

2Am

(12)特許協力条約に基づいて公開された国際出願

(19) 世界知的所有権機関
国際事務局(43) 国際公開日
2003 年 8 月 28 日 (28.08.2003)

PCT

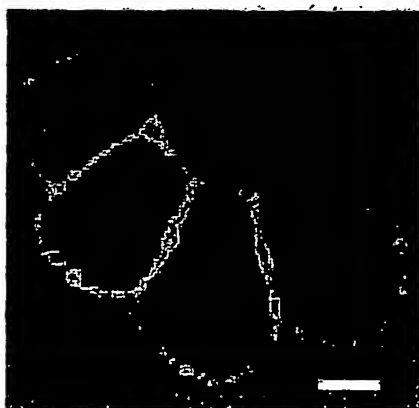
(10) 国際公開番号
WO 03/071272 A1

- (51) 国際特許分類⁷: G01N 33/50, 33/15, C12N 15/09
- (21) 国際出願番号: PCT/JP03/01901
- (22) 国際出願日: 2003 年 2 月 21 日 (21.02.2003)
- (25) 国際出願の言語: 日本語
- (26) 国際公開の言語: 日本語
- (30) 優先権データ:
特願2002-45728 2002 年 2 月 22 日 (22.02.2002) JP
特願2002-213949 2002 年 7 月 23 日 (23.07.2002) JP
特願2002-298237 2002 年 10 月 11 日 (11.10.2002) JP
- (71) 出願人 (米国を除く全ての指定国について): 武田薬品工業株式会社 (TAKEDA CHEMICAL INDUSTRIES, LTD.) [JP/JP]; 〒541-0045 大阪府 大阪市 中央区道修町四丁目 1 番 1 号 Osaka (JP).
- (72) 発明者; および
(75) 発明者/出願人 (米国についてのみ): 日沼 州司 (HINUMA, Shuji) [JP/JP]; 〒305-0821 茨城県 つくば市 春日 1 丁目 7 番地 9 武田春日ハイツ 1 4 0 2 号 Ibaraki (JP). 藤井 亮 (FUJII, Ryo) [JP/JP]; 〒305-0821 茨城県 つくば市 春日 2 丁目 3 3 番地 1 6 Ibaraki (JP). 大儀 和宏 (OGI, Kazuhiro) [JP/JP]; 〒305-0045 茨城県 つくば市 梅園 2 丁目 1 6 番 1 号 ルンビーニ梅園 2 0 6 号 Ibaraki (JP). 小松 秀俊 (KOMATSU, Hidetoshi) [JP/JP]; 〒305-0821 茨城県 つくば市 春日 1 丁目 7 番地 9 武田春日ハイツ 8 0 3 号 Ibaraki (JP). 川俣 裕二 (KAWAMATA, Yuji) [JP/JP]; 〒305-0035 茨城県 つくば市 松代 4 丁目 2 2 番地 松代 4 丁目団地 2 号棟 2 0 3 号 Ibaraki (JP). 細谷 昌樹 (HOSOYA, Masaki) [JP/JP]; 〒300-0007 茨城県 土浦市 板谷 1 丁目 7 1 1 番地の 8 3 Ibaraki (JP).
- (74) 代理人: 小林 浩, 外 (KOBAYASHI, Hiroshi et al.); 〒104-0028 東京都 中央区 八重洲 2 丁目 8 番 7 号 福岡ビル 9 階 Tokyo (JP).

/続葉有/

(54) Title: METHOD OF DETERMINING LIGAND

(54) 発明の名称: リガンドの決定方法



(57) Abstract: It is intended to provide a method of determining a ligand to an orphan receptor. More specifically speaking, it is intended to provide a method of a ligand to a receptor protein, to which no ligand has been determined, characterized by using a fused protein of the receptor protein with a fluorescent protein.

(57) 要約:

本発明は、オーファンレセプターのリガンドの決定方法の提供を目的とする。

具体的には、本発明はリガンドが決定されていないレセプタータンパク質と蛍光タンパク質との融合タンパク質を用いることを特徴とする該レセプタータンパク質に対するリガンドの決定方法等を提供する。

BEST AVAILABLE COPY

WO 03/071272 A1



(81) 指定国 (国内): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, SE, SI, SK, TR), OAPI 特許 (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

添付公開書類:

— 国際調査報告書

(84) 指定国 (広域): ARIPO 特許 (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), ユーラシア特許 (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), ヨーロッパ特許

2文字コード及び他の略語については、定期発行される各PCTガゼットの巻頭に掲載されている「コードと略語のガイダンスノート」を参照。

1

明細書

リガンドの決定方法

技術分野

- 5 本発明は、細胞膜に存在するレセプタータンパク質に対するリガンドの決定方法、特にリガンドが全く未知である、いわゆるオーファンレセプターのリガンドの決定方法に関する。

背景技術

- 10 多くのホルモンや神経伝達物質などの生理活性物質は、細胞膜に存在する特異的なレセプタータンパク質を通じて生体の機能を調節している。これらのレセプタータンパク質のうち多くは共役しているguanine nucleotide-binding protein (以下、Gタンパク質と略称する)の活性化を通じて細胞内のシグナル伝達を行ない、また、7個の膜貫通領域を有する共通した構造をもっていることから、G
- 15 タンパク質共役型レセプタータンパク質あるいは7回膜貫通型レセプタータンパク質(7TMR)と総称される。

Gタンパク質共役型レセプタータンパク質は生体の細胞や臓器の各機能細胞表面に存在し、それら細胞や臓器の機能を調節する分子、例えば、ホルモン、神経伝達物質および生理活性物質等の標的として生理的に重要な役割を担っている。

- 20 レセプターは生理活性物質との結合を介してシグナルを細胞内に伝達し、このシグナルにより細胞の賦活や抑制といった種々の反応が惹起される。

- 各種生体の細胞や臓器の機能を調節する物質と、その特異的なレセプタータンパク質、特にGタンパク質共役型レセプタータンパク質との関係を明らかにすることは、各種生体の細胞や臓器の機能を解明し、それら機能と密接に関連した医薬品開発に非常に重要な手段を提供することとなる。
- 25

従来、Gタンパク質共役型レセプタータンパク質と生理活性物質(すなわち、リガンド)との結合を阻害する物質や、結合して生理活性物質(すなわち、リガンド)と同様なシグナル伝達を引き起こす物質は、これらレセプターの特異的なアンタゴニストまたはアゴニストとして、生体機能を調節する医薬品として活用

されてきた。

しかし、現時点でもなお、対応するリガンドが同定されていない、いわゆるオーファンレセプターが多数存在しており、そのリガンドの決定および機能解明が切望されている。

- 5 Gタンパク質共役型レセプターのシグナル伝達作用を指標とする、新たな生理活性物質（すなわち、リガンド）の探索、また、該レセプターに対するアゴニストまたはアンタゴニストの探索は有用である。これら該レセプターに対するリガンド、アゴニストまたはアンタゴニストなどは、Gタンパク質共役型レセプターの機能不全に関連する疾患の予防および／または治療薬や診断薬として活用することが期待できる。

GFP (Green Fluorescent Protein) は中生動物のオワンクラゲに由来する発光タンパク質の一種である (WO 96/23810、WO 96/27675、WO 97/26333、WO 97/28261、WO 97/42320)。

- 15 Multiple レスポンスエレメント (MRE) および cAMP レスポンスエレメント (CRE) とレポーター活性とを組み合わせ、Gi、Gs または Gq 共役型オーファン受容体のリガンドを決定する方法が報告されている (Analytical Biochemistry, 275, 54-61, 1999)。

- 20 cAMP レスポンスエレメント (CRE) とレポーター活性とを組み合わせ、Gs または Gq 共役型オーファン受容体と相互作用する分子をスクリーニングする方法が報告されている (Analytical Biochemistry, 226, 349-354, 1995)。

- 25 cAMP レスポンスエレメント (CRE) とレポーター活性とを組み合わせ、リガンドが知られている Gi または Gs 共役型受容体の特徴を調べる方法が報告されている (Current Opinion in Biotechnology, 1995, 6: 574-581)。

Gタンパク質共役型レセプターとの共役関係の曖昧さを増大させたキメラGタンパク質αサブユニット、キメラGタンパク質を発現させた細胞を用いてGタンパク質共役型レセプターの反応を検出する方法が報告されている (WO 01/36481)

組換え型酵母発現ライブラリーを用いたオーファンG蛋白質共役型レセプターのリガンドの同定方法が報告されている (US P 6, 255, 059)。

- 5 受容体と試験ペプチドの両方を含有する細胞からなり、オーファン受容体の同定あるいはスクリーニングに有用な細胞の受容体活性修飾物質の同定方法が報告されている (US 2001/0026926)。

オーファン受容体のリガンドを同定するための *Saccharomyces* 有性生殖系を利用した発現システムが報告されている (WO 00/031261)。

- 10 従来のリガンドの探索・決定方法では、例えば真核生物由来の細胞を用いて、リガンドをスクリーニングする場合、該レセプターを安定的に発現する、いわゆる安定細胞株 (stable cell line) を樹立しなければならず、この細胞株の樹立には特別な細胞を必要とした。またスクリーニングには複数の測定の実行が必要であり、試験化合物が複数存在すると、時間がかかるためにその実施が困難であった。つまり、従来のリガンド等の探索・決定方法には、(1) 使用可能な細胞系が限定される、(2) 該細胞系の樹立に時間がかかる、(3) 複数の測定法を組み合わせるために、検体数が多くなるとその実施が困難になる等の問題があった。これらの問題を解決するための、各種の細胞系が使用でき、かつ短時間で実施できるリガンドの決定方法が望まれている。

20

発明の開示

- 本発明者らは、鋭意研究を重ねた結果、リガンドが決定されていないレセプタータンパク質と GFP 等の蛍光タンパク質との融合タンパク質を安定的にあるいは一過性に発現させた細胞を作製することにより、GFP 等の蛍光タンパク質の
25 蛍光または GFP 抗体等の蛍光タンパク質抗体を利用した免疫染色法やウエスタンブロット法などを用いて、

(1) タンパク質レベルでレセプタータンパク質が発現していることを確認でき

(2) 細胞膜にレセプタータンパク質が発現していることを確認でき、

- (3) レセプタータンパク質の発現量を見積もることができ、
(4) レセプタータンパク質の高発現細胞を選択でき、そして
(5) リガンドによるレセプターの特異的反応を、レセプターと蛍光タンパク質との融合タンパク質の細胞内へのインターナリゼーションとして検出できること
5 等を見出し、これらの特徴を利用することにより、リガンドが決定されていないレセプタータンパク質（以下、オーファンレセプターと略記する場合がある）のリガンドを効率よく決定できることを見出した。本発明者らは、これらの知見に基づいて、さらに研究を重ねた結果、本発明を完成するに至った。

すなわち、本発明は、

- 10 [1] リガンドが決定されていないレセプタータンパク質と蛍光タンパク質との融合タンパク質を用いることを特徴とする該レセプタータンパク質に対するリガンドの決定方法、
[2] リガンドが決定されていないレセプタータンパク質とGFPとの融合タンパク質を用いることを特徴とする上記[1]記載のリガンドの決定方法、
15 [3] リガンドが決定されていないレセプタータンパク質とGFPとの融合タンパク質を発現している細胞またはその細胞膜画分と、試験化合物とを接触させることを特徴とする上記[1]記載のリガンドの決定方法、
[4] (1) アラキドン酸遊離、アセチルコリン遊離、細胞内 Ca^{2+} 遊離、細胞内cAMP生成、細胞内cGMP生成、イノシトールリン酸産生、細胞膜電位
20 変動、細胞内タンパク質のリン酸化、c-fos活性化またはpHの低下を促進する活性または抑制する活性、(2) MAPキナーゼの活性化、(3) 転写因子の活性化、(4) ジアシルグリセロール産生、(5) 細胞膜上のイオンチャネルの開閉、(6) アポトーシスの誘導、(7) 形態変化、(8) 該融合タンパク質の細胞膜から細胞質への移行、(9) 低分子量Gタンパク質の活性化、(10)
25) 細胞分裂促進活性または(11) DNA合成促進活性を測定することを特徴とする上記[1]記載のリガンドの決定方法、
[5] 該融合タンパク質の細胞膜から細胞質への移行を測定することを特徴とする上記[1]記載のリガンドの決定方法、
[6] GFP蛍光を観察することにより該融合タンパク質の細胞膜から細胞質へ

の移行を測定する上記〔5〕記載のリガンドの決定方法、

〔7〕リガンドが決定されていないレセプタータンパク質と蛍光タンパク質との融合タンパク質を発現し、かつ、cAMPレスポンスエレメント／プロモーターの下流にレポータータンパク質をコードするDNAを連結したプラスミドを含有する細胞と試験化合物とを接触させて、レポータータンパク質の活性を測定することを特徴とする上記〔1〕記載のリガンドの決定方法、

〔8〕（1）リガンドが決定されていないレセプタータンパク質と蛍光タンパク質との融合タンパク質をコードするDNAを含有するプラスミドおよび（2）cAMPレスポンスエレメント／プロモーターの下流にレポータータンパク質をコードするDNAを連結したプラスミドを含有する細胞を培養し、試験化合物と接触させてレポータータンパク質の活性を測定することを特徴とする上記〔7〕記載の方法、

〔9〕リガンドが決定されていないレセプタータンパク質とGFPとの融合タンパク質を発現し、かつ、cAMPレスポンスエレメント／プロモーターの下流にレポータータンパク質をコードするDNAを連結したプラスミドを含有する細胞と試験化合物とを接触させて、レポータータンパク質の活性を測定することを特徴とする上記〔2〕記載のリガンドの決定方法、

〔10〕（1）リガンドが決定されていないレセプタータンパク質とGFPとの融合タンパク質をコードするDNAを含有するプラスミドおよび（2）cAMPレスポンスエレメント／プロモーターの下流にレポータータンパク質をコードするDNAを連結したプラスミドを含有する細胞を培養し、試験化合物と接触させてレポータータンパク質の活性を測定することを特徴とする上記〔9〕記載の方法、

〔11〕レセプタータンパク質がGタンパク質共役型レセプタータンパク質である上記〔1〕記載の方法、

〔12〕GFPが配列番号：1、配列番号：3、配列番号：5または配列番号：7で表わされるアミノ酸配列と同一または実質的に同一のアミノ酸配列を含有するタンパク質である上記〔1〕記載の方法、

〔13〕プロモーターがTATA様配列である上記〔7〕記載の方法、

6

- [14] レポータータンパク質がルシフェラーゼである上記[7]記載の方法、
[15] プラスミドがcAMPレスポンスエレメントの下流にTATA様プロモーターおよびレポータータンパク質をコードする遺伝子を連結したものである上記[7]記載の方法、
- 5 [16] 細胞が、リガンドが決定されていない2種類以上のレセプタータンパク質を発現している上記[7]記載の方法、
[17] 細胞が、抑制性Gタンパク質 α サブユニットGiをコードする遺伝子を含有するプラスミドを更に含有する上記[7]記載の方法、
[18] さらにフォルスコリンを添加する上記[7]記載の方法、
- 10 [19] 2種類以上のレセプタータンパク質が類似の特徴を有することを特徴とする上記[16]記載の方法、
[20] 類似の特徴がレポータータンパク質の基礎発現量および（または）フォルスコリン添加時のレポータータンパク質の発現量である上記[19]記載の方法、
- 15 [21] 予め2種類以上のレセプタータンパク質をそれぞれ単独で発現させた時のレポータータンパク質の基礎発現量および／またはフォルスコリン添加時のレポータータンパク質の発現量を測定し、該レポータータンパク質の発現量が同程度である2種類以上のレセプタータンパク質を組み合わせ発現させることを特徴とする上記[16]記載の方法、
- 20 [22] リガンドが決定されていないレセプタータンパク質と蛍光タンパク質との融合タンパク質またはその塩、
[23] 蛍光タンパク質がGFPである上記[22]記載の融合タンパク質またはその塩、
[24] 上記[22]記載の融合タンパク質をコードするDNAを含有するDNA、
- 25 A、
[25] 上記[22]記載のDNAを含有する組換えベクター、
[26] 上記[25]記載の組換えベクターで形質転換させた形質転換体、
[27] リガンドが決定されていないレセプタータンパク質に対するリガンドを決定するための蛍光タンパク質の使用、

[28] リガンドが決定されていないレセプタータンパク質に対するリガンドを決定するためのGFPの使用に関する。

図面の簡単な説明

- 5 図1は、TGR5発現ベクターを導入したHEK293細胞(A)および元のベクターのみを導入したHEK293細胞(B)における、コレステロール代謝関連物質によるレポーター活性化の検出(n=2)の結果を示す。

図2は、HEK293細胞におけるリガンド刺激に対するレポーター遺伝子の発現誘導の結果を示す。

- 10 図3は、Gi共存下でのTGR5のリトコール酸に対する反応の結果を示す。

図4は、リガンド非存在下における、CHO細胞に発現させたTGR5-GFP融合タンパク質の局在を示す。図中の白線は4μmを示す。

図5は、TGR5-GFPを発現させたCHO細胞にTLCAを添加して30分後の融合タンパク質の局在を示す。図中の白線は4μmを示す。

15

発明を実施するための最良の形態

本発明のリガンド決定方法は、(1) リガンドが決定されていないレセプタータンパク質と蛍光タンパク質との融合タンパク質を用いることを特徴とする方法であり、具体的には、リガンドが決定されていないレセプタータンパク質と蛍光

20 タンパク質との融合タンパク質を発現している細胞またはその細胞膜画分と、試験化合物とを接触させることを特徴とする方法である(リガンド決定方法A)。

- さらには、本発明のリガンドの決定方法は、(1) リガンドが決定されていないレセプタータンパク質と蛍光タンパク質との融合タンパク質を発現し、かつエンハンサー/プロモーターの下流にレポータータンパク質をコードするDNAを連結したプラスミドを含有する細胞と試験化合物とを接触させて、発現誘導され
- 25 るレポータータンパク質の活性を測定する方法、(2) (i) リガンドが決定されていないレセプタータンパク質と蛍光タンパク質との融合タンパク質をコードするDNAを含有するプラスミドおよび(ii) エンハンサー/プロモーターの下流にレポータータンパク質をコードするDNAを連結したプラスミドを含有す

る細胞を培養し、試験化合物と接触させて、発現誘導されるレポータータンパク質の活性を測定する方法である（以上、リガンド決定法B）。

本発明に用いられるオーファンレセプターとしては、例えばGタンパク質共役型レセプタータンパク質などが用いられる。具体例としては、配列番号：9で表わされるアミノ酸配列と同一もしくは実質的に同一のアミノ酸配列を含有するGタンパク質共役型レセプタータンパク質や、WO 96/05302、EP-A-711831、EP-A-789076、EP-A-1103563、EP-A-1103562、特開平8-154682号公報、特開平8-283295号公報、特開平8-196278号公報、特開平8-245697号公報、特開平8-266280号公報、特開平9-51795号公報、特開平9-121865号公報、特開平9-2388686号公報、特開平10-146192号公報に記載のGタンパク質共役型レセプタータンパク質などが挙げられる。

蛍光タンパク質としては、視覚によって認識し得るタンパク質であれば特に限定されることはなく、例えば、GFP (Green Fluorescent Protein)、Tag配列、EGFP (enhanced greenfluorescent protein)、ECFP (enhanced cyan fluorescent protein)、EYFP (Enhanced yellow fluorescent protein)、DsRED (Discosoma sp. Red Fluorescent Protein)、EBFP (Enhanced blue fluorescent protein) などが用いられる。

GFPは、中生動物のオワンクラゲに由来する発光タンパク質の一種であり、配列番号：1、配列番号：3、配列番号：5または配列番号：7で表わされるアミノ酸配列と同一もしくは実質的に同一のアミノ酸配列を含有するタンパク質などである。

配列番号：1、配列番号：3、配列番号：5または配列番号：7で表わされるアミノ酸配列と実質的に同一のアミノ酸配列としては、例えば、配列番号：1、配列番号：3、配列番号：5または配列番号：7で表わされるアミノ酸配列と約70%以上、好ましくは約80%以上、さらに好ましくは約90%以上、最も好ましくは約95%以上の相同性を有するアミノ酸配列などが挙げられる。

本発明の配列番号：1、配列番号：3、配列番号：5または配列番号：7で表わされるアミノ酸配列と実質的に同一のアミノ酸配列を含有するタンパク質とし

ては、例えば、配列番号：1、配列番号：3、配列番号：5または配列番号：7で表わされるアミノ酸配列と実質的に同一のアミノ酸配列を有し、かつ配列番号：1、配列番号：3、配列番号：5または配列番号：7で表わされるアミノ酸配列からなるタンパク質と実質的に同質の活性を有するタンパク質などが好ましい

5 .

GFPの活性としては、例えば、励起光照射による発光などが挙げられる。実質的に同質の活性とは、それらの活性が性質的に同質であることを示す。したがって、それらの活性が同等（例、約0.01～100倍、好ましくは約0.5～20倍、より好ましくは約0.5～2倍）であることが好ましいが、活性の程度

10 やタンパク質の分子量などの量的要素は異なってもよい。

GFPにおける励起光照射による発光などの活性の測定は、公知の方法に準じて行なうことができる。

また、GFPとしては、(1) 配列番号：1、配列番号：3、配列番号：5または配列番号：7で表わされるアミノ酸配列中の1または2個以上（好ましくは、1～30個程度、より好ましくは1～10個程度、さらに好ましくは数個（1～5個））のアミノ酸が欠失したアミノ酸配列、(2) 配列番号：1、配列番号：3、配列番号：5または配列番号：7で表わされるアミノ酸配列に1または2個以上（好ましくは、1～30個程度、より好ましくは1～10個程度、さらに好ましくは数個（1～5個））のアミノ酸が付加または挿入したアミノ酸配列、

15 (3) 配列番号：1、配列番号：3、配列番号：5または配列番号：7で表わされるアミノ酸配列中の1または2個以上（好ましくは、1～30個程度、より好ましくは1～10個程度、さらに好ましくは数個（1～5個））のアミノ酸が他のアミノ酸で置換されたアミノ酸配列、または(4) それらの欠失・付加・置換を組み合わせたアミノ酸配列を含有するタンパク質なども用いられ、なかでも（

20 i) 配列番号：1、配列番号：3、配列番号：5または配列番号：7で表わされるアミノ酸配列のN末端のメチオニン残基が欠失しているアミノ酸配列または（

25 ii) 配列番号：1で表わされるアミノ酸配列のN末端のメチオニン残基が欠失し、さらに次のアラニン残基がスレオニン残基またはセリン残基に置換されたアミノ酸配列を含有するタンパク質などが好ましく用いられる。

- 具体的には、例えば、(i) 配列番号：1、配列番号：3、配列番号：5または配列番号：7で表わされるアミノ酸配列からなるGFP、(ii) 配列番号：1、配列番号：3、配列番号：5または配列番号：7で表わされるアミノ酸配列のN末端のメチオニン残基が欠失しているアミノ酸配列からなるGFP、(iii)
- 5 配列番号：1で表わされるアミノ酸配列のN末端のメチオニン残基が欠失し、さらに次のアラニン残基がスレオニン残基またはセリン残基に置換されたアミノ酸配列からなるGFPなどが用いられる。

Tag配列としては、例えば、以下の公知配列が用いられる。

- (1) His-tag (PCDNA3.1/His A)
- 10 His His His His His His (配列番号：17)
- (2) V5-tag (PCDNA3.1/V5-His A)
- Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr (配列番号：18)
-)
- (3) myc-tag (pCDNA3.1/myc-His A)
- 15 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu (配列番号：19)
- (4) Xpress-tag (PCDNA3.1/His A)
- Asp Leu Tyr Asp Asp Asp Asp Lys (配列番号：20)
- (5) HA-tag (PCLuzHA Expression vector)
- Met Gly Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser Leu Glu Phe (配列番号：21)
- 20

EGFPとしては、配列番号：7で表わされるアミノ酸配列からなるタンパク質が用いられる。

ECFPとしては、配列番号：22で表わされるアミノ酸配列からなるタンパク質が用いられる。

- 25 EYFPとしては、配列番号：24で表わされるアミノ酸配列からなるタンパク質が用いられる。

DsREDとしては、配列番号：26で表わされるアミノ酸配列からなるタンパク質が用いられる。

EBFPとしては、配列番号：28で表わされるアミノ酸配列からなるタンパ

ク質が用いられる。

これらEGFP、ECFP、EYFP、DsRED、EBFPは、励起光照射による発光などの活性を有する限り、（１）上記したアミノ酸配列中の１または２個以上（好ましくは、１～３０個程度、より好ましくは１～１０個程度、さらに好ましくは数個（１～５個））のアミノ酸が欠失したアミノ酸配列、（２）上記したアミノ酸配列に１または２個以上（好ましくは、１～３０個程度、より好ましくは１～１０個程度、さらに好ましくは数個（１～５個））のアミノ酸が付加または挿入しているアミノ酸配列、（３）上記したアミノ酸配列中の１または２個以上（好ましくは、１～３０個程度、より好ましくは１～１０個程度、さらに好ましくは数個（１～５個））のアミノ酸が他のアミノ酸で置換されているアミノ酸配列、または（４）それらの欠失・付加・置換を組み合わせたアミノ酸配列を有するタンパク質であってもよい。

GFPをコードするDNAとしては、具体的には、例えば、配列番号：２、配列番号：４、配列番号：６または配列番号：８で表される塩基配列を含有するDNA、または配列番号：２、配列番号：４、配列番号：６または配列番号：８で表わされる塩基配列の相補的塩基配列とハイストリンジェントな条件下でハイブリダイズする塩基配列を有し、かつ配列番号：１、配列番号：３、配列番号：５または配列番号：７で表されるアミノ酸配列からなるGFPと実質的に同質の活性（例、励起光照射による発光など）を有するタンパク質をコードするDNAであれば何れのものでよい。

配列番号：２、配列番号：４、配列番号：６または配列番号：８で表わされる塩基配列とハイブリダイズできるDNAとしては、例えば、配列番号：２、配列番号：４、配列番号：６または配列番号：８で表わされる塩基配列と約７０％以上、好ましくは約８０％以上、より好ましくは約９０％以上、最も好ましくは約９５％以上の相同性を有する塩基配列を含有するDNAなどが用いられる。

ハイブリダイゼーションは、公知の方法あるいはそれに準じる方法、例えば、モレキュラー・クローニング（Molecular Cloning）2nd（J. Sambrook et al., Cold Spring Harbor Lab. Press, 1989）に記載の方法などに従って行なうことができる。また、市販のハイブリダイゼーション用試薬を使用する場合、添付の

使用説明書に記載の方法に従って行なうことができる。より好ましくは、ハイス
トリンジエントな条件に従って行なうことができる。

該ハイストリンジエントな条件とは、例えば、ナトリウム濃度が約19～40
mM、好ましくは約19～20 mMで、温度が約50～70℃、好ましくは約6
5 0～65℃の条件を示す。特に、ナトリウム濃度が約19 mMで温度が約65℃
の場合が最も好ましい。

より具体的には、配列番号：1で表わされるアミノ酸配列からなるGFPをコ
ードするDNAは、配列番号：2で表わされる塩基配列を含有するDNA（WO
97/42320）などであり、配列番号：3で表わされるアミノ酸配列からな
るGFPをコードするDNAは、配列番号：4で表わされる塩基配列を含有する
10 DNA（WO96/23810）などであり、配列番号：5で表わされるアミノ
酸配列からなるGFP（GFPuv）をコードするDNAは、配列番号：6で表
わされる塩基配列を含有するDNA（WO97/26333）などであり、配列
番号：7で表わされるアミノ酸配列からなるGFP（EGFP）をコードするD
15 NAは、配列番号：8で表わされる塩基配列を含有するDNA（NCBI Accessio
n No. AAB0572）などである。

配列番号：7で表わされるアミノ酸配列からなるEGFPをコードするDNA
としては、配列番号：8で表わされる塩基配列からなるDNAなどが用いられる
。

20 配列番号：22で表わされるアミノ酸配列からなるECFPをコードするDNA
としては、配列番号：23で表わされる塩基配列からなるDNAなどが用いられ
る。

配列番号：24で表わされるアミノ酸配列からなるEYFPをコードするDNA
としては、配列番号：25で表わされる塩基配列からなるDNAなどが用いられ
25 る。

配列番号：26で表わされるアミノ酸配列からなるDsREDをコードするDN
Aとしては、配列番号：27で表わされる塩基配列からなるDNAなどが用いら
れる。

配列番号：28で表わされるアミノ酸配列からなるEBFPをコードするDN

Aとしては、配列番号：29で表わされる塩基配列からなるDNAなどが用いられる。

オーファンレセプターと蛍光タンパク質との融合タンパク質は、オーファンレセプタータンパク質をコードするDNAとGFPをコードするDNAとを連結したDNAを用いて製造することができる。

該連結DNAは、オーファンレセプターをコードするDNAの塩基配列の3'末端に、インフレームでGFPをコードするDNAの5'末端を連結して構築する。

なお、両DNAの間にAla、Gly、Serなど分子量の小さいアミノ酸残基から選ばれる1～5個程度のリンカーと呼ばれるアミノ酸配列をコードするDNAを挿入してもよい。

オーファンレセプターと蛍光タンパク質との融合タンパク質（以下、融合タンパク質と略記する場合がある）の発現ベクターは、例えば、（1）融合タンパク質をコードするDNA断片を調製し、（2）該DNA断片を適当な発現ベクター中のプロモーターの下流に連結することにより製造することができる。

リガンドが決定されていないレセプタータンパク質と蛍光タンパク質との融合タンパク質としては、例えば、配列番号：30～配列番号：131のいずれかの配列番号で表されるアミノ酸配列からなる、リガンドが決定されていない102種類の各レセプタータンパク質と配列番号：1で表されるアミノ酸配列からなるGFPとの融合タンパク質が好ましく用いられる。これら配列番号：30～配列番号：131のいずれかの配列番号で表されるアミノ酸配列においては、配列番号：1で表されるアミノ酸配列のN末端のメチオニン残基が欠失しており、場合によっては、さらに次のアラニン残基がスレオニン残基またはセリン残基に置換されている。

この融合タンパク質をコードするDNAは、リガンドが決定されていない102種類の各レセプタータンパク質をコードする部分の下流に、配列番号：1で表されるアミノ酸配列からなるGFPをコードするDNA（配列番号：2）を連結することによって調製でき、具体的には配列番号132～配列番号：233のいずれかの配列番号で表される塩基配列からなるDNAが用いられる。これら配列

番号：132～配列番号：233のいずれかの配列番号で表される塩基配列においては、配列番号：2で表される塩基配列の5'末端のメチオニン残基コドンが欠失しており、場合によっては、さらに次のアラニン残基コドンがスレオニン残基コドンまたはセリン残基コドンに置換されている。

- 5 発現ベクターとしては、大腸菌由来のプラスミド（例、pCR4、pCR2.1、pBR322、pBR325、pUC12、pUC13）、枯草菌由来のプラスミド（例、pUB110、pTP5、pC194）、酵母由来プラスミド（例、pSH19、pSH15）、 λ ファージなどのバクテリオファージ、レトロウイルス、ワクシニアウイルス、バキュロウイルスなどの動物ウイルスなどの他、
- 10 pA1-11、pXT1、pRc/CMV、pRc/RSV、pcDNA1/Neoなどが用いられる。

- 該ベクターで用いられるプロモーターは、遺伝子発現に用いる宿主内で機能する適切なプロモーターであればいかなるものでもよい。例えば、動物細胞を宿主として用いる場合は、SR α プロモーター、SV40プロモーター、LTRプロモーター、CMVプロモーター、HSV-TKプロモーターなどが用いられる。
- 15 これらのうち、CMVプロモーター、SR α プロモーターなどが好ましい。

- また、各種組織において発現させる場合、インスリンII・プロモーター（膵臓）、Glycoprotein- α サブユニット・プロモーター（下垂体）、トランスサイレチン・プロモーター（肝臓）、レニン・プロモーター（腎臓）、
- 20 PSE・プロモーター（前立腺）、CD2・プロモーター（T細胞）、IgG-heavy chain・プロモーター（B細胞）、スカベンジャーレセプターA・プロモーター（マクロファージ）などが用いられる。

- 宿主がエシェリヒア属菌である場合は、trpプロモーター、lacプロモーター、recAプロモーター、 λ P_Lプロモーター、lppプロモーターなどが
- 25 、宿主がバチルス属菌である場合は、SPO1プロモーター、SPO2プロモーター、penPプロモーターなど、宿主が酵母である場合は、PHO5プロモーター、PGKプロモーター、GAPプロモーター、ADHプロモーターなどが好ましい。宿主が昆虫細胞である場合は、ポリヘドリンプロモーター、P10プロモーターなどが好ましい。

該発現ベクターは、以上の他に、所望によりエンハンサー、スプライシングシグナル、ポリA付加シグナル、選択マーカー、SV40複製オリジン（以下、SV40oriと略称する場合がある）などを含有しうる。選択マーカーとして、例えば、ジヒドロ葉酸還元酵素（以下、dhfrと略称する場合がある）遺伝子

5 [メソトレキセート（MTX）耐性]、アンピシリン耐性遺伝子（以下、Amp^rと略称する場合がある）、ネオマイシン耐性遺伝子（以下、Neo^rと略称する場合がある、G418耐性）等が挙げられる。特に、CHO（dhfr⁻）細胞を用いてdhfr遺伝子を選択マーカーとして使用する場合、目的遺伝子をチミジンを含まない培地によっても選択できる。

- 10 また、必要に応じて、宿主に合ったシグナル配列を、本発明のレセプタータンパク質のN末端側に付加する。宿主がエシェリヒア属菌である場合は、PhoA・シグナル配列、OmpA・シグナル配列などが、宿主がバチルス属菌である場合は、 α -アミラーゼ・シグナル配列、サブチリシン・シグナル配列などが、宿主が酵母である場合は、MF α ・シグナル配列、SUC2・シグナル配列など、
- 15 宿主が動物細胞である場合には、インシュリン・シグナル配列、 α -インターフェロン・シグナル配列、抗体分子・シグナル配列などがそれぞれ利用できる。

このようにして構築されたレセプタータンパク質と蛍光タンパク質との融合タンパク質をコードするDNAを含有する発現ベクターを用いて、形質転換体を製造することができる。

- 20 宿主としては、例えば、エシェリヒア属菌、バチルス属菌、酵母、昆虫細胞、昆虫、動物細胞などが用いられる。

エシェリヒア属菌の具体例としては、エシェリヒア・コリ（*Escherichia coli*）K12・DH1（Proc. Natl. Acad. Sci. USA, 60, 160 (1968)）、JM103（Nucleic Acids Research, 9, 309 (1981)）、JA221（Journal of Molecular Biology, 120, 517 (1978)）、HB101（Journal of Molecular Biology, 41, 459 (1969)）、C600（Genetics, 39, 440 (1954)）、DH5 α （Inoue, H., Nojima, H. and Okayama, H., Gene, 96, 23-28 (1990)）、DH10B（Proc. Natl. Acad. Sci. USA, 87, 4645-4649 (1990)）などが用いられる。

25

バチルス属菌としては、例えば、バチルス・ズブチルス（*Bacillus subtilis*

) M I 1 1 4 (Gene, 24, 255 (1983))、2 0 7 - 2 1 (Journal of Biochemistry, 95, 87 (1984)) などが用いられる。

酵母としては、例えば、サッカロマイセス・セレビスエ (*Saccharomyces cerevisiae*) A H 2 2, A H 2 2 R⁻, N A 8 7 - 1 1 A, D K D - 5 D、2 0 B -
5 1 2、シゾサッカロマイセス・ポンベ (*Schizosaccharomyces pombe*) N C Y C 1 9 1 3, N C Y C 2 0 3 6、ピキア・パストリス (*Pichia pastoris*) などが用いられる。

昆虫細胞としては、例えば、ウイルスが A c N P V の場合は、ヨトウガの幼虫由来株化細胞 (*Spodoptera frugiperda* cell; S f 細胞)、*Trichoplusia ni* の
10 中腸由来の M G 1 細胞、*Trichoplusia ni* の卵由来の High FiveTM 細胞、*Mamestra brassicae* 由来の細胞または *Estigmena acrea* 由来の細胞などが用いられる。ウイルスが B m N P V の場合は、カイコ由来株化細胞 (*Bombyx mori* N; B m N 細胞) などが用いられる。該 S f 細胞としては、例えば、S f 9 細胞 (ATCC CRL17
11)、S f 2 1 細胞 (以上、Vaughn, J. L. ら、In Vivo, 13, 213-217 (1977))
15 などが用いられる。

昆虫としては、例えば、カイコの幼虫などが用いられる〔前田ら、Nature, 315, 592 (1985)〕。

動物細胞としては、例えば、サル細胞 C O S - 7, V e r o, チャイニーズハムスター細胞 C H O (以下、C H O 細胞と略記)、d h f r 遺伝子欠損チャイニ
20 ーズハムスター細胞 C H O (以下、C H O (d h f r⁻) 細胞と略記)、マウス L 細胞、マウス A t T - 2 0、マウスミエローマ細胞、ラット G H 3、ヒト F L 細胞、脾臓由来細胞 (R I N m 5 F、H I T - T 1 5 など)、下垂体由来細胞 (G H 3、G H 1、R C 4 / B C など)、胎盤由来細胞 (B e W o, J A R, J E G - 3 など)、肝臓由来細胞 (H e p G 2 など)、腎臓由来細胞 (A C H N など)
25)、血球細胞由来細胞 (H 9, T H P - 1, U - 9 3 7 など)、H e L a 細胞などが用いられる。

エシェリヒア属菌を形質転換するには、例えば、Proc. Natl. Acad. Sci. USA, 69, 2110 (1972) や、Gene, 17, 107 (1982) などに記載の方法に従って行なうことができる。

バチルス属菌を形質転換するには、例えば、Molecular & General Genetics, 168, 111 (1979)などに記載の方法に従って行なうことができる。

酵母を形質転換するには、例えば、Methods in Enzymology, 194, 182-187 (1991)、Proc. Natl. Acad. Sci. USA, 75, 1929 (1978)などに記載の方法に従っ

5 て行なうことができる。

昆虫細胞または昆虫を形質転換するには、例えば、Bio/Technology, 6, 47-55 (1988)などに記載の方法に従って行なうことができる。

動物細胞を形質転換するには、例えば、細胞工学別冊8新細胞工学実験プロト
コール、263-267 (1995) (秀潤社発行)、Virology, 52, 456 (197

10 3)に記載の方法に従って行なうことができる。

このようにして、上記融合タンパク質をコードするDNAを含有する発現ベク
ターで形質転換された形質転換体を得られる。

宿主がエシェリヒア属菌、バチルス属菌である形質転換体を培養する際、培養
に使用される培地としては液体培地が適当であり、その中には該形質転換体の生
15 育に必要な炭素源、窒素源、無機物その他が含有せしめられる。炭素源としては
、例えば、グルコース、デキストリン、可溶性澱粉、ショ糖など、窒素源として
は、例えば、アンモニウム塩類、硝酸塩類、コーンスチープ・リカー、ペプトン
、カゼイン、肉エキス、大豆粕、バレイショ抽出液などの無機または有機物質、
無機物としては、例えば、塩化カルシウム、リン酸二水素ナトリウム、塩化マグ
20 ネシウムなどが挙げられる。また、酵母エキス、ビタミン類、生長促進因子など
を添加してもよい。培地のpHは約5～8が望ましい。

エシェリヒア属菌を培養する際の培地としては、例えば、グルコース、カザミ
ノ酸を含むM9培地〔ミラー (Miller)、Journal of Experiments in Molecula
r Genetics, 431-433, Cold Spring Harbor Laboratory, New York (1972)〕が
25 好ましい。ここに必要によりプロモーターを効率よく働かせるために、例えば、
3β-インドリルアクリル酸のような薬剤を加えることができる。

宿主がエシェリヒア属菌の場合、培養は通常約15～43℃で約3～24時間
行ない、必要により、通気や攪拌を加えることもできる。

宿主がバチルス属菌の場合、培養は通常約30～40℃で約6～24時間行な

い、必要により通気や攪拌を加えることもできる。

宿主が酵母である形質転換体を培養する際、培地としては、例えば、パークホルダー (Burkholder) 最小培地 [Bostian, K. L. ら、Proc. Natl. Acad. Sci. USA, 77, 4505 (1980)] や 0.5% カザミノ酸を含有する SD 培地 [Bitter, G. A. ら、Proc. Natl. Acad. Sci. USA, 81, 5330 (1984)] が挙げられる。培地の pH は約 5~8 に調整するのが好ましい。培養は通常約 20℃~35℃ で約 24~72 時間行ない、必要に応じて通気や攪拌を加える。

宿主が昆虫細胞または昆虫である形質転換体を培養する際、培地としては、Grace's Insect Medium (Grace, T. C. C., Nature, 195, 788 (1962)) に非働化した 10% ウシ血清等の添加物を適宜加えたものなどが用いられる。培地の pH は約 6.2~6.4 に調整するのが好ましい。培養は通常約 27℃ で約 3~5 日間行ない、必要に応じて通気や攪拌を加える。

宿主が動物細胞である形質転換体を培養する際、培地としては、例えば、約 5~20% の胎児牛血清を含む MEM 培地 [Science, 122, 501 (1952)]、DME M 培地 [Virology, 8, 396 (1959)]、RPMI 1640 培地 [The Journal of the American Medical Association, 199, 519 (1967)]、199 培地 [Proceeding of the Society for the Biological Medicine, 73, 1 (1950)] などが用いられる。pH は約 6~8 であるのが好ましい。培養は通常約 30℃~40℃ で約 15~60 時間行ない、必要に応じて通気や攪拌を加える。

各種宿主について適当な培地、培養条件などについては公知である（特に、WO 00/14227 号公報第 24 頁第 24 行~第 26 頁第 8 行、EP 1111047 A2 号公報段落 [0090]~[0096] 参照）。

以上のようにして、形質転換体の細胞膜に融合タンパク質を発現させることができる。

上記培養物から融合タンパク質を分離精製するには、例えば、下記の方法により行なうことができる。

融合タンパク質を培養菌体あるいは細胞から抽出するに際しては、培養後、公知の方法で菌体あるいは細胞を集め、これを適当な緩衝液に懸濁し、超音波、リゾチームおよび/または凍結融解などによって菌体あるいは細胞を破壊したのち

- 、遠心分離やろ過により融合タンパク質の粗抽出液を得る方法などが適宜用いられる。緩衝液の中に尿素や塩酸グアニジンなどのタンパク質変性剤や、トリトン X-100TMなどの界面活性剤が含まれていてもよい。培養液中にレセプタータンパク質が分泌される場合には、培養終了後、公知の方法で菌体あるいは細胞と
- 5 上清とを分離し、上清を集める。

- このようにして得られた培養上清、あるいは抽出液中に含まれる融合タンパク質の精製は、公知の分離・精製法を適切に組み合わせて行なうことができる。これらの公知の分離、精製法としては、塩析や溶媒沈澱法などの溶解度を利用する方法、透析法、限外ろ過法、ゲルろ過法、および SDS-ポリアクリルアミドゲル電気泳動法などの主として分子量の差を利用する方法、イオン交換クロマトグラフィーなどの荷電の差を利用する方法、アフィニティークロマトグラフィーなどの特異的親和性を利用する方法、逆相高速液体クロマトグラフィーなどの疎水性の差を利用する方法、等電点電気泳動法などの等電点の差を利用する方法などが用いられる。
- 10

- 15 かくして得られる融合タンパク質が遊離体で得られた場合には、公知の方法あるいはそれに準じる方法によって塩に変換することができ、逆に塩で得られた場合には公知の方法あるいはそれに準じる方法により、遊離体または他の塩に変換することができる。

- なお、組換え体が産生する融合タンパク質を、精製前または精製後に適当なタンパク質修飾酵素を作用させることにより、任意に修飾を加えたり、ポリペプチドを部分的に除去することもできる。タンパク質修飾酵素としては、例えば、トリプシン、キモトリプシン、アルギニルエンドペプチダーゼ、プロテインキナーゼ、グリコシダーゼなどが用いられる。
- 20

- かくして生成する融合タンパク質またはその塩の活性または存在は、標識したリガンドとの結合実験および特異抗体を用いたエンザイムイムノアッセイなどにより測定することができる。
- 25

本発明のリガンドの決定方法に用いられる試験化合物としては、公知のリガンド（例えば、アンギオテンシン、ボンベシン、カナビノイド、コレシストキニン、グルタミン、セロトニン、メラトニン、ニューロペプチド Y、オピオイド、プ

リン、バソプレッシン、オキシトシン、PACAP（例、PACAP 27、PACAP 38）、セクレチン、グルカゴン、カルシトニン、アドレノメジュリン、ソマトスタチン、GHRH、CRF、ACTH、GRP、PTH、VIP（バソアクティブ・インテスティナル・アンド・リレイテッド・ポリペプチド）、ソマトスタチン、ドーパミン、モチリン、アミリン、ブラジキニン、CGRP（カルシトニンジーンリレーティッドペプチド）、ロイコトリエン、パンクレアスタチン、プロスタグランジン、トロンボキサン、アデノシン、アドレナリン、ケモカインスーパーファミリー（例、IL-8、GRO α 、GRO β 、GRO γ 、NAP-2、ENA-78、GCP-2、PF4、IP-10、Mig、PBSF/SDF-1などのCXCケモカインサブファミリー；MCAF/MCP-1、MCP-2、MCP-3、MCP-4、eotaxin、RANTES、MIP-1 α 、MIP-1 β 、HCC-1、MIP-3 α /LARC、MIP-3 β /ELC、I-309、TARC、MIPF-1、MIPF-2/eotaxin-2、MDC、DC-CK1/PARC、SLCなどのCCケモカインサブファミリー；lymphotactinなどのCケモカインサブファミリー；fractalkineなどのCX3Cケモカインサブファミリー等）、エンドセリン、エンテロガストリン、ヒスタミン、ニューロテンシン、TRH、パンクレアティックポリペプチド、ガラニン、リゾホスファチジン酸（LPA）、スフィンゴシン1-リン酸、リゾホスファチジルセリン、スフィンゴシルホスホリルコリン、リゾホスファチジルコリン、ステロイド類、胆汁酸類、イソプレノイド、アラキドン酸代謝物、アミン類、アミノ酸、ヌクレオチド、ヌクレオシド、飽和脂肪酸または不飽和脂肪酸など）の他に、例えば、ヒトまたは哺乳動物（例えば、マウス、ラット、ブタ、ウシ、ヒツジ、サルなど）の組織抽出物、細胞培養上清などが用いられる。例えば、該組織抽出物、細胞培養上清などを、オーファンレセプターとGFPとの融合タンパク質を発現させた細胞に添加し、その細胞刺激活性などを測定しながらスクリーニングを行い、最終的に単一のリガンドを決定することができる。

本発明のリガンド決定方法Aは、具体的には、該融合タンパク質の発現細胞を構築し、該発現細胞やその細胞膜画分を用いて細胞刺激活性アッセイやレセプタ

一結合アッセイを行うことによって、オーファンレセプターに結合して細胞刺激活性（例えば、アラキドン酸遊離、アセチルコリン遊離、細胞内 Ca^{2+} 遊離、細胞内 cAMP 生成、細胞内 cGMP 生成、イノシトールリン酸産生、細胞膜電位変動、細胞内タンパク質のリン酸化、c-fos 活性化、pH の低下などを促進する活性または抑制する活性）、MAP キナーゼの活性化、転写因子（例、CRE、AP1、NFkB など）の活性化、ジアシルグリセロール産生、細胞膜上のイオンチャンネル（例、 K^+ 、 Ca^{2+} 、 Na^+ 、 Cl^- など）の開閉、アポトーシスの誘導、細胞の形態変化、レセプター（融合タンパク質）の細胞膜から細胞質への移行、低分子量 G タンパク質（例、Ras、Rap、Rho、Rab など）の活性化、細胞分裂促進活性、DNA 合成促進活性などを有する化合物、すなわちリガンド（例えば、ペプチド、タンパク質、非ペプチド性化合物、合成化合物、発酵生産物など）を決定する方法である。

本発明のリガンド決定方法は、融合タンパク質を発現している細胞またはその細胞膜画分と試験化合物とを接触させた場合の、例えば、該オーファンレセプターに対する試験化合物の結合量や細胞刺激活性などを測定することを特徴とする。

より具体的には、本発明は、次のようなりガンド決定方法を提供する。

（１）標識した試験化合物を、融合タンパク質を発現している細胞またはその細胞膜画分に接触させた場合における、標識した試験化合物の該細胞またはその細胞膜画分に対する結合量を測定することを特徴とするオーファンレセプターに対するリガンドの決定方法、

（２）標識した試験化合物を、融合タンパク質をコードする DNA を含有する形質転換体を培養することによって細胞膜上に発現した融合タンパク質に接触させた場合における、標識した試験化合物のオーファンレセプターに対する結合量を測定することを特徴とするオーファンレセプターに対するリガンドの決定方法

（３）試験化合物を、融合タンパク質を発現している細胞に接触させた場合における、オーファンレセプターを介した前記細胞刺激活性、MAP キナーゼの活性化、転写因子（例、CRE、AP1、NFkB など）の活性化、ジアシルグリ

セロール産生、細胞膜上のイオンチャンネル（例、 K^+ 、 Ca^{2+} 、 Na^+ 、 Cl^- など）の開閉、アポトーシスの誘導、細胞の形態変化、レセプター（融合タンパク質）の細胞膜から細胞質への移行、低分子量Gタンパク質（例、Ras、Rap、Rho、Rabなど）の活性化、細胞分裂促進活性、DNA合成促進活性などを測定することを特徴とするオーファンレセプターに対するリガンドの決定方法、および

（４）試験化合物を、融合タンパク質をコードするDNAを含有する形質転換体を培養することによって細胞膜上に発現した融合タンパク質に接触させた場合における、オーファンレセプターを介する前記細胞刺激活性、MAPキナーゼの活性化、転写因子（例、CRE、AP1、NFkBなど）の活性化、ジアシルグリセロール産生、細胞膜上のイオンチャンネル（例、 K^+ 、 Ca^{2+} 、 Na^+ 、 Cl^- など）の開閉、アポトーシスの誘導、細胞の形態変化、レセプター（融合タンパク質）の細胞膜から細胞質への移行、低分子量Gタンパク質（例、Ras、Rap、Rho、Rabなど）の活性化、細胞分裂促進活性、DNA合成促進活性などを測定することを特徴とするオーファンレセプターに対するリガンドの決定方法を提供する。

特に、上記（１）～（２）の試験を行ない、試験化合物がオーファンレセプターに結合することを確認した後に、上記（３）～（４）の試験を行なうことが好ましい。

場合によっては、上記発現細胞から融合タンパク質を単離精製し、それを用いてレセプター結合アッセイ等を行うこともできる。リガンド決定方法に用いる融合タンパク質としては、前記細胞を用いて大量発現させた融合タンパク質が適している。

融合タンパク質を製造するには、上記の発現方法が用いられるが、該融合タンパク質をコードするDNAを哺乳動物細胞や昆虫細胞などで発現させることが好ましい。融合タンパク質をコードするDNA断片を宿主細胞に導入し、それらを効率よく発現させるためには、該DNA断片をバキュロウイルスに属する核多角体病ウイルス（nuclear polyhedrosis virus；NPV）のポリヘドリンプロモーター、SV40由来のプロモーター、レトロウイルスのプロモーター、メタロチ

オネインプロモーター、ヒトヒートショックプロモーター、サイトメガロウイルスプロモーター、SR α プロモーターなどの下流に組み込むのが好ましい。発現した融合タンパク質の量と質の検査は公知の方法で行うことができる。例えば、文献〔Nambi, P. ら、J. Biol. Chem., 267, 19555-19559 (1992)〕に記載の方法に従って行うことができる。

本発明のリガンド決定方法において、融合タンパク質を発現している細胞またはその細胞膜画分を用いるのが好ましい。

本発明のリガンド決定方法において、融合タンパク質を発現している細胞を用いる場合、該細胞をグルタルアルデヒド、ホルマリンなどで固定化してもよい。

10 固定化方法は公知の方法に従って行なうことができる。

融合タンパク質を発現している細胞とは、融合タンパク質を発現した宿主細胞をいうが、該宿主細胞としては、大腸菌、枯草菌、酵母、昆虫細胞、動物細胞などが用いられる。

細胞膜画分としては、細胞を破碎した後、公知の方法で得られる細胞膜が多く含まれる画分のことをいう。細胞の破碎方法としては、Potter-Elvehjem型ホモジナイザーで細胞を押し潰す方法、ワーリングブレンダーやポリトロン (Kinematica社製) による破碎、超音波による破碎、フレンチプレスなどで加圧しながら細胞を細いノズルから噴出させることによる破碎などが挙げられる。細胞膜の分画には、分画遠心分離法や密度勾配遠心分離法などの遠心力による分画法が主として用いられる。例えば、細胞破碎液を低速 (500rpm~3000rpm) で短時間 (通常、約1分~10分) 遠心し、上清をさらに高速 (15000rpm~30000rpm) で通常30分~2時間遠心し、得られる沈澱を膜画分とする。該膜画分中には、発現した融合タンパク質と細胞由来のリン脂質や膜タンパク質などの膜成分が多く含まれる。

25 該融合タンパク質を発現している細胞やその膜画分中の融合タンパク質の量は、1細胞当たり 10^3 ~ 10^8 分子であるのが好ましく、 10^5 ~ 10^7 分子であるのが好適である。なお、発現量が多いほど膜画分当たりのリガンド結合活性 (比活性) が高くなり、高感度なスクリーニング系の構築が可能になるばかりでなく、同一ロットで大量の試料を測定できるようになる。この融合タンパク質の発

現量を、蛍光顕微鏡や蛍光光度計を用いて、細胞や細胞膜におけるGFP発光量から概算することができる。

- 5 オーフアンレセプターに対するリガンドを決定する上記の(1)～(2)の方法を実施するためには、融合タンパク質を含有する適当な細胞または細胞膜画分および標識した試験化合物が必要である。融合タンパク質画分としては、天然型のオーファンレセプターと同等の活性を有する組換え型融合レセプターを含有するものが望ましい。ここで、同等の活性とは、同等のリガンド結合活性、シグナル情報伝達作用などを示す。

- 10 標識した試験化合物として、 $[^3\text{H}]$ 、 $[^{125}\text{I}]$ 、 $[^{14}\text{C}]$ 、 $[^{35}\text{S}]$ などで標識した、前述のリガンド化合物群から選ばれる化合物が用いられる。

- 具体的には、本発明のリガンドの決定方法を行なうには、まず融合タンパク質を発現している細胞またはその細胞膜画分を、決定方法に適したバッファーに懸濁することにより融合タンパク質標品を調製する。バッファーには、pH4～10（望ましくはpH6～8）のリン酸バッファー、トリス-塩酸バッファーなどのリガンドとオーファンレセプターとの結合を阻害しないバッファーであればい
- 15 ずれでもよい。また、非特異的結合を低減させる目的で、CHAPS、Tween-80TM（花王-アトラス社）、ジギトニン、デオキシコレートなどの界面活性剤やウシ血清アルブミンやゼラチンなどの各種タンパク質をバッファーに加えることもできる。さらに、プロテアーゼによるレセプターやリガンドの分解を抑える目的でPMSF、ロイペプチン、E-64（ペプチド研究所製）、ペプスタチンなどのプロテアーゼ阻害剤を添加することもできる。そして、例えば0.01ml～10mlの該レセプター標品に、一定量（5000cpm～500000cpm）の $[^3\text{H}]$ 、 $[^{125}\text{I}]$ 、 $[^{14}\text{C}]$ 、 $[^{35}\text{S}]$ などで標識した試験化合物を共存させる。非特異的結合量（NSB）を知るために大過剰の未標識の
- 20 試験化合物を加えた反応チューブも用意する。反応は約0℃～50℃、望ましくは約4℃～37℃で、約20分～24時間、望ましくは約30分～3時間行なう。反応後、ガラス繊維濾紙等で濾過し、適量の同バッファーで洗浄した後、ガラス繊維濾紙に残存する放射活性を液体シンチレーションカウンターあるいはγ-カウンターで計測する。全結合量（B）から非特異的結合量（NSB）を引いた

カウント（B-N S B）が0 c p mを越える試験化合物をオーファンレセプターに対するリガンド（アゴニストを含む）として選択することができる。

本発明のリガンドを決定する上記の（3）～（4）の方法を実施するためには、オーファンレセプターを介する前記細胞刺激活性、例えばMAPキナーゼの活性化、転写因子（例、CRE、AP1、NF κ Bなど）の活性化、ジアシルグリセロール産生、細胞膜上のイオンチャンネル（例、K⁺、Ca²⁺、Na⁺、Cl⁻など）の開閉、アポトーシスの誘導、細胞の形態変化、レセプター（融合タンパク質）の細胞膜から細胞質への移行、低分子量Gタンパク質（例、Ras、Rap、Rho、Rabなど）の活性化、細胞分裂促進活性、DNA合成促進活性などを公知の方法または市販の測定用キットを用いて測定することができる。具体的には、まず、融合タンパク質を発現している細胞をマルチウェルプレート等に培養する。リガンド決定を行なうにあたっては前もって新鮮な培地あるいは細胞に毒性を示さない適当なバッファーに交換し、試験化合物などを添加して一定時間インキュベートした後、細胞を抽出あるいは上清液を回収して、生成した代謝産物をそれぞれの方法に従って定量する。細胞刺激活性の指標とする物質（例えば、アラキドン酸など）の生成が、細胞が含有する分解酵素によって検定困難な場合は、該分解酵素に対する阻害剤を添加してアッセイを行なってもよい。また、cAMP産生抑制などの活性については、フォルスコリンなどで細胞の基礎的産生量を増大させておいた細胞に対する産生抑制作用として検出することができる。

上記細胞刺激活性のうち「レセプターの細胞質内への移行」の測定では、GFPなどの蛍光タンパク質の蛍光を測定することで、融合タンパク質の細胞膜から細胞質への移動を観察することができる。融合タンパク質の細胞膜から細胞質への移動の観察するためには、前記した融合タンパク質を安定的にまたは一過性に発現している動物細胞を用いるのが適している。適当な培養器に通常の培地を用いて培養した当該細胞に、適当な濃度に希釈した試験化合物を添加する。その際培地に直接希釈した試験化合物溶液を添加しても良いが、細胞をハンス平衡塩溶液（HBSS、BSAを0から10%、好ましくは0.1から1%添加しても良い）で洗浄した後、試験化合物を含有する同液を添加しても良い。該細胞はリ

ガンド添加後、4℃から37℃、好ましくは20℃から37℃で1分から6時間、好ましくは10分から2時間放置後に、融合タンパク質の細胞膜から細胞質への移動を観察する。該細胞はそのままでも観察可能であるが、グルタルアルデヒドやホルマリンで固定してもよい。固定方法は公知の方法に従って行うことがで

5 きる。

観察は通常の蛍光顕微鏡や共焦点レーザー顕微鏡を用いればよいが、励起光を照射できる機能と蛍光像を取り込む機能を備えたプレートリーダーなども使用できる。その際、レセプターと、配列番号：3または配列番号：5で示した野生型GFPまたはGFPuvとの融合タンパク質を検出するためには紫外光、好ましくは395nmで励起し、フルオレセイン・イソシアネート（FITC）や一般に市販されるGFP検出用のフィルターを用いて観察できる。また、配列番号：10 1または配列番号：7で示したGFPとの融合タンパク質を検出するためには460～500nm、好ましくは488nmの励起光で励起し、FITCや一般に市販されるGFP検出用のフィルターを用いて観察すればよい。

15 レセプター（融合タンパク質）の細胞質内への移行の他に、レセプターの凝集、レセプターの局在化、あるいはレセプターの発現の低下または増加など、顕微鏡的に観察できるレセプターの形態学的な変化を観察することもできる。

本発明のリガンド決定法Bを実施する場合、融合タンパク質の発現ベクター以外に、特定のエンハンサー／プロモーターの下流にレポータータンパク質をコードするDNAを含有するプラスミドを、細胞、好ましくは真核生物由来の細胞に組み込むことが必要である。このプラスミドは、細胞、好ましくは真核生物由来の細胞内で該レポータータンパク質を発現させることのできるプロモーターを含有し、更に原核生物内で増殖させる場合の選択マーカーとして薬剤耐性遺伝子（例えば、アンピシリン耐性遺伝子）などを含有してもよい。

25 エンハンサー／プロモーターの下流にレポータータンパク質をコードするDNAを含有するプラスミドは、そのエンハンサーの制御下に細胞内でレポータータンパク質を発現することでき、かつ細胞内に導入できるプラスミドであれば、市販のプラスミドなどのいかなるプラスミドでもよい。

エンハンサーとしては、例えば、SV40、パピローマウイルス等のウイルス

由来のエンハンサー、レトロウイルスのLTR、cAMPレスポンスエレメント（cAMP応答配列）（CRE）、あるいはTPAレスポンスエレメント（TPA応答配列）（TRE）等が用いられ、好ましくはcAMPレスポンスエレメントである。該細胞が発現するオーファンレセプターによって仲介される上記細胞刺激活性によって活性化されるエンハンサーが適当である。

プロモーターとしては、例えば、SV40プロモーター、CMVプロモーター、HSVのチミジンキナーゼ遺伝子のTATA様プロモーター等が用いられ、好ましくはTATA様プロモーターである。

レポータータンパク質遺伝子としては、例えば、ルシフェラーゼ遺伝子、 β -ガラクトシダーゼ遺伝子、GFP遺伝子、アルカリフォスファターゼ遺伝子等が用いられる。公知の方法にて酵素活性を検出できるような酵素遺伝子であれば、レポータータンパク質として用いる。

かかるプラスミドの具体例として、cAMPレスポンスエレメントの下流にTATA様プロモーターおよびレポータータンパク質（例、ルシフェラーゼ遺伝子）をコードする遺伝子を連結したプラスミド、例えばpCRE-Luc（Clontech社）などがある。

リガンド決定方法Bで用いられる細胞としては、前記した宿主細胞が用いられ、好ましくは真核生物由来の細胞、より好ましくは動物細胞（例、サル細胞COS-7、Vero、CHO細胞、CHO(dhfr⁻)細胞、マウスL細胞、マウスAtT-20、マウスミエローマ細胞、ラットGH3、ヒトFL細胞、ヒトHEK293細胞など）などが用いられる。

該細胞は、2種以上（好ましくは2～3種）の融合タンパク質を発現しているもよい。

2種類以上の融合タンパク質を発現させる場合は、類似の生物学的特徴を有する2種類以上のオーファンレセプターを用いるのが良い。

類似の特徴としては、例えば、使用する2種類以上のオーファンレセプターをそれぞれ単独で発現させた時のレポータータンパク質の発現量などが挙げられる。具体的には、2種類以上のオーファンレセプターをそれぞれ単独で発現させた場合における(1)レポータータンパク質の基礎発現量および/または(2)フォルス

コリン添加時のレポータータンパク質の発現量を指標として、各レセプタータンパク質の特徴を区別することができる。

従って、2種類以上のオーファンレセプターを発現させてリガンドを決定する場合、あらかじめレポータータンパク質の基礎発現量が低いもの、中程度のもの
5、明らかに高いものなどに区分けをしたり、あるいはフォルスコリン添加によってレポータータンパク質の発現量が上昇しにくいレセプタータンパク質を明らかにしておくことが望ましい。なぜならば、例えばレポータータンパク質の基礎発現量が高いレセプタータンパク質とレポータータンパク質の基礎発現量が低いレセプターの2種類のレセプタータンパク質を発現させた場合、後者にリガンドが
10結合した場合にレポータータンパク質発現量の上昇が検出しにくくなるからである。すなわち：

- (1) レポータータンパク質の基礎発現量が高いオーファンレセプターと低いレセプタータンパク質の混合は避けるのが好ましい、
- (2) フォルスコリン添加によるレポータータンパク質の発現量の上昇が顕著な
15レセプタータンパク質とそうでないオーファンレセプターは混合しないほうが好ましい、
- (3) レポータータンパク質の基礎発現量が同程度であるオーファンレセプター同士を組み合わせ発現させるのが好ましい。

このように類似の特徴を有するオーファンレセプターの組合わせとしては、例
20例えば、APJ（アペリンレセプター；Gene, 136, 355 (1993)）とTGR-1（特開2002-078492号）との組み合わせが挙げられる。

リガンドの決定方法Bの具体例を以下に記載する。

細胞を96ウェルプレートに播種し、例えば10%ウシ胎児血清を含むDMEMで一晩培養する。ここで、例えば市販のトランスフェクションキットを用いて
25、融合タンパク質の発現プラスミドおよびレポータープラスミドを同時に細胞に導入し、細胞をさらに一晩培養することにより、細胞内でオーファンレセプターを一過性に発現させる。細胞を洗浄し、さらに培地を無血清化した後、試験化合物を添加する。エンハンサーがCREである場合、試験化合物と同時にフォルスコリンを添加してもよい。一定時間インキュベーションを行った後、細胞を溶解

し、レポータータンパク質の活性を測定する。

前記の決定方法において、レポータータンパク質活性のベースラインが高く、試験化合物による活性の変化の検出が困難な場合には、ベースラインを低下させる手段を講じるとよい。例えばオーファンレセプターがGタンパク質共役型レセ

- 5 プタータンパク質（GPCR）の場合、Gタンパク質の α サブユニットのうち、cAMP抑制効果を示すGiタンパク質を加えることにより、活性変化の検出が容易となる。Giタンパク質を発現させるために、Giタンパク質をコードするDNAを発現するプラスミドを、オーファンレセプタープラスミドおよびレポ
- 10 ド（オーファンレセプタープラスミド：レポータープラスミド：Giプラスミド）の混合比は、好ましくは5～15：1：1～6程度、さらに好ましくは7：1：3程度である。

- 本発明のリガンド決定方法Bにおいて、試験化合物を添加した場合に、レポータータンパク質の活性が約20%以上、好ましくは約50%以上、上昇または減少した時、当該試験化合物をリガンドとして同定することができる。
- 15

本発明のリガンド決定方法Bにおいて用いられる試験化合物は、前述の試験化合物などから選択される化合物である。

更に、本発明のリガンド決定用キットは、本発明の融合タンパク質を発現し得る細胞またはその細胞膜画分などを含有するものである。

- 20 本発明のリガンド決定用キットの例としては、次のものが挙げられる。

1. リガンド決定用試薬

(1) 測定用緩衝液および洗浄用緩衝液

Hanks' Balanced Salt Solution（ギブコ社製）に、0.05%のウシ血清アルブミン（シグマ社製）を加えたもの。

- 25 孔径0.45 μ mのフィルターで濾過滅菌し、4℃で保存するか、あるいは用時調製しても良い。

(2) 融合タンパク質標品

融合タンパク質を発現しているCHO細胞を、12穴プレートに 5×10^5 個/穴で継代し、37℃、5%CO₂、95%airで2日間培養したもの。

(3) 標識試験化合物

市販の [^3H]、 [^{125}I]、 [^{14}C]、 [^{35}S] などで標識した化合物、または適当な方法で標識化したもの。

- 5 水溶液の状態のものを 4°C あるいは -20°C にて保存し、用時に測定用緩衝液にて $1\ \mu\text{M}$ に希釈する。水に難溶性を示す試験化合物については、ジメチルホルムアミド、DMSO、メタノール等に溶解する。

(4) 非標識試験化合物

標識化合物と同じものを $100\sim 1000$ 倍濃い濃度に調製する。

2. 測定法

- 10 (1) 12 穴組織培養用プレートにて培養した本発明のレセプタータンパク質発現CHO細胞を、測定用緩衝液 1 ml で2回洗浄した後、 $490\ \mu\text{l}$ の測定用緩衝液を各穴に加える。

(2) 標識試験化合物を $5\ \mu\text{l}$ 加え、室温にて1時間反応させる。非特異的結合量を知るためには非標識試験化合物を $5\ \mu\text{l}$ 加えておく。

- 15 (3) 反応液を除去し、 1 ml の洗浄用緩衝液で3回洗浄する。細胞に結合した標識試験化合物を $0.2\text{ N NaOH}-1\% \text{ SDS}$ で溶解し、 4 ml の液体シンチレーターA（和光純薬製）と混合する。

(4) 液体シンチレーションカウンター（ベックマン社製）を用いて放射活性を測定する。

- 20 この様に、本発明のリガンド決定方法（A及びB）によれば、GFPなどの蛍光タンパク質の蛍光またはGFP抗体などの蛍光タンパク質抗体を利用した免疫染色法やウエスタンブロット法など用いて、

(1) タンパク質レベルでレセプタータンパク質が発現していることを確認でき

- 25 (2) 細胞膜にレセプタータンパク質が発現していることを確認でき、

(3) レセプタータンパク質の発現量を見積もることができ、

(4) レセプタータンパク質の高発現細胞を選択でき、そして

(5) リガンドによるレセプターの特異的反応を、レセプターと蛍光タンパク質との融合タンパク質の細胞内へのインターナリゼーションとして検出できる。こ

れらの特徴を利用することにより、リガンドが決定されていないレセプタータンパク質（オーファンレセプター）のリガンドを効率よく決定できる。

- このようにして決定されたリガンドは、そのレセプタータンパク質に結合して、その生理的機能を調節するので、そのレセプタータンパク質の機能に関連する疾患の予防及び／又は治療剤として用いることができる。さらには、リガンドとそのレセプタータンパク質を用いて、該レセプターのアゴニスト／アンタゴニストのスクリーニングを行うことができる。

- 本明細書および図面において、塩基やアミノ酸などを略号で表示する場合、IUPAC-IUB Commission on Biochemical Nomenclature による略号あるいは当該分野における慣用略号に基づく。またアミノ酸に関し光学異性体があり得る場合は、特に明示しなければL体を示すものとする。

本明細書の配列表の配列番号は、以下の配列を示す。

配列番号：1

- 15 実施例1で使用したGFP（以下、GFP-1と略記する）のアミノ酸配列を示す。

配列番号：2

実施例1で使用したGFPをコードするDNAの塩基配列を示す。

配列番号：3

- 20 野生型GFPのアミノ酸配列を示す。

配列番号：4

野生型GFPをコードするDNAの塩基配列を示す。

配列番号：5

GFPuvのアミノ酸配列を示す。

- 25 配列番号：6

GFPuvをコードするDNAの塩基配列を示す。

配列番号：7

EGFPのアミノ酸配列を示す。

配列番号：8

E G F Pをコードするc D N Aの塩基配列を示す。

配列番号：9

実施例1で用いるヒト由来Gタンパク質共役型レセプタータンパク質T G R 5
のアミノ酸配列を示す。

5 配列番号：10

実施例1で用いるヒト由来Gタンパク質共役型レセプタータンパク質T G R 5
をコードするc D N Aの塩基配列を示す。

配列番号：11

参考例1におけるP C R反応で使用したプライマー1の塩基配列を示す。

10 配列番号：12

参考例1におけるP C R反応で使用したプライマー2の塩基配列を示す。

配列番号：13

ヒト由来副甲状腺ホルモン受容体（P T H-R）のアミノ酸配列を示す。

配列番号：14

15 ヒト由来副甲状腺ホルモン受容体（P T H-R）をコードするc D N Aの塩基
配列を示す。

配列番号：15

ヒト由来G P R 40のアミノ酸配列を示す。

配列番号：16

20 ヒト由来G P R 40をコードするc D N Aの塩基配列を示す。

配列番号：17

H i s-T a gのアミノ酸配列を示す。

配列番号：18

V 5-t a gのアミノ酸配列を示す。

25 配列番号：19

m y c-t a gのアミノ酸配列を示す。

配列番号：20

X p r e s s-t a gのアミノ酸配列を示す。

配列番号：21

HA-t a gのアミノ酸配列を示す。

配列番号：22

ECFPのアミノ酸配列を示す。

配列番号：23

- 5 ECFPをコードするcDNAの塩基配列を示す。

配列番号：24

EYFPのアミノ酸配列を示す。

配列番号：25

EYFPをコードするcDNAの塩基配列を示す。

- 10 配列番号：26

DsREDのアミノ酸配列を示す。

配列番号：27

DsREDをコードするcDNAの塩基配列を示す。

配列番号：28

- 15 EBFPAのアミノ酸配列を示す。

配列番号：29

EBFPAをコードするcDNAの塩基配列を示す。

配列番号：30

- 20 オーフアンレセプターhBL5とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：31

オーファンレセプターh7TBA62とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：32

- 25 オーフアンレセプター14273とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：33

オーファンレセプターEMR3とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：34

オーファンレセプターGPR15とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：35

- 5 オーファンレセプターGPR31とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：36

オーファンレセプターGPCR5BとGFP-1との融合タンパク質のアミノ酸配列を示す。

- 10 配列番号：37

オーファンレセプターPSEC0142とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：38

- 15 オーファンレセプターHE6とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：39

オーファンレセプターGPR61とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：40

- 20 オーファンレセプターTGR9とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：41

オーファンレセプターTGR24とGFP-1との融合タンパク質のアミノ酸配列を示す。

- 25 配列番号：42

オーファンレセプターZGPR1とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：43

オーファンレセプターEMR1とGFP-1との融合タンパク質のアミノ酸配

列を示す。

配列番号：44

オーファンレセプターGPR25とGFP-1との融合タンパク質のアミノ酸配列を示す。

5 配列番号：45

オーファンレセプターGPR55とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：46

10 オーファンレセプターAXOR14とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：47

オーファンレセプターTM7SF1とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：48

15 オーファンレセプターPSP24BとGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：49

オーファンレセプターSREB3とGFP-1との融合タンパク質のアミノ酸配列を示す。

20 配列番号：50

オーファンレセプターTGR37とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：51

25 オーファンレセプターH963とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：52

オーファンレセプターGPR87とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：53

オーファンレセプターGPR91とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：54

5 オーファンレセプターPNRとGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：55

オーファンレセプターTGR29とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：56

10 オーファンレセプターTGR36とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：57

オーファンレセプターH9とGFP-1との融合タンパク質のアミノ酸配列を示す。

15 配列番号：58

オーファンレセプターTGR18とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：59

20 オーファンレセプターTGR19とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：60

オーファンレセプターAM-RとGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：61

25 オーファンレセプターGPR19とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：62

オーファンレセプターGPR45とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：63

オーファンレセプターGPRC5DとGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：64

- 5 オーファンレセプターLGR6とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：65

オーファンレセプターRUP3とGFP-1との融合タンパク質のアミノ酸配列を示す。

- 10 配列番号：66

オーファンレセプターTGR14とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：67

- 15 オーファンレセプターTPRA40とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：68

オーファンレセプターGPR22とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：69

- 20 オーファンレセプターGPR52とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：70

オーファンレセプターFLH2882とGFP-1との融合タンパク質のアミノ酸配列を示す。

- 25 配列番号：71

オーファンレセプターSNORF36とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：72

オーファンレセプターMRGとGFP-1との融合タンパク質のアミノ酸配列

を示す。

配列番号：73

オーファンレセプターSREB2とGFP-1との融合タンパク質のアミノ酸配列を示す。

5 配列番号：74

オーファンレセプターGPR12とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：75

10 配列番号：76
オーファンレセプターGPR30とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：77

15 配列番号：78
オーファンレセプターGPR82とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：79

20 配列番号：80
オーファンレセプターRECAPとGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：81

25 配列番号：82
オーファンレセプターHB954とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：83

30 配列番号：84
オーファンレセプターRDC1とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：85

35 配列番号：86
オーファンレセプターTGR6とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：87

40 配列番号：88
オーファンレセプターA-2とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：89

オーファンレセプターJEG18とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：83

- 5 オーファンレセプターGPR17とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：84

オーファンレセプターGPR35とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：85

- 10 オーファンレセプターGPCR5CとGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：86

オーファンレセプターHM74とGFP-1との融合タンパク質のアミノ酸配列を示す。

- 15 配列番号：87

オーファンレセプターRPEとGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：88

- 20 オーファンレセプターTGR13とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：89

オーファンレセプターTGR27とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：90

- 25 オーファンレセプターDEZとGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：91

オーファンレセプターratGPR1とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号： 9 2

オーファンレセプターGPR3とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号： 9 3

- 5 オーファンレセプターGPR6とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号： 9 4

オーファンレセプターRAIG1とGFP-1との融合タンパク質のアミノ酸配列を示す。

- 10 配列番号： 9 5

オーファンレセプターTGR2-1とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号： 9 6

- 15 オーファンレセプターTGR2-2とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号： 9 7

オーファンレセプターTGR21とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号： 9 8

- 20 オーファンレセプターGPR56とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号： 9 9

オーファンレセプターKIAA0758とGFP-1との融合タンパク質のアミノ酸配列を示す。

- 25 配列番号： 1 0 0

オーファンレセプターRE2とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号： 1 0 1

オーファンレセプターP40とGFP-1との融合タンパク質のアミノ酸配列

を示す。

配列番号：102

オーファンレセプターGPR27とGFP-1との融合タンパク質のアミノ酸配列を示す。

5 配列番号：103

オーファンレセプターHG38とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：104

10 オーファンレセプターDRR1とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：105

オーファンレセプターTGR12とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：106

15 オーファンレセプターTGR11とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：107

オーファンレセプターTGR15とGFP-1との融合タンパク質のアミノ酸配列を示す。

20 配列番号：108

オーファンレセプターTGR8とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：109

25 オーファンレセプターGPR20とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：110

オーファンレセプターTGR10とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：111

オーファンレセプターTGR30とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：112

- 5 オーファンレセプターGPR18とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：113

オーファンレセプターTGR25とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：114

- 10 オーファンレセプターGPR23とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：115

オーファンレセプターP2Y10とGFP-1との融合タンパク質のアミノ酸配列を示す。

- 15 配列番号：116

オーファンレセプターGPR37とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：117

- 20 オーファンレセプターET(B)R-LP-2とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：118

オーファンレセプターFPRL2とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：119

- 25 オーファンレセプターGPR32とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：120

オーファンレセプターdj287G14.2とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：1 2 1

オーファンレセプターBRS-3とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：1 2 2

- 5 オーファンレセプターGPR39とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：1 2 3

オーファンレセプター63A2とGFP-1との融合タンパク質のアミノ酸配列を示す。

- 10 配列番号：1 2 4

オーファンレセプターGPR84とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：1 2 5

- 15 オーファンレセプターGPR21とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：1 2 6

オーファンレセプターGPR48とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：1 2 7

- 20 オーファンレセプターSNORF1とGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：1 2 8

オーファンレセプターBA12とGFP-1との融合タンパク質のアミノ酸配列を示す。

- 25 配列番号：1 2 9

オーファンレセプターMASとGFP-1との融合タンパク質のアミノ酸配列を示す。

配列番号：1 3 0

オーファンレセプターOT7T009とGFP-1との融合タンパク質のアミ

ノ酸配列を示す。

配列番号：131

オーファンレセプターTGR34とGFP-1との融合タンパク質のアミノ酸配列を示す。

5 配列番号：132

オーファンレセプターhBL5とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：133

10 オーファンレセプターh7TBA62とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：134

オーファンレセプター14273とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：135

15 オーファンレセプターEMR3とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：136

オーファンレセプターGPR15とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

20 配列番号：137

オーファンレセプターGPR31とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：138

25 オーファンレセプターGPRC5BとGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：139

オーファンレセプターPSEC0142とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：140

オーファンレセプターHE 6 とGFP-1 との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：141

- 5 オーファンレセプターGPR 61 とGFP-1 との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：142

オーファンレセプターTGR 9 とGFP-1 との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：143

- 10 オーファンレセプターTGR 24 とGFP-1 との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：144

オーファンレセプターZGPR 1 とGFP-1 との融合タンパク質をコードするDNAの塩基配列を示す。

- 15 配列番号：145

オーファンレセプターEMR 1 とGFP-1 との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：146

- 20 オーファンレセプターGPR 25 とGFP-1 との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：147

オーファンレセプターGPR 55 とGFP-1 との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：148

- 25 オーファンレセプターAXOR 14 とGFP-1 との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：149

オーファンレセプターTM7SF 1 とGFP-1 との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：150

オーファンレセプターPSP24BとGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：151

- 5 オーファンレセプターSREB3とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：152

オーファンレセプターTGR37とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

- 10 配列番号：153

オーファンレセプターH963とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：154

- 15 オーファンレセプターGPR87とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：155

オーファンレセプターGPR91とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：156

- 20 オーファンレセプターPNRとGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：157

オーファンレセプターTGR29とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

- 25 配列番号：158

オーファンレセプターTGR36とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：159

オーファンレセプターH9とGFP-1との融合タンパク質をコードするDN

Aの塩基配列を示す。

配列番号：160

オーファンレセプターTGR18とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

5 配列番号：161

オーファンレセプターTGR19とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：162

10 オーファンレセプターAM-RとGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：163

オーファンレセプターGPR19とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：164

15 オーファンレセプターGPR45とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：165

オーファンレセプターGPRC5DとGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

20 配列番号：166

オーファンレセプターLGR6とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：167

25 オーファンレセプターRUP3とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：168

オーファンレセプターTGR14とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：169

オーファンレセプターTPRA40とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：170

- 5 オーファンレセプターGPR22とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：171

オーファンレセプターGPR52とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：172

- 10 オーファンレセプターFLH2882とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：173

オーファンレセプターSNORF36とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

- 15 配列番号：174

オーファンレセプターMRGとGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：175

- 20 オーファンレセプターSREB2とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：176

オーファンレセプターGPR12とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：177

- 25 オーファンレセプターGPR30とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：178

オーファンレセプターGPR82とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：179

オーファンレセプターRECAPとGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：180

- 5 オーファンレセプターHB954とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：181

オーファンレセプターRDC1とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

- 10 配列番号：182

オーファンレセプターTGR6とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：183

- 15 オーファンレセプターA-2とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：184

オーファンレセプターJEG18とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：185

- 20 オーファンレセプターGPR17とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：186

オーファンレセプターGPR35とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

- 25 配列番号：187

オーファンレセプターGPRC5CとGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：188

オーファンレセプターHM74とGFP-1との融合タンパク質をコードする

DNAの塩基配列を示す。

配列番号：189

オーファンレセプターRPEとGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

5 配列番号：190

オーファンレセプターTGR13とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：191

10 オーファンレセプターTGR27とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：192

オーファンレセプターDEZとGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：193

15 オーファンレセプターratGPR1とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：194

オーファンレセプターGPR3とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

20 配列番号：195

オーファンレセプターGPR6とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：196

25 オーファンレセプターRAIG1とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：197

オーファンレセプターTGR2-1とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：198

51

オーファンレセプターTGR 2-2とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：199

- 5 オーファンレセプターTGR 21とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：200

オーファンレセプターGPR 56とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：201

- 10 オーファンレセプターKIAA 0758とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：202

オーファンレセプターRE 2とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

- 15 配列番号：203

オーファンレセプターP 40とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：204

- 20 オーファンレセプターGPR 27とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：205

オーファンレセプターHG 38とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：206

- 25 オーファンレセプターDRR 1とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：207

オーファンレセプターTGR 12とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：208

オーファンレセプターTGR11とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：209

- 5 オーファンレセプターTGR15とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：210

オーファンレセプターTGR8とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

- 10 配列番号：211

オーファンレセプターGPR20とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：212

- 15 オーファンレセプターTGR10とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：213

オーファンレセプターTGR30とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：214

- 20 オーファンレセプターGPR18とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：215

オーファンレセプターTGR25とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

- 25 配列番号：216

オーファンレセプターGPR23とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：217

オーファンレセプターP2Y10とGFP-1との融合タンパク質をコードす

るDNAの塩基配列を示す。

配列番号：218

オーファンレセプターGPR37とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

5 配列番号：219

オーファンレセプターET(B)R-LP-2とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：220

10 オーファンレセプターFPRL2とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：221

オーファンレセプターGPR32とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：222

15 オーファンレセプターdj287G14.2とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：223

オーファンレセプターBRS-3とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

20 配列番号：224

オーファンレセプターGPR39とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：225

25 オーファンレセプター63A2とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：226

オーファンレセプターGPR84とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：227

オーファンレセプターGPR21とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：228

5 オーファンレセプターGPR48とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：229

オーファンレセプターSNORF1とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：230

10 オーファンレセプターBA12とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：231

オーファンレセプターMASとGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

15 配列番号：232

オーファンレセプターOT7T009とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

配列番号：233

20 オーファンレセプターTGR34とGFP-1との融合タンパク質をコードするDNAの塩基配列を示す。

25 参考例1で得られた形質転換体エシェリヒア・コリ (*Escherichia coli*) JM109/pCR4-hTGR5は、平成12(2000)年4月3日から茨城県つくば市東1丁目1番地1 中央第6(郵便番号305-8566)の独立行政法人産業技術総合研究所 特許生物寄託センター(旧 通商産業省工業技術院生命工学工業技術研究所(NIBH))に寄託番号FERM BP-7114として、また平成12(2000)年3月23日から大阪府大阪市淀川区十三本町2丁目17番85号(郵便番号532-8686)の財団法人・発酵研究所(IFO)に寄託番号IFO 16410として寄託されている。

実施例

以下に参考例および実施例を示して、本発明をより詳細に説明するが、これらは本発明の範囲を限定するものではない。なお、大腸菌を用いての遺伝子操作は、モレキュラー・クローニング (Molecular cloning) に記載されている方法に従った。

参考例 1 ヒト脾臓の G タンパク質共役型レセプタータンパク質をコードする cDNA のクローニングと塩基配列の決定

- 10 ヒト脾臓 cDNA (Clontech) を鋳型とし、2 個のプライマー、プライマー 1 (配列番号: 11) およびプライマー 2 (配列番号: 12) を用いて PCR 反応を行った。該反応における反応液の組成は、上記鋳型 cDNA 1/10 量、Advantage-GC2 Polymerase Mix (Clontech) 1/50 量、プライマー 1 (配列番号: 11) およびプライマー 2 (配列番号: 12) 各 0.5 μ M、dNTPs 200 μ M、および該酵素製品に添付のバッファー 1/5 量、GC Melt 1/5 量からなり、最終量を 20 μ l とした。PCR 反応では、94℃・5 分の後、94℃・30 秒、60℃・30 秒、68℃・2 分のサイクルを 30 回繰り返し、最後に 68℃・5 分の伸長反応を行った。該 PCR 反応産物を TA クローニングキット (Invitrogen) の処方に従いプラスミドベクター
- 20 pCR4 (Invitrogen) へサブクローニングした。これを大腸菌 JM109 に導入し、該 PCR 産物の cDNA を持つクローンをアンピシリンを含む LB 寒天培地中で選択した。個々のクローンの配列を解析した結果、新規 G タンパク質共役型レセプタータンパク質をコードする cDNA 配列 (配列番号: 10) を得た。この cDNA 配列から推定されるアミノ酸配列 (配列番号: 9) を有する新規 G
- 25 タンパク質共役型レセプタータンパク質を TGR5 と命名した。また配列番号: 10 で表わされる DNA を含有する形質転換体は大腸菌 (*Escherichia coli*) JM109/pCR4-hTGR5 と命名した。

参考例 2 TGR5 を一過性に発現させたヒト HEK293 細胞における、コレ

ステロール代謝関連物質によるレポーター活性化の検出

コレステロール代謝関連物質によるTGR 5特異的な刺激活性の検出は、CREプロモーターの発現誘導によって産生されるレポーター遺伝子産物（ルシフェラーゼ）の発現量を指標に行った。

- 5 ヒト由来のHEK 293細胞を増殖培地（DMEM（Dulbecco's Modified Eagle Medium）（GibcoBRL）に10%ウシ胎児血清（GibcoBRL）を添加したもの）に懸濁し、 1×10^5 cells/wellの濃度にてコラーゲンでコートされたBlack well 96ウェルプレート（ベクトンディッキンソン社）にまいた。37℃、5%CO₂条件下で一晩培養した後、レポーター遺伝子を含む
- 10 るプラスミドpCRE-Luc（Clontech）と共に、公知の方法により動物細胞用発現ベクターpAKKO-111H（Biochem. Biophys. Acta, Hinuma, S. et al., 1219, 251-259, 1994記載のpAKKO-1. 111Hと同一のプラスミドベクター）にTGR 5遺伝子を挿入して作製したTGR 5発現ベクタープラスミド、または、TGR 5遺伝子を含まない元のpAKKO-111Hを該細胞に
- 15 以下の通りにトランスフェクションした。

- OPTI-MEM-I（GibcoBRL）とLipofectamine™ 2000試薬（GibcoBRL）を24:1にて混合することにより、リポフェクトアミン希釈液を調製した。また、OPTI-MEM-I、TGR 5発現ベクタープラスミドまたは元のベクタープラスミド（240 ng/μl）およびpCRE-Luc
- 20 c（240 ng/μl）を24:0.9:0.1にて混合することによりDNA希釈液を調製した。リポフェクトアミン希釈液とDNA希釈液を等量混合し、20分間室温で静置することによりDNAとリポフェクトアミンの複合体を形成させた後、その溶液25 μlを上記のHEK 293細胞を培養したプレートに添加し、さらに37℃、5%CO₂条件下で一晩培養した。

- 25 トランスフェクトしたHEK 293細胞をアッセイ用培地（DMEMに0.1%ウシ血清アルブミンを添加したもの）にて洗浄した後、アッセイ用培地にて希釈したリトコール酸（和光純薬）およびプロゲステロン（和光純薬）を 2×10^{-5} Mとなるようプレートに添加し、37℃、5%CO₂条件下で4時間培養した。培養上清を捨てて、ルシフェラーゼ活性測定用の基質であるピッカジーンLT

2. 0 (東洋インキ製造株式会社) を $50 \mu\text{l}$ 添加し、プレートリーダー (ARVO s x マルチラベルカウンター、Wallac 社) を用いてルシフェラーゼの発光量を測定した。

5 その結果、配列番号: 10 で表される塩基配列を有する TGR5 遺伝子を導入した HEK293 細胞特異的に、リトコール酸およびプロゲステロンによるルシフェラーゼ活性の上昇が認められた (図1)。

参考例 3 Gタンパク質共役型レセプタータンパク質発現プラスミドおよびレポータープラスミドの宿主細胞への導入

10 公知の方法によって作製した各種 Gタンパク質共役型レセプタータンパク質 cDNA、すなわち甲状腺ホルモン刺激因子レセプター (TRHR)、ニューロメジン Uレセプター (FM-3 および TGR-1)、プロラクチン放出因子レセプター (hGR3)、アペリンレセプター (APJ) などを挿入した動物細胞用発現プラスミドを用いて、大腸菌 JM109 を形質転換し、得られたコロニーを単
15 離・培養後、QIAGEN Plasmid Maxi Kit (キアゲン) を用いてプラスミドの調製を行なった。また、cAMP レスポンスエレメント (CRE) の下流にレポーターとしてルシフェラーゼ遺伝子が連結された pCRE-Luc (Clontech) のレポータープラスミドを同様にして調製した。

Gタンパク質共役型レセプタータンパク質発現プラスミドおよびレポータープ
20 ラスミドを導入する宿主細胞として、ヒト HEK293 細胞を I 型コラーゲンでコートした 96 ウェル黒色プレート (ベクトンディッキンソン社) に 100,000 cells/well、培養液量 $100 \mu\text{l}$ で播種し、一晚培養した。同じく CHO (dhfr⁻) 細胞を pAKK0-111H で形質転換した CHO-mock 細胞をコスター社の 96 ウェル黒色プレートに 40,000 cells/well、培養液量 $100 \mu\text{l}$ で播種し、
25 一晚培養した。いずれの細胞についても、プレート培養するための培地として DMEM (GibcoBRL 社) に 10% のウシ胎児血清のみを添加したものを用了。

上記各プラスミドを $240 \text{ ng}/\mu\text{l}$ の濃度に希釈し、Gタンパク質共役型レセプタータンパク質の発現プラスミド $9 \mu\text{l}$ とレポータープラスミド $1 \mu\text{l}$ の割合で $240 \mu\text{l}$ の Opti-MEM-I (GibcoBRL 社) に添加した。これを、同じく 240

μ lのOpti-MEM-Iに10 μ lのリポフェクトアミン2000 (GibcoBRL社) を添加したものと等量混合して、リポフェクトアミン2000に添付の説明書の方法に従ってリポソームとプラスミドとの複合体を形成させた。また、効率的なスクリーニングの実施のためには、240 ng/ μ lの濃度で3種類のレセプター発現プラスミドを5 μ lずつ添加し、他の試薬の比率は前出と同じものを調製した。これらを25 μ l/wellずつHEK293あるいはCHO-mock細胞の培養液に添加し、37℃で一晩培養してプラスミドの導入を行った。CHO-mock細胞については、プラスミド添加後4時間以降に培養液をアッセイバッファー(0.1%のウシ血清アルブミンを添加したDMEM)に交換し、無血清化をおこなった。

参考例4 レポーターアッセイによるリガンド活性の検出

HEK293細胞についてはアッセイの1時間前に培養液を、参考例3に記載のアッセイバッファーに交換し、プレインキュベーションを行なった。アッセイバッファーにリガンドあるいはリガンド候補化合物を溶解したものを用意し、参考例3で準備したHEK293細胞またはCHO-mock細胞に添加した。また、アッセイバッファーに終濃度2 μ Mのフォルスコリンを添加した条件でのアッセイも同様にして実施した。リガンドまたは試験化合物の添加後4時間のインキュベーションを行ない、レセプターを介したリガンドのアゴニスト活性によって惹起される細胞内シグナル伝達に由来するレポーター遺伝子の転写・翻訳の促進あるいは抑制を誘導した。インキュベーション終了後に各ウェルのアッセイバッファーを除去し、ピッカジーンLT2.0 (東洋インキ社) 発光基質を50 μ lずつ加えた。細胞が溶解し、基質と十分に混合した後、各ウェルのレポーター遺伝子の発現誘導量に相当する発光量を参考例2記載のプレートリーダーにて測定した。

参考例3および4に記載の方法に従って各種のGタンパク質共役型レセプタータンパク質cDNAを挿入した発現プラスミドを用い、HEK293細胞においてリガンド刺激によるレポーター遺伝子の発現誘導を測定した。細胞内へシグナルを伝達するGタンパク質の α サブユニットとしてGsに共役するCRFRにつ

いては、フォルスコリン非添加、添加のいずれの条件においてもリガンド添加によるレポーター遺伝子の活性化が検出された。また、抑制性であるG i に共役するAP Jについては、フォルスコリン添加条件において、リガンド添加によるレポーター遺伝子発現の抑制が検出された。また、G q に共役するレセプターTR HR、FM-3、TGR-1については、フォルスコリン添加条件においてレポーター遺伝子の発現の促進が検出された。G q およびG i の両方に共役するレセプターhGR3についても、同様にフォルスコリン添加条件においてレポーター遺伝子の発現の促進が検出された（図2）。

10 参考例5 抑制性Gタンパク質 α サブユニットG i 発現プラスミドを用いたレポーターアッセイ

参考例3に示したGタンパク質レセプター発現プラスミドと同様の方法によって、抑制性Gタンパク質 α サブユニット(G i)の発現プラスミドを調製した（ここで、G i については、動物種を問わない）。これを3 μ l、レセプター発現プラスミドを7 μ l、レポータープラスミドを1 μ lの割合で240 μ lのOpti-ME M-Iに添加し、その他の条件は実施例2と同様の方法でHEK293あるいはCHO-mock細胞にDNAを導入した。これら3種のプラスミドの混合比は全体の量を11 μ lとした場合、G i が1から6 μ l、好ましくは1から3 μ lが
15 適当である。これらを実施例3の方法に従ってアッセイを行いリガンド活性を検出した。

すなわち、G i 共存下でのTGR5のリトコール酸に対する反応を検出した結果、CHO-mock細胞を用いたGタンパク質レセプターTGR5のアッセイにおいて、G i をTGR5と同時に発現させることにより、リガンド非添加時（リガンド（-））のルシフェラーゼ活性を大幅に低下させることができ、その結果リガンド（リトコール酸、 2×10^{-5} M、リガンド（+））による活性の上昇
25 を検出することが可能となった（図3）。

実施例1 CHO細胞に発現させたTGR5-GFP融合タンパク質のタウロリトコール酸添加による細胞内移行

TGR5のC末端にオワンクラゲより単離されたGreen Fluorescent Protein (GFP)をつないだ融合タンパク質を発現させるための発現プラスミドを構築した。その際GFPのcDNA (配列番号: 2) としてGFPの発現ベクターpQB125 (宝酒造) から切り出した断片を用いた。TGR5のcDNAはPCR法によりその終止コドン制限酵素Nhe Iの認識配列に修正し、ここにGFPのcDNA断片を連結して、実施例1に記載の発現ベクターpAKKO-111Hに挿入した。このようにして得たTGR5とGFPとの融合タンパク質 (以下、TGR5-GFP) の発現ベクタープラスミドを以下の方法でCHO-mock細胞にトランスフェクションした。CHO-mock細胞は増殖培地 [DMEM (Dulbecco's Modified Eagle Medium) (GIBCO BRL社) に10%ウシ胎児血清 (GIBCO BRL社) を添加したもの] に懸濁し、 0.6×10^5 cells/チャンバーの濃度にてチャンバー数4つのLab-Tek IIカバーガラスチャンバー (Nalgen Nunc社) にまき、37℃、5%CO₂条件下で一晩培養した後にトランスフェクションした。トランスフェクションにはLipofectamine™ 2000試薬 (GIBCO BRL社) を用いた。まず、Lipofectamine™ 2000 試薬 2μlとOPTI-MEM-I (GIBCO BRL社) 50μlを混合し、5分間放置後、これを0.48μgのDNAとOPTI-MEM-I 50μlの混合液と混ぜ合わせ、20分間室温で静置することによりDNAとリポフェクトアミンの複合体を形成させた。この混合液を上記のCHO細胞を培養したチャンバーに100μl添加し、さらに37℃、5%CO₂条件下で一晩培養した。培地を共焦点顕微鏡観察用培地 [Hanks' Balanced Salt Solution (GIBCO BRL社) に0.1%ウシアルブミン (Essentially Fatty Acid Free (GIBCO BRL社)) を懸濁したもの] に置き換え、共焦点顕微鏡 (ライカ社) でGFPの蛍光像を観察した。その際、GFPの励起は488nmで行った。

その結果TGR5-GFP融合タンパク質は細胞膜に観察された (図4)。この細胞にタウロリトコール酸を 10^{-5} Mとなるように培地に添加した30分後には、GFPの蛍光が細胞膜ではなく、細胞質に移動していることが見出された

(図5)。このことはTGR5が細胞膜に発現するGタンパク質共役型のレセプターであるとともに、TGR5がタウロリトコール酸に反応して細胞質へ移行、すなわちインタナリゼーションしたことを示す。

5 実施例2 膵臓β細胞株RINm5Fに一過性発現による副甲状腺ホルモン受容体(PTH-R)とGFP融合タンパク質の発現

- 実施例1と同様の方法でヒトPTH-R(配列番号:13)のC末端にGFPをつないだ融合タンパク質を発現させるための発現プラスミドを参考例2に記載の発現ベクターpAKKO-111Hに挿入した発現ベクターを作製した。この
- 10 ようにして得たPTH-RとGFPとの融合タンパク質(以下、PTH-GFP)の発現ベクタープラスミドを以下の方法でRINm5F細胞にトランスフェクションした。RINm5F細胞は増殖培地[RPMI1640(GIBCO BRL社)にCharcoal/Dextran処理済のウシ胎児血清(Hyclone社)を10%添加したもの]に懸濁し、 0.3×10^5 cells/チャ
- 15 ンバーの濃度にてチェンバー数8つのLab-TekIIカバーグラスチェンバー(Nalgen Nunc社)にまき、37℃、5%CO₂条件下で一晩培養した後、トランスフェクションした。トランスフェクションにはLipofectamine™ 2000 試薬(GIBCO BRL社)を用いた。まずLipofectamine™ 2000 試薬 3.3μlとOPTI-ME
- 20 M-I(GIBCO BRL社)80μlを混合し、5分間放置後、これを0.72μgのDNAとOPTI-MEM-I 80μlの混合液と混ぜ合わせ、20分間室温で静置することによりDNAとリポフェクトアミンの複合体を形成させた。この混合液を上記のRINm5F細胞を培養したチェンバーに160μl添加し、さらに37℃、5%CO₂条件下で一晩培養した。共焦点顕微鏡での観
- 25 察は実施例1と同様の方法で行った。

その結果PTH-GFP融合タンパク質の細胞膜での発現が観察された。

実施例3 インスリンIIプロモーターを用いたGPCRとGFP融合タンパク質の発現

実施例1と同様の方法で、マウスゲノムからクローニングしたマウスインスリンIIプロモーターの下流に、ヒトGPR40（配列番号：15）のC末端にGFPをつないだ断片を挿入し、GPR40とGFPとの融合タンパク質（以下、GPR40-GFP）を発現させるための発現ベクターを作製した。このようにして得たGPR40-GFPの発現ベクタープラスミドを以下の方法でMIN6細胞にトランスフェクションした。MIN6細胞は増殖培地 [DMEM (4.5 g/l Glucose含有) (Invitrogen社) に最終濃度ウシ胎児血清 (Trace社) を15%、55 μ M 2-mercaptoethanol (Invitrogen社)、20mM HEPES (大日本製薬社) をそれぞれ添加したもの] に懸濁し、 1.2×10^5 cells/チャンバーの濃度にてチャンバー数4つのLab Tek IIカバーグラスチャンバー (Nalge Nunc社) にまき、37℃、5% CO₂条件下で二晩培養した後にトランスフェクションした。トランスフェクションにはLipofectamineTM 2000 試薬 (Invitrogen社) を用いた。まずLipofectamineTM 2000 試薬4 μ lとOpti-MEM培地 (Invitrogen社) 100 μ lを混合し、5分間放置後、これを2 μ gのDNAとOpti-MEM培地100 μ lの混合液と混ぜ合わせ、20分間室温で静置することによりDNAとリポフェクトアミンの複合体を形成させた。この混合液を上記のMIN6細胞を培養したチャンバーに100 μ l添加し、37℃、5% CO₂条件下で4時間培養後、新たな増殖培地400 μ lに交換し、さらに一晩培養した。共焦点顕微鏡での観察は実施例1と同様の方法で行った。

その結果、GPR40-GFP融合タンパク質がMIN6細胞の細胞膜で発現しているのが観察された。

25 実施例4 102種類の融合タンパク質をそれぞれ発現し得る形質転換体の製造

実施例1の方法に準じて、リガンドが決定されていない102種類の各レセプタータンパク質と配列番号：1で表されるアミノ酸配列またはその改変アミノ酸配列からなるGFPとの融合タンパク質をコードするDNA（配列番号132～配列番号：233）をそれぞれ含有する102種類の発現ベクタープラスミドを

調製し、CHO-mock細胞にトランスフェクションした。これらのCHO細胞を実施例1と同様に培養したところ、融合タンパク質の発現がCHO-mock細胞に観察された。

5 産業上の利用可能性

本発明の、リガンドが決定されていないレセプタータンパク質のリガンドの決定方法は、各種の細胞系を使用できるため簡便であり、かつ短時間で実施することができる。

請求の範囲

1. リガンドが決定されていないレセプタータンパク質と蛍光タンパク質との融合タンパク質を用いることを特徴とする該レセプタータンパク質に対するリガンドの決定方法。
- 5 2. リガンドが決定されていないレセプタータンパク質とGFPとの融合タンパク質を用いることを特徴とする請求項1記載のリガンドの決定方法。
3. リガンドが決定されていないレセプタータンパク質とGFPとの融合タンパク質を発現している細胞またはその細胞膜画分と、試験化合物とを接触させることを特徴とする請求項1記載のリガンドの決定方法。
- 10 4. (1) アラキドン酸遊離、アセチルコリン遊離、細胞内Ca²⁺遊離、細胞内cAMP生成、細胞内cGMP生成、イノシトールリン酸産生、細胞膜電位変動、細胞内タンパク質のリン酸化、c-fos活性化またはpHの低下を促進する活性または抑制する活性、(2) MAPキナーゼの活性化、(3) 転写因子の活性化、(4) ジアシルグリセロール産生、(5) 細胞膜上のイオンチャネルの開閉、(6) アポトーシスの誘導、(7) 形態変化、(8) 該融合タンパク質の細胞膜から細胞質への移行、(9) 低分子量Gタンパク質の活性化、(10) 細胞分裂促進活性または(11) DNA合成促進活性を測定することを特徴とする請求項1記載のリガンドの決定方法。
- 15 5. 該融合タンパク質の細胞膜から細胞質への移行を測定することを特徴とする請求項1記載のリガンドの決定方法。
6. GFP蛍光を観察することにより該融合タンパク質の細胞膜から細胞質への移行を測定する請求項5記載のリガンドの決定方法。
7. リガンドが決定されていないレセプタータンパク質と蛍光タンパク質との融合タンパク質を発現し、かつ、cAMPレスポンスエレメント/プロモーターの下流にレポータータンパク質をコードするDNAを連結したプラスミドを含有する細胞と試験化合物とを接触させて、レポータータンパク質の活性を測定することを特徴とする請求項1記載のリガンドの決定方法。
- 25 8. (1) リガンドが決定されていないレセプタータンパク質と蛍光タンパク質との融合タンパク質をコードするDNAを含有するプラスミドおよび(2) cA

MPレスポンスエレメント／プロモーターの下流にレポータータンパク質をコードするDNAを連結したプラスミドを含有する細胞を培養し、試験化合物と接触させてレポータータンパク質の活性を測定することを特徴とする請求項7記載の方法。

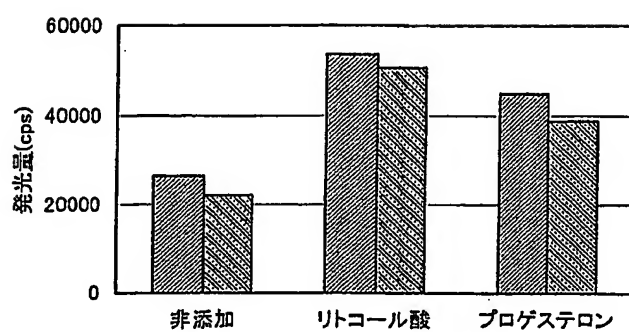
- 5 9. リガンドが決定されていないレセプタータンパク質とGFPとの融合タンパク質を発現し、かつ、cAMPレスポンスエレメント／プロモーターの下流にレポータータンパク質をコードするDNAを連結したプラスミドを含有する細胞と試験化合物とを接触させて、レポータータンパク質の活性を測定することを特徴とする請求項2記載のリガンドの決定方法。
- 10 10. (1) リガンドが決定されていないレセプタータンパク質とGFPとの融合タンパク質をコードするDNAを含有するプラスミドおよび(2) cAMPレスポンスエレメント／プロモーターの下流にレポータータンパク質をコードするDNAを連結したプラスミドを含有する細胞を培養し、試験化合物と接触させてレポータータンパク質の活性を測定することを特徴とする請求項9記載の方法。
- 15 11. レセプタータンパク質がGタンパク質共役型レセプタータンパク質である請求項1記載の方法。
12. GFPが配列番号：1、配列番号：3、配列番号：5または配列番号：7で表わされるアミノ酸配列と同一または実質的に同一のアミノ酸配列を含有するタンパク質である請求項1記載の方法。
- 20 13. プロモーターがTATA様配列である請求項7記載の方法。
14. レポータータンパク質がルシフェラーゼである請求項7記載の方法。
15. プラスミドがcAMPレスポンスエレメントの下流にTATA様プロモーターおよびレポータータンパク質をコードする遺伝子を連結したものである請求項7記載の方法。
- 25 16. 細胞が、リガンドが決定されていない2種類以上のレセプタータンパク質を発現している請求項7記載の方法。
17. 細胞が、抑制性Gタンパク質 α サブユニットGiをコードする遺伝子を含有するプラスミドを更に含有する請求項7記載の方法。
18. さらにフォルスコリンを添加する請求項7記載の方法。

19. 2種類以上のレセプタータンパク質が類似の特徴を有することを特徴とする請求項16記載の方法。
20. 類似の特徴がレポータータンパク質の基礎発現量および（または）フォルスコリン添加時のレポータータンパク質の発現量である請求項19記載の方法。
- 5 21. 予め2種類以上のレセプタータンパク質をそれぞれ単独で発現させた時のレポータータンパク質の基礎発現量および／またはフォルスコリン添加時のレポータータンパク質の発現量を測定し、該レポータータンパク質の発現量が同程度である2種類以上のレセプタータンパク質を組み合わせることを特徴とする請求項16記載の方法。
- 10 22. リガンドが決定されていないレセプタータンパク質と蛍光タンパク質との融合タンパク質またはその塩。
23. 蛍光タンパク質がGFPである請求項22記載の融合タンパク質またはその塩。
24. 請求項22記載の融合タンパク質をコードするDNAを含有するDNA。
- 15 25. 請求項24記載のDNAを含有する組換えベクター。
26. 請求項25記載の組換えベクターで形質転換させた形質転換体。
27. リガンドが決定されていないレセプタータンパク質に対するリガンドを決定するための蛍光タンパク質の使用。
28. リガンドが決定されていないレセプタータンパク質に対するリガンドを決定するためのGFPの使用。
- 20

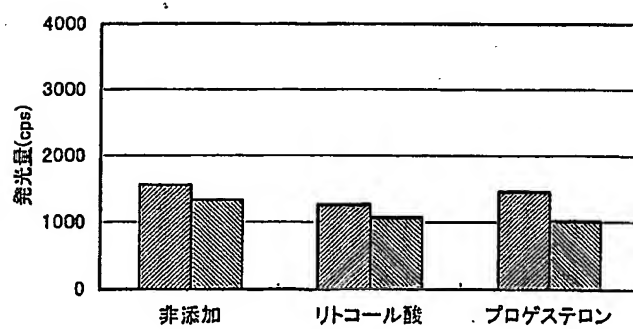
1/5

図 1

A

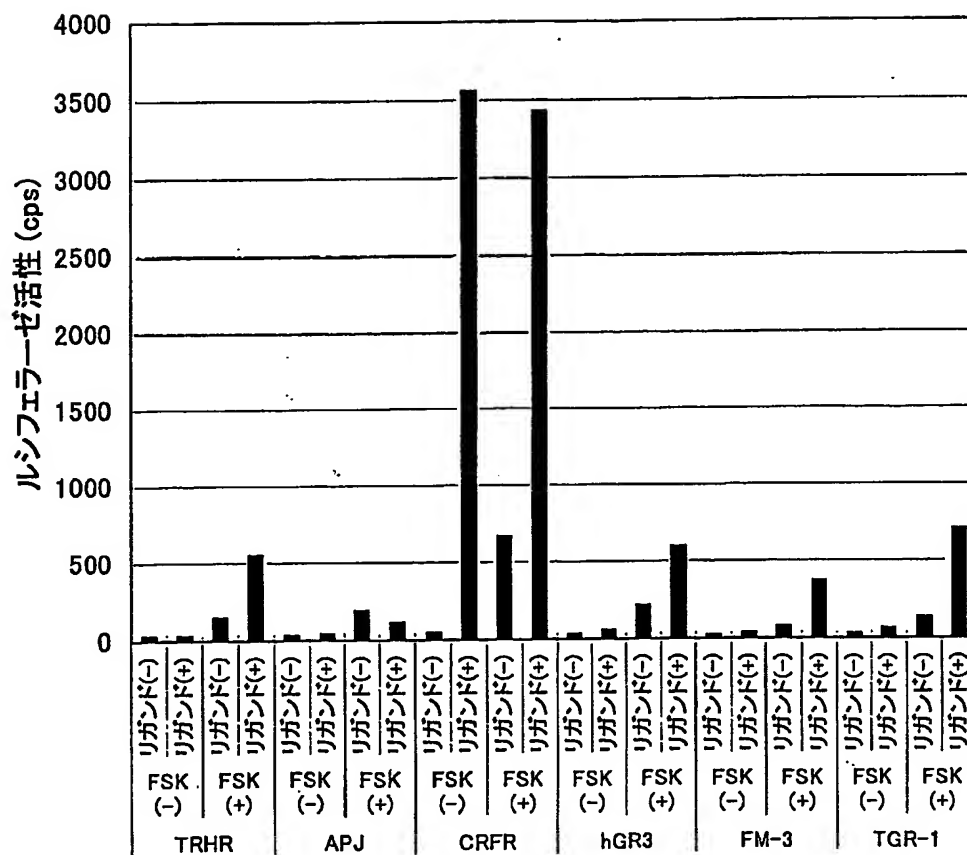


B



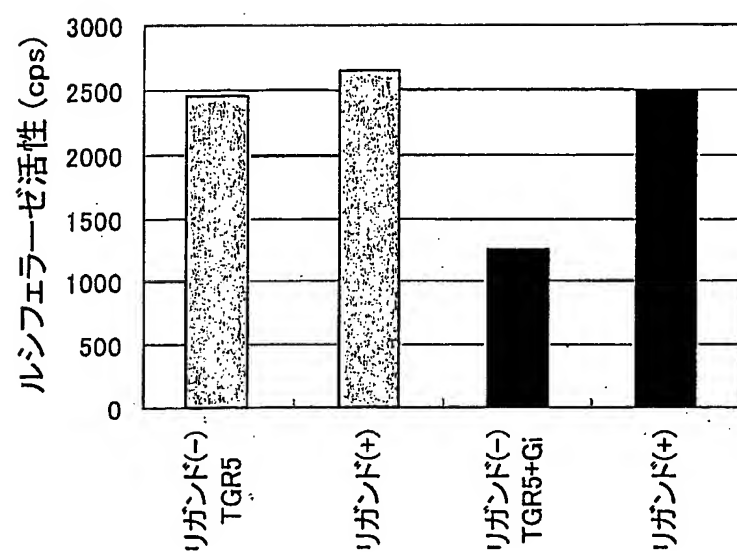
2/5

図 2



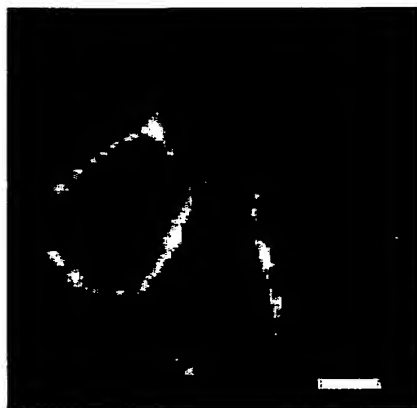
3/5

図 3



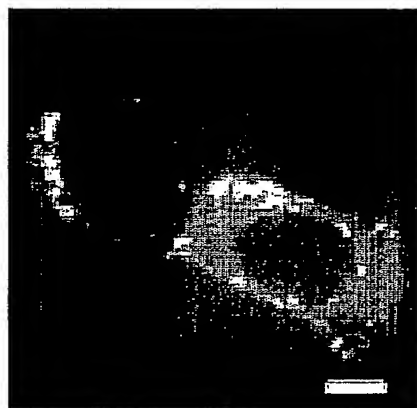
4/5

図 4



5/5

図 5



1/518

SEQUENCE LISTING

<110> Takeda Chemical Industries, Ltd.

<120> Determination of a ligand

<130> P03-0006PCT

<150> JP 2002-45728

<151> 2002-02-22

<150> JP 2002-213949

<151> 2002-07-23

<150> JP 2002-298237

<151> 2002-10-11

<160> 233

<210> 1

<211> 239

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of wild-type GFP

<400> 1

Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu

2/518

	5		10		15
Val	Glu	Leu	Asp	Gly	Asp
		Val	Asn	Gly	His
			Lys	Phe	Ser
				Val	Ser
				Gly	
	20		25		30
Glu	Gly	Glu	Gly	Asp	Ala
		Thr	Tyr	Gly	Lys
			Leu	Thr	Leu
				Lys	Phe
				Ile	
	35		40		45
Cys	Thr	Thr	Gly	Lys	Leu
		Pro	Val	Pro	Trp
			Pro	Thr	Leu
				Val	Thr
				Thr	
	50		55		60
Leu	Cys	Tyr	Gly	Val	Gln
		Cys	Phe	Ser	Arg
			Tyr	Pro	Asp
				His	Met
				Lys	
	65		70		75
					80
Arg	His	Asp	Phe	Phe	Lys
		Ser	Ala	Met	Pro
			Glu	Gly	Tyr
				Val	Gln
				Glu	
	85		90		95
Arg	Thr	Ile	Phe	Phe	Lys
		Asp	Asp	Gly	Asn
			Tyr	Lys	Thr
				Arg	Ala
				Glu	
	100		105		110
Val	Lys	Phe	Glu	Gly	Asp
		Thr	Leu	Val	Asn
			Arg	Ile	Glu
				Leu	Lys
				Gly	
	115		120		125
Ile	Asp	Phe	Lys	Glu	Asp
		Gly	Asn	Ile	Leu
			Gly	His	Lys
				Leu	Glu
				Tyr	
	130		135		140
Asn	Tyr	Asn	Ser	His	Asn
		Val	Tyr	Ile	Met
			Ala	Asp	Lys
				Gln	Lys
				Asn	
	145		150		155
					160
Gly	Ile	Lys	Val	Asn	Phe
		Lys	Thr	Arg	His
			Asn	Ile	Glu
				Asp	Gly
				Ser	
	165		170		175
Val	Gln	Leu	Ala	Asp	His
		Tyr	Gln	Gln	Asn
			Thr	Pro	Ile
				Gly	Asp
				Gly	
	180		185		190
Pro	Val	Leu	Leu	Pro	Asp
		Asn	His	Tyr	Leu
			Ser	Thr	Gln
				Ser	Ala
				Leu	
	195		200		205
Ser	Lys	Asp	Pro	Asn	Glu
		Lys	Arg	Asp	His
			Met	Val	Leu
				Leu	Glu
				Phe	
	210		215		220
Val	Thr	Ala	Ala	Gly	Ile
		Thr	His	Gly	Met
			Asp	Glu	Leu
				Tyr	Asn
	225		230		235

3/518

<210> 2

<211> 717

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of wild-type GFP cDNA

<400> 2

```
atggctagca aaggagaaga actcttcact ggagttgtcc caattcttgt tgaattagat    60
ggtgatgitta acggccacaa gttctctgtc agtggagagg gtgaaggta tgcaacatac    120
ggaaaactta cctgaagtt catctgcact actggcaaac tgcctgttcc atggccaaca    180
ctagtcacta ctctgtgcta tggigttaa tgcttttcaa gatacccgga tcatatgaaa    240
cggcatgact ttttcaagag tgccatgccc gaaggttatg tacaggaaag gaccatcttc    300
ttcaaagatg acggcaacta caagacacgt gctgaagtca agtttgaagg tgataccctt    360
gttaatagaa tcgagttaaa aggtattgac ttcaaggaag atggcaacat tctgggacac    420
aaattggaat acaactataa ctacacaaat gtatacatca tggcagacaa acaaaagaat    480
ggaatcaaag tgaacttcaa gaccgcccac aacattgaag atggaagcgt tcaactagca    540
gaccattatc aacaaaatac tccaattggc gatggccctg tccttttacc agacaacat    600
tacctgtcca cacaatctgc cttttcgaaa gatcccaacg aaaagagaga ccacatggtc    660
cttcttgagt ttgtaacagc tgctgggatt acacatggca tggatgaact gtacaac    717
```

<210> 3

<211> 238

<212> PRT

<213> *Aequorea coerulescens*

<400> 3

4/518

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 5 10 15
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60
 Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140
 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160
 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
 165 170 175
 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
 180 185 190
 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
 195 200 205
 Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
 210 215 220
 Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys

5/518

225

230

235

<210> 4

<211> 714

<212> DNA

<213> *Aequorea coerulescens*

<400> 4

```

atgagtaaag gagaagaact tttcactgga gtigtcccaa ttcttgttga attagatggt    60
gatgttaatg ggcacaaatt ttctgtcagt ggagagggig aaggtgatgc aacatacgga    120
aaacttacc ttaaatttat tggcactact ggaaaactac ctgttccatg gccaacactt    180
gtcactactt tctcttatgg tgttcaatgc ttttcaagat acccagatca tatgaaacgg    240
catgactttt tcaagagtgc catgcccga ggttatgtac aggaaagaac tatatttttc    300
aaagatgacg ggaactacaa gacacgtgct gaagtcaagt ttgaaggatg tacccttggt    360
aatagaatcg agttaaaagg tattgatit t aaagaagatg gaaacattct tggacacaaa    420
ttggaataca actataactc acacaatgta tacatcatgg cagacaaaca aaagaatgga    480
atcaaagtta acttcaaaat tagacacaac attgaagatg gaagcgttca actagcagac    540
cattatcaac aaaatactcc aatigggcat ggccctgtcc ttttaccaga caaccattac    600
ctgtccacac aatctgccct ttcgaaagat cccaacgaaa agagagacca catggtcctt    660
cttgagtttg taacagctgc tgggattaca catggcatgg atgaactata caaa          714

```

<210> 5

<211> 238

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of wild-type GFP

6/518

<400> 5

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val

5

10

15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu

20

25

30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys

35

40

45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe

50

55

60

Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg

65

70

75

80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg

85

90

95

Thr Ile Ser Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val

100

105

110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile

115

120

125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn

130

135

140

Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly

145

150

155

160

Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val

165

170

175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro

180

185

190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser

195

200

205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val

210

215

220

7/518

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys

225

230

235

<210> 6

<211> 714

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of wild-type GFP cDNA

<400> 6

```

atgagtaaag gagaagaact ttctactgga gttgtcccaa ttcttggtga attagatggt    60
gatgttaatg ggcacaaatt ttctgtcagt ggagagggtg aaggatgatc aacatacggg    120
aaacttaccc tttaaatttat ttgcactact ggaaaactac ctgttccatg gccaacactt    180
gtcactactt tctcttatgg tgttcaatgc ttttcccggt atccggatca tatgaaacgg    240
catgactttt tcaagagtgc catgcccga ggttatgtac aggaacgcac tatatctttc    300
aaagatgacg ggaactacaa gacgcgtgct gaagtcaagt ttgaaggatg tacccttggt    360
aatcgtatcg agttaaaagg tattgatatt aaagaagatg gaaacattct cggacacaaa    420
ctcgagtaca actataactc acacaatgta tacatcacgg cagacaaaca aaagaatgga    480
atcaaagcta acttcaaaat tcgccacaac attgaagatg gatccgttca actagcagac    540
cattatcaac aaaatactcc aattggcgat ggccctgtcc ttttaccaga caaccattac    600
ctgtcgacac aatctgccct ttcgaaagat cccaacgaaa agcgtgacca catggtcctt    660
cttgagtttg taactgctgc tgggattaca catggcatgg atgagctcta caaa          714

```

<210> 7

<211> 239

<212> PRT

<213> Artificial Sequence

8/518

<220>

<223> Variant of wild-type GFP

<400> 7

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 5 10 15
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60
 Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80
 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160
 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190

9/518

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220
 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 225 230 235

<210> 8

<211> 717

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of wild-type GFP cDNA

<400> 8

atggtgagca agggcgagga gctgttcacc ggggtggtgc ccatcctggt cgagctggac 60
 ggcgacgtaa acggccacaa gttcagcgtg tccggcgagg gcgagggcga tgccacctac 120
 ggcaagctga ccctgaagtt catctgcacc accggcaagc tgcccgtgcc ctggcccacc 180
 ctcgtgacca ccctgacctg cggcgtgcag tgcttcagcc gctaccccga ccacatgaag 240
 cagcacgact tcttcaagtc cgccatgccc gaaggctacg tccaggagcg caccatcttc 300
 ttcaaggacg acggcaacta caagacccgc gccgaggtga agttcgaggg cgacaccctg 360
 gtgaaccgca tcgagctgaa gggcatcgac ttcaaggagg acggcaacat cctggggcac 420
 aagctggagt acaactacaa cagccacaac gtctatatca tggccgacaa gcagaagaac 480
 ggcataaagg tgaacttcaa gatccgccac aacatcgagg acggcagcgt gcagctcgcc 540
 gaccactacc agcagaacac ccccatcggc gacggccccg tgcgtgctgcc cgacaaccac 600
 tacctgagca cccagtcgcg cctgagcaaa gaccccaacg agaagcgcgga tcacatggtc 660
 ctgctggagi tcgtgaccgc cgccgggatc actctcggca tggacgagct gtacaag 717

10/518

<210> 9

<211> 330

<212> PRT

<213> Human

<400> 9

Met Thr Pro Asn Ser Thr Gly Glu Val Pro Ser Pro Ile Pro Lys Gly
 5 10 15
 Ala Leu Gly Leu Ser Leu Ala Leu Ala Ser Leu Ile Ile Thr Ala Asn
 20 25 30
 Leu Leu Leu Ala Leu Gly Ile Ala Trp Asp Arg Arg Leu Arg Ser Pro
 35 40 45
 Pro Ala Gly Cys Phe Phe Leu Ser Leu Leu Leu Ala Gly Leu Leu Thr
 50 55 60
 Gly Leu Ala Leu Pro Thr Leu Pro Gly Leu Trp Asn Gln Ser Arg Arg
 65 70 75 80
 Gly Tyr Trp Ser Cys Leu Leu Val Tyr Leu Ala Pro Asn Phe Ser Phe
 85 90 95
 Leu Ser Leu Leu Ala Asn Leu Leu Leu Val His Gly Glu Arg Tyr Met
 100 105 110
 Ala Val Leu Arg Pro Leu Gln Pro Pro Gly Ser Ile Arg Leu Ala Leu
 115 120 125
 Leu Leu Thr Trp Ala Gly Pro Leu Leu Phe Ala Ser Leu Pro Ala Leu
 130 135 140
 Gly Trp Asn His Trp Thr Pro Gly Ala Asn Cys Ser Ser Gln Ala Ile
 145 150 155 160
 Phe Pro Ala Pro Tyr Leu Tyr Leu Glu Val Tyr Gly Leu Leu Leu Pro
 165 170 175
 Ala Val Gly Ala Ala Ala Phe Leu Ser Val Arg Val Leu Ala Thr Ala

11/518

180	185	190	
His Arg Gln Leu Gln Asp Ile Cys Arg Leu Glu Arg Ala Val Cys Arg			
195	200	205	
Asp Glu Pro Ser Ala Leu Ala Arg Ala Leu Thr Trp Arg Gln Ala Arg			
210	215	220	
Ala Gln Ala Gly Ala Met Leu Leu Phe Gly Leu Cys Trp Gly Pro Tyr			
225	230	235	240
Val Ala Thr Leu Leu Leu Ser Val Leu Ala Tyr Glu Gln Arg Pro Pro			
245	250	255	
Leu Gly Pro Gly Thr Leu Leu Ser Leu Leu Ser Leu Gly Ser Ala Ser			
260	265	270	
Ala Ala Ala Val Pro Val Ala Met Gly Leu Gly Asp Gln Arg Tyr Thr			
275	280	285	
Ala Pro Tyr Arg Ala Ala Ala Gln Arg Cys Leu Gln Gly Leu Trp Gly			
290	295	300	
Arg Ala Ser Arg Asp Ser Pro Gly Pro Ser Ile Ala Tyr His Pro Ser			
305	310	315	320
Ser Gln Ser Ser Val Asp Leu Asp Leu Asn			
325	330		

<210> 10

<211> 990

<212> DNA

<213> Human

<400> 10

atgacgccca acagcactgg cgaggtgccc agccccattc ccaagggggc ttggggctc	60
tccctggccc tggcaagcct catcatcacc gcgaacctgc tcctagccct gggcatcgcc	120
tgggaccgcc gccctgcgag cccacctgct ggctgcttct tcctgagcct actgctggct	180

12/518

```

gggctgctca cgggtctggc attgcccaca ttgccagggc tgtggaacca gagtcgccgg 240
ggttactggg cctgcctcct cgtctacttg gctcccaact tctccttctt ctccttgctt 300
gccaaacctt tgctggigca cggggagcgc tacatggcag tcctgaggcc actccagccc 360
cctgggagca ttcggctggc cctgtccttc acctgggctg gtcccttctt ctttgccagt 420
ctgcccgttc tgggtggaa ccactggacc cctggtgcca actgcagctc ccaggctatc 480
ttcccagccc cctacctgta cctcgaagtc tatgggtccc tgctgccgcg cgtgggtgct 540
gtgccttccc tctctgtccg cgtgtggcc actgcccacc gccagctgca ggacatctgc 600
cggctggagc gggcagtggt ccgcgatgag cctccgccc tggcccgggc cttacctgg 660
aggcaggcaa gggcacaggc tggagccatg ctgtcttctg ggctgtgctg ggggccctac 720
gtggccacac tgctcctctc agtcttggcc tatgagcagc gcccgccact ggggcctggg 780
acactgttgt cctcctcttc cctaggaagt gccagtgcag cggcagtgcc cgtagccatg 840
gggctgggcg atcagcgcta cacagcccc tggagggcag ccgccc aaag gtgcctgcag 900
gggctgtggg gaagagcctc ccgggacagt cccggcccca gcattgccta ccaccaagc 960
agccaaagca gtgtcgacct ggacttgaac 990

```

<210> 11

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer to amplify DNA encoding TGR5

<400> 11

```

gatgacgccc aacagcactg gcgaggtgcc 30

```

<210> 12

<211> 31

<212> DNA

13/518

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer to amplify DNA encoding TGR5

<400> 12

ttagttcaag tccaggtcga cactgctttg g 31

<210> 13

<211> 593

<212> PRT

<213> Human

<400> 13

Met Gly Thr Ala Arg Ile Ala Pro Gly Leu Ala Leu Leu Leu Cys Cys

5

10

15

Pro Val Leu Ser Ser Ala Tyr Ala Leu Val Asp Ala Asp Asp Val Met

20

25

30

Thr Lys Glu Glu Gln Ile Phe Leu Leu His Arg Ala Gln Ala Gln Cys

35

40

45

Glu Lys Arg Leu Lys Glu Val Leu Gln Arg Pro Ala Ser Ile Met Glu

50

55

60

Ser Asp Lys Gly Trp Thr Ser Ala Ser Thr Ser Gly Lys Pro Arg Lys

65

70

75

80

Asp Lys Ala Ser Gly Lys Leu Tyr Pro Glu Ser Glu Glu Asp Lys Glu

85

90

95

Ala Pro Thr Gly Ser Arg Tyr Arg Gly Arg Pro Cys Leu Pro Glu Trp

100

105

110

Asp His Ile Leu Cys Trp Pro Leu Gly Ala Pro Gly Glu Val Val Ala

14/518

115	120	125
Val Pro Cys Pro Asp Tyr Ile Tyr Asp Phe Asn His Lys Gly His Ala		
130	135	140
Tyr Arg Arg Cys Asp Arg Asn Gly Ser Trp Glu Leu Val Pro Gly His		
145	150	155
Asn Arg Thr Trp Ala Asn Tyr Ser Glu Cys Val Lys Phe Leu Thr Asn		
165	170	175
Glu Thr Arg Glu Arg Glu Val Phe Asp Arg Leu Gly Met Ile Tyr Thr		
180	185	190
Val Gly Tyr Ser Val Ser Leu Ala Ser Leu Thr Val Ala Val Leu Ile		
195	200	205
Leu Ala Tyr Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His Met		
210	215	220
His Leu Phe Leu Ser Phe Met Leu Arg Ala Val Ser Ile Phe Val Lys		
225	230	235
Asp Ala Val Leu Tyr Ser Gly Ala Thr Leu Asp Glu Ala Glu Arg Leu		
245	250	255
Thr Glu Glu Glu Leu Arg Ala Ile Ala Gln Ala Pro Pro Pro Pro Ala		
260	265	270
Thr Ala Ala Ala Gly Tyr Ala Gly Cys Arg Val Ala Val Thr Phe Phe		
275	280	285
Leu Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly Leu		
290	295	300
Tyr Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser Glu Lys Lys Tyr		
305	310	315
Leu Trp Gly Phe Thr Val Phe Gly Trp Gly Leu Pro Ala Val Phe Val		
325	330	335
Ala Val Trp Val Ser Val Arg Ala Thr Leu Ala Asn Thr Gly Cys Trp		
340	345	350

15/518

Asp Leu Ser Ser Gly Asn Lys Lys Trp Ile Ile Gln Val Pro Ile Leu
 355 360 365
 Ala Ser Ile Val Leu Asn Phe Ile Leu Phe Ile Asn Ile Val Arg Val
 370 375 380
 Leu Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys Asp Thr Arg
 385 390 395 400
 Gln Gln Tyr Arg Lys Leu Leu Lys Ser Thr Leu Val Leu Met Pro Leu
 405 410 415
 Phe Gly Val His Tyr Ile Val Phe Met Ala Thr Pro Tyr Thr Glu Val
 420 425 430
 Ser Gly Thr Leu Trp Gln Val Gln Met His Tyr Glu Met Leu Phe Asn
 435 440 445
 Ser Phe Gln Gly Phe Phe Val Ala Ile Ile Tyr Cys Phe Cys Asn Gly
 450 455 460
 Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala
 465 470 475 480
 Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr
 485 490 495
 Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Val
 500 505 510
 Gly Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala Thr Thr
 515 520 525
 Asn Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr Pro Ala
 530 535 540
 Leu Glu Thr Leu Glu Thr Thr Pro Pro Ala Met Ala Ala Pro Lys Asp
 545 550 555 560
 Asp Gly Phe Leu Asn Gly Ser Cys Ser Gly Leu Asp Glu Glu Ala Ser
 565 570 575
 Gly Pro Glu Arg Pro Pro Ala Leu Leu Gln Glu Glu Trp Glu Thr Val

16/518

580

585

590

Met

<210> 14

<211> 1779

<212> DNA

<213> Human

<400> 14

```

atggggaccg cccggatcgc acccggcctg gcgctcctgc tctgctgcc cgtgctcagc   60
tccgcgtacg cgctgggtga tgcagatgac gtcatgacta aagaggaaca gatcttccig  120
ctgcaccgtg ctccaggcca gtgcgaaaaa cggctcaagg aggtcctgca gaggccagcc  180
agcataatgg aatcagacaa gggatggaca tctgcgtcca catcaggga gcccaggaaa  240
gataaggcat ctgggaagct ctacctgag tctgaggagg acaaggaggc acccactggc  300
agcaggtacc gagggcgccc ctgtctgcc gaatgggacc acatcctgtg ctggccgctg  360
ggggcaccag gtgaggtggt ggctgtgcc tgtccgact acatttatga cttcaatcac  420
aaaggccatg cctaccgacg ctgtgaccgc aatggcagct gggagctggt gcctgggcac  480
aacaggacgt gggccaacta cagcgagtgt gtcaaatttc tcaccaatga gactcgtgaa  540
cgggaggtgt ttgaccgcct gggcatgatt tacaccgtgg gctactccgt gtccttgccg  600
tccctcaccg tagctgtgct catcctggcc tactttaggc ggctgcactg cacgcgcaac  660
tacatccaca tgcacctgtt cctgtccttc atgtgcgcg ccgtgagcat cttcgtcaag  720
gacgctgtgc tctactctgg cgccacgctt gatgaggctg agcgccctac cgaggaggag  780
ctgcgcgcca tcgccaggc gccccgccg cctgccaccg ccgtgccgg ctacgcgggc  840
tgcagggtgg ctgtgacctt cttcctttac ttctggcca ccaactacta ctggattctg  900
gtggaggggc tgtacctgca cagcctcatc ttcatggcct tcttctcaga gaagaagtac  960
ctgtggggct tcacagtctt cggctggggt ctgccgctg tcttcgtggc tgtgtgggtc 1020
agtgtcagag ctacctggc caacaccggg tgctgggact tgagctccgg gaacaaaaag 1080
tggatcatcc agtgcccat cctggcctcc attgtgtca acttcatcct cttcatcaat 1140
atcgtccggg tgctgccac caagctgcg gagaccaacg ccggccggtg tgacacacgg 1200

```

17/518

```

cagcagtacc ggaagctgct caaatccacg ctggtgctca tgccctctt tggcgctccac 1260
tacattgtct tcatggccac accatacacc gaggctcag ggacgctctg gcaagtcag 1320
atgcactatg agatgctctt caactccttc cagggatit tigtcgcaat catatactgt 1380
ttctgcaatg gcgaggtaca agctgagatc aagaaatctt ggagccgctg gacactggca 1440
ctggacttca agcgaaaggc acgcagcggg agcagcagct atagctacgg ccccatgggtg 1500
tcccacacaa gtgtgaccaa tgtcggcccc cgtgtgggac tcggcctgcc cctcagcccc 1560
cgcctactgc ccactgccac caccaacggc caccctcagc tgccitggcca tgccaagcca 1620
gggaccccag ccttgagac cctcgagacc acaccacctg ccatggctgc tcccaaggac 1680
gatgggttcc tcaacggctc ctgctcaggc ctggacgagg aggcctctgg gcctgagcgg 1740
ccacctgccc tgctacagga agagtgggag acagtcatg 1779

```

<210> 15

<211> 300

<212> PRT

<213> Human

<400> 15

Met Asp Leu Pro Pro Gln Leu Ser Phe Gly Leu Tyr Val Ala Ala Phe

5

10

15

Ala Leu Gly Phe Pro Leu Asn Val Leu Ala Ile Arg Gly Ala Thr Ala

20

25

30

His Ala Arg Leu Arg Leu Thr Pro Ser Leu Val Tyr Ala Leu Asn Leu

35

40

45

Gly Cys Ser Asp Leu Leu Leu Thr Val Ser Leu Pro Leu Lys Ala Val

50

55

60

Glu Ala Leu Ala Ser Gly Ala Trp Pro Leu Pro Ala Ser Leu Cys Pro

65

70

75

80

Val Phe Ala Val Ala His Phe Phe Pro Leu Tyr Ala Gly Gly Gly Phe

85

90

95

18/518

Leu Ala Ala Leu Ser Ala Gly Arg Tyr Leu Gly Ala Ala Phe Pro Leu
 100 105 110
 Gly Tyr Gln Ala Phe Arg Arg Pro Cys Tyr Ser Trp Gly Val Cys Ala
 115 120 125
 Ala Ile Trp Ala Leu Val Leu Cys His Leu Gly Leu Val Phe Gly Leu
 130 135 140
 Glu Ala Pro Gly Gly Trp Leu Asp His Ser Asn Thr Ser Leu Gly Ile
 145 150 155 160
 Asn Thr Pro Val Asn Gly Ser Pro Val Cys Leu Glu Ala Trp Asp Pro
 165 170 175
 Ala Ser Ala Gly Pro Ala Arg Phe Ser Leu Ser Leu Leu Leu Phe Phe
 180 185 190
 Leu Pro Leu Ala Ile Thr Ala Phe Cys Tyr Val Gly Cys Leu Arg Ala
 195 200 205
 Leu Ala Arg Ser Gly Leu Thr His Arg Arg Lys Leu Arg Ala Ala Trp
 210 215 220
 Val Ala Gly Gly Ala Leu Leu Thr Leu Leu Leu Cys Val Gly Pro Tyr
 225 230 235 240
 Asn Ala Ser Asn Val Ala Ser Phe Leu Tyr Pro Asn Leu Gly Gly Ser
 245 250 255
 Trp Arg Lys Leu Gly Leu Ile Thr Gly Ala Trp Ser Val Val Leu Asn
 260 265 270
 Pro Leu Val Thr Gly Tyr Leu Gly Arg Gly Pro Gly Leu Lys Thr Val
 275 280 285
 Cys Ala Ala Arg Thr Gln Gly Gly Lys Ser Gln Lys
 290 295 300

<210> 16

<211> 900

19/518

<212> DNA

<213> Human

<400> 16

```
atggacctgc ccccgagct ctccctcggc ctctatgtgg ccgccittgc gctgggcttc    60
ccgctcaacg tccitggccat ccgaggcgcg acggcccacg cccggctccg tctcaccct    120
agcctggict acgccctgaa cctgggctgc tccgacctgc tctgacagt ctctctgccc    180
ctgaaggcgg tggaggcgct agcctccggg gccitggcctc tgccggcctc gctgtgcccc    240
gtcttcgcgg tggcccactt ctccccactc tatgccggcg ggggcttctt ggccgccctg    300
agtgcaggcc gctacctggg agcagccttc cctitgggct accaagcctt ccggaggccg    360
tgctattcct ggggggtgtg cgcggccatc tgggccctcg tctgtgtca cctgggtctg    420
gtctttgggt tggaggctcc aggaggctgg ctggaccaca gcaacacctc cctgggcac    480
aacacaccgg tcaacggctc tccggtctgc ctggaggcct gggaccggc ctctgccggc    540
ccggcccgtt tcagcctctc tctcctgctc tttttctgc ccttggccat cacagccttc    600
tgctacgtgg gctgccctcg ggcactggcc cgctccggcc tgacgcacag gcggaagctg    660
cgggccgcct ggggtggccg cggggccctc ctacagctgc tgctctgctt aggaccctac    720
aacgcctcca acgtggccag ctccctgtac cccaatctag gaggtcctg gcggaagctg    780
gggctcalca cgggtgcctg gagtgtgtg cttaatccgc tggtgaccgg ttacttggga    840
aggggtcctg gcctgaagac agtgtgtgcg gcaagaacgc aagggggcaa gtcccagaag    900
```

<210> 17

<211> 6

<212> PRT

<213> Artificial sequence

<220>

<223> His-tag

<400> 17

20/518

His His His His His His

1 5

<210> 18

<211> 14

<212> PRT

<213> Artificial sequence

<220>

<223> V5-tag

<400> 18

Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr

1 5 10

<210> 19

<211> 10

<212> PRT

<213> Artificial sequence

<220>

<223> myc-tag

<400> 19

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu

1 5 10

<210> 20

<211> 8

21/518

<212> PRT

<213> Artificial sequence

<220>

<223> Xpress-tag

<400> 20

Asp Leu Tyr Asp Asp Asp Asp Lys

1 5

<210> 21

<211> 16

<212> PRT

<213> Artificial sequence

<220>

<223> HA-tag

<400> 21

Met Gly Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser Leu Glu Phe

1 5 10 15

<210> 22

<211> 239

<212> PRT

<213> Artificial sequence

<220>

<223> Variant of wild-type GFP

22/518

<400> 22

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 5 10 15
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60
 Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80
 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140
 Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
 145 150 155 160
 Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe

23/518

210	215	220
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys		
225	230	235

<210> 23

<211> 720

<212> DNA

<213> Artificial sequence

<220>

<223> Variant of wild-type GFP cDNA

<400> 23

```

atggtgagca agggcgagga gctgttcacc ggggtggtgc ccatcctggt cgagctggac    60
ggcgacglaa acggccacaa gttcagcgtg tccggcgagg gcgagggcga tgccacctac    120
ggcaagctga ccctgaagtt catctgcacc accggcaagc tggccgtgcc ctggcccacc    180
ctcgtgacca ccctgacctg gggcgtgcag tgcctcagcc gctaccccga ccacatgaag    240
cagcagcact tcttcaagtc cgccatgccc gaaggctacg tccaggagcg caccatcttc    300
ttcaaggacg acggcaacta caagaccgcg gccgaggtga agttcgaggg cgacaccctg    360
gtgaaccgca tcgagctgaa gggcatcgac ttcaaggagg acggcaacat cctggggcac    420
aagctggagt acaactacat cagccacaac gtctatatca ccgccgacaa gcagaagaac    480
ggcatcaagg ccaacttcaa gatccgccac aacatcgagg acggcagcgt gcagctcgcc    540
gaccactacc agcagaacac ccccatcggc gacggccccg tgctgctgcc cgacaaccac    600
tacctgagca ccagtcctgc cctgagcaaa gaccccaacg agaagcgcga tcacatggtc    660
ctgctggagt tcgtgaccgc cgccgggatc actctcggca tggacgagct gtacaagtaa    720

```

<210> 24

<211> 239

<212> PRT

24/518

<213> Artificial sequence

<220>

<223> Variant of wild-type GFP

<400> 24

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 5 10 15
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60
 Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80
 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160
 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly

25/518

	180		185		190	
Pro	Val	Leu	Leu	Pro	Asp	Asn
				His	Tyr	Leu
				Ser	Tyr	Gln
				Ser	Ala	Leu
	195		200		205	
Ser	Lys	Asp	Pro	Asn	Glu	Lys
				Arg	Asp	His
				Met	Val	Leu
				Leu	Glu	Phe
	210		215		220	
Val	Thr	Ala	Ala	Gly	Ile	Thr
				Leu	Gly	Met
				Asp	Glu	Leu
				Tyr	Lys	.
225		230		235		

<210> 25

<211> 720

<212> DNA

<213> Artificial sequence

<220>

<223> Variant of wild-type GFP cDNA

<400> 25

atggtgagca agggcgagga gctgttcacc ggggtggtgc ccatcctggt cgagctggac	60
ggcgacgtaa acggccacaa gticagcgtg tccggcgagg gcgagggcga tgccacctac	120
ggcaagctga cctgaagtt catctgcacc accggcaagc tgcccgtgcc ctggcccacc	180
ctcgtgacca ccttcggcta cggcctgcag tgcttcgccc gctaccccgga ccacatgaag	240
cagcagcact tcttcaagtc cgccatgccc gaaggctacg tccaggagcg caccatcttc	300
ttcaaggacg acggcaacta caagaccgc gccgaggtga agttcgagg cgacaccctg	360
gtgaaccgca tcgagctgaa gggcatcgac ttcaaggagg acggcaacat cctggggcac	420
aagctggagt acaactacaa cagccacaac gctatatca tggccgacaa gcagaagaac	480
ggcatcaagg tgaacttcaa gatccgccac aacatcgagg acggcagcgt gcagctcgcc	540
gaccactacc agcagaacac ccccatcggc gacggccccg tgcctgctgcc cgacaaccac	600
tacctgagct accagtcgcg cctgagcaaa gaccccaacg agaagcgcg tcacatggtc	660
ctgctggagt tcgtgaccgc cgccgggatc actctcgga tggacgagct gtacaagtaa	720

26/518

<210> 26

<211> 225

<212> PRT

<213> Discosoma sp.

<400> 26

Met Arg Ser Ser Lys Asn Val Ile Lys Glu Phe Met Arg Phe Lys Val

5

10

15

Arg Met Glu Gly Thr Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu

20

25

30

Gly Glu Gly Arg Pro Tyr Glu Gly His Asn Thr Val Lys Leu Lys Val

35

40

45

Thr Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln

50

55

60

Phe Gln Tyr Gly Ser Lys Val Tyr Val Lys His Pro Ala Asp Ile Pro

65

70

75

80

Asp Tyr Lys Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val

85

90

95

Met Asn Phe Glu Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser

100

105

110

Leu Gln Asp Gly Cys Phe Ile Tyr Lys Val Lys Phe Ile Gly Val Asn

115

120

125

Phe Pro Ser Asp Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu

130

135

140

Ala Ser Thr Glu Arg Leu Tyr Pro Arg Asp Gly Val Leu Lys Gly Glu

145

150

155

160

Ile His Lys Ala Leu Lys Leu Lys Asp Gly Gly His Tyr Leu Val Glu

165

170

175

27/518

Phe Lys Ser Ile Tyr Met Ala Lys Lys Pro Val Gln Leu Pro Gly Tyr
 180 185 190
 Tyr Tyr Val Asp Ser Lys Leu Asp Ile Thr Ser His Asn Glu Asp Tyr
 195 200 205
 Thr Ile Val Glu Gln Tyr Glu Arg Thr Glu Gly Arg His His Leu Phe
 210 215 220
 Leu
 225

<210> 27

<211> 678

<212> DNA

<213> Discosoma sp.

<400> 27

atgaggtctt ccaagaatgt tatcaaggag ttcattgaggt ttaaggttcg catggaagga 60
 acggitcaatg ggcacgagtt tgaaatagaa ggccaaggag aggggaggcc atacgaaggc 120
 cacaataaccg taaagcctaa ggtaaccaag gggggacctt tgccatttgc ttgggatatt 180
 ttgtcaccac aatttcagta tggaagcaag gtatatgtca agcaccttgc cgacatacca 240
 gactataaaa agctgtcatt tcctgaagga tttaaatggg aaagggtcat gaactttgaa 300
 gacggtagcg tcgttactgt aaccaggat tccagtttgc aggatggctg tttcatctac 360
 aagggtcaagt tcattggcgt gaactttcct tccgatggac ctgttatgca aaagaagaca 420
 atgggctggg aagccagcac tgagcgtttg tatcctcgtg atggcgtgtt gaaaggagag 480
 attcataagg ctctgaagct gaaagacggt ggtcattacc tagttgaatt caaaagtatt 540
 tacatggcaa agaagcctgt gcagctacca ggttactact atgttgactc caaactggat 600
 ataacaagcc acaacgaaga ctatacaatc gttgagcagt atgaaagaac cgagggacgc 660
 caccatctgt tccttttag 678

<210> 28

28/518

<211> 239

<212> PRT

<213> Artificial sequence

<220>

<223> Variant of wild-type GFP

<400> 28

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu

5

10

15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly

20

25

30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile

35

40

45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr

50

55

60

Leu Thr His Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys

65

70

75

80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu

85

90

95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu

100

105

110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly

115

120

125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr

130

135

140

Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn

145

150

155

160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser

29/518

	165	170	175
Val	Gln	Leu	Ala
Asp	His	Tyr	Gln
Gln	Asn	Thr	Pro
Ile	Gly	Asp	Gly
	180	185	190
Pro	Val	Leu	Leu
Pro	Asp	Asn	His
Tyr	Leu	Ser	Thr
Gln	Ser	Ala	Leu
	195	200	205
Ser	Lys	Asp	Pro
Asn	Glu	Lys	Arg
Asp	His	Met	Val
Leu	Leu	Glu	Phe
	210	215	220
Val	Thr	Ala	Ala
Gly	Ile	Thr	Leu
Gly	Met	Asp	Glu
Leu	Tyr	Lys	
	225	230	235

<210> 29

<211> 720

<212> DNA

<213> Artificial sequence

<220>

<223> Variant of wild-type GFP cDNA

<400> 29

atggtgagca agggcgagga gctgttcacc ggggtggtgc ccatcctggt cgagctggac	60
ggcgacglaa acggccacaa gttcagcgtg tccggcgagg gcgagggcga tgccacctac	120
ggcaagctga ccctgaagtt catctgcacc accggcaagc tgcccgtgcc ctggcccacc	180
ctcgtgacca ccctgaccca cggcgtgcag tgcctcagcc gctaccccga ccacatgaag	240
cagcagcact tcttcaagtc cgccatgccc gaaggctacg tccaggagcg caccatcttc	300
ttcaaggacg acggcaacta caagacccgc gccgaggtga agttcgaggg cgacaccctg	360
gtgaaccgca tcgagctgaa gggcatcgac ttcaaggagg acggcaacat cctggggcac	420
aagctggagt acaacttcaa cagccacaac gtctatatca tggccgacaa gcagaagaac	480
ggcatcaagg tgaacttcaa gatccgccac aacatcgagg acggcagcgt gcagctcgcc	540
gaccactacc agcagaacac ccccatcggc gacggccccg tgctgctgcc cgacaaccac	600

30/518

tacctgagca cccagtcgc cctgagcaaa gaccccaacg agaagcgcga tcacatggtc 660
 ctgctggagt tcgtgaccgc cgccgggatac actctcggca tggacgagct gtacaagtaa 720

<210> 30

<211> 544

<212> PRT

<213> Human

<400> 30

Met Tyr Ser Phe Met Ala Gly Ser Ile Phe Ile Thr Ile Phe Gly Asn
 5 10 15
 Leu Ala Met Ile Ile Ser Ile Ser Tyr Phe Lys Gln Leu His Thr Pro
 20 25 30
 Thr Asn Phe Leu Ile Leu Ser Met Ala Ile Thr Asp Phe Leu Leu Gly
 35 40 45
 Phe Thr Ile Met Pro Tyr Ser Met Ile Arg Ser Val Glu Asn Cys Trp
 50 55 60
 Tyr Phe Gly Leu Thr Phe Cys Lys Ile Tyr Tyr Ser Phe Asp Leu Met
 65 70 75 80
 Leu Ser Ile Thr Ser Ile Phe His Leu Cys Ser Val Ala Ile Asp Arg
 85 90 95
 Phe Tyr Ala Ile Cys Tyr Pro Leu Leu Tyr Ser Thr Lys Ile Thr Ile
 100 105 110
 Pro Val Ile Lys Arg Leu Leu Leu Leu Cys Trp Ser Val Pro Gly Ala
 115 120 125
 Phe Ala Phe Gly Val Val Phe Ser Glu Ala Tyr Ala Asp Gly Ile Glu
 130 135 140
 Gly Tyr Asp Ile Leu Val Ala Cys Ser Ser Ser Cys Pro Val Met Phe
 145 150 155 160

31/518

Asn Lys Leu Trp Gly Thr Thr Leu Phe Met Ala Gly Phe Phe Thr Pro			
165	170	175	
Gly Ser Met Met Val Gly Ile Tyr Gly Lys Ile Phe Ala Val Ser Arg			
180	185	190	
Lys His Ala His Ala Ile Asn Asn Leu Arg Glu Asn Gln Asn Asn Gln			
195	200	205	
Val Lys Lys Asp Lys Lys Ala Ala Lys Thr Leu Gly Ile Val Ile Gly			
210	215	220	
Val Phe Leu Leu Cys Trp Phe Pro Cys Phe Phe Thr Ile Leu Leu Asp			
225	230	235	240
Pro Phe Leu Asn Phe Ser Thr Pro Val Val Leu Phe Asp Ala Leu Thr			
245	250	255	
Trp Phe Gly Tyr Phe Asn Ser Thr Cys Asn Pro Leu Ile Tyr Gly Phe			
260	265	270	
Phe Tyr Pro Trp Phe Arg Arg Ala Leu Lys Tyr Ile Leu Leu Gly Lys			
275	280	285	
Ile Phe Ser Ser Cys Phe His Asn Thr Ile Leu Cys Met Gln Lys Glu			
290	295	300	
Ser Glu Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile			
305	310	315	320
Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser			
325	330	335	
Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe			
340	345	350	
Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr			
355	360	365	
Thr Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met			
370	375	380	
Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln			

32/518

385 390 395 400
 Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala
 405 410 415
 Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys
 420 425 430
 Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu
 435 440 445
 Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
 450 455 460
 Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly
 465 470 475 480
 Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 485 490 495
 Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala
 500 505 510
 Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
 515 520 525
 Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn
 530 535 540

<210> 31

<211> 612

<212> PRT

<213> Human

<400> 31

Met Pro Thr Leu Asn Thr Ser Ala Ser Pro Pro Thr Phe Phe Trp Ala
 5 10 15
 Asn Ala Ser Gly Gly Ser Val Leu Ser Ala Asp Asp Ala Pro Met Pro

33/518

20	25	30
Val Lys Phe Leu Ala Leu Arg Leu Met Val Ala Leu Ala Tyr Gly Leu		
35	40	45
Val Gly Ala Ile Gly Leu Leu Gly Asn Leu Ala Val Leu Trp Val Leu		
50	55	60
Ser Asn Cys Ala Arg Arg Ala Pro Gly Pro Pro Ser Asp Thr Phe Val		
65	70	75
Phe Asn Leu Ala Leu Ala Asp Leu Gly Leu Ala Leu Thr Leu Pro Phe		
85	90	95
Trp Ala Ala Glu Ser Ala Leu Asp Phe His Trp Pro Phe Gly Gly Ala		
100	105	110
Leu Cys Lys Met Val Leu Thr Ala Thr Val Leu Asn Val Tyr Ala Ser		
115	120	125
Ile Phe Leu Ile Thr Ala Leu Ser Val Ala Arg Tyr Trp Val Val Ala		
130	135	140
Met Ala Ala Gly Pro Gly Thr His Leu Ser Leu Phe Trp Ala Arg Ile		
145	150	155
Ala Thr Leu Ala Val Trp Ala Ala Ala Ala Leu Val Thr Val Pro Thr		
165	170	175
Ala Val Phe Gly Val Glu Gly Glu Val Cys Gly Val Arg Leu Cys Leu		
180	185	190
Leu Arg Phe Pro Ser Arg Tyr Trp Leu Gly Ala Tyr Gln Leu Gln Arg		
195	200	205
Val Val Leu Ala Phe Met Val Pro Leu Gly Val Ile Thr Thr Ser Tyr		
210	215	220
Leu Leu Leu Leu Ala Phe Leu Gln Arg Arg Gln Arg Arg Arg Gln Asp		
225	230	235
Ser Arg Val Val Ala Arg Ser Val Arg Ile Leu Val Ala Ser Phe Phe		
245	250	255

34/518

Leu Cys Trp Phe Pro Asn His Val Val Thr Leu Trp Gly Val Leu Val
 260 265 270
 Lys Phe Asp Leu Val Pro Trp Asn Ser Thr Phe Tyr Thr Ile Gln Thr
 275 280 285
 Tyr Val Phe Pro Val Thr Thr Cys Leu Ala His Ser Asn Ser Cys Leu
 290 295 300
 Asn Pro Val Leu Tyr Cys Leu Leu Arg Arg Glu Pro Arg Gln Ala Leu
 305 310 315 320
 Ala Gly Thr Phe Arg Asp Leu Arg Ser Arg Leu Trp Pro Gln Gly Gly
 325 330 335
 Gly Trp Val Gln Gln Val Ala Leu Lys Gln Val Gly Arg Arg Trp Val
 340 345 350
 Ala Ser Asn Pro Arg Glu Ser Arg Pro Ser Thr Leu Leu Thr Asn Leu
 355 360 365
 Asp Arg Gly Thr Pro Gly Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly
 370 375 380
 Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys
 385 390 395 400
 Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu
 405 410 415
 Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro
 420 425 430
 Thr Leu Val Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr
 435 440 445
 Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu
 450 455 460
 Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr
 465 470 475 480
 Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg

35/518

	485	490	495
Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly			
500	505	510	
His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala			
515	520	525	
Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn			
530	535	540	
Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr			
545	550	555	560
Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser			
565	570	575	
Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met			
580	585	590	
Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp			
595	600	605	
Glu Leu Tyr Asn			
610			

<210> 32

<211> 599

<212> PRT

<213> Human

<400> 32

Met Ser Pro Glu Cys Ala Arg Ala Ala Gly Asp Ala Pro Leu Arg Ser			
5	10	15	
Leu Glu Gln Ala Asn Arg Thr Arg Phe Pro Phe Phe Ser Asp Val Lys			
20	25	30	
Gly Asp His Arg Leu Val Leu Ala Ala Val Glu Thr Thr Val Leu Val			

36/518

35	40	45
Leu Ile Phe Ala Val Ser Leu Leu Gly Asn Val Cys Ala Leu Val Leu		
50	55	60
Val Ala Arg Arg Arg Arg Arg Gly Ala Thr Ala Cys Leu Val Leu Asn		
65	70	75
Leu Phe Cys Ala Asp Leu Leu Phe Ile Ser Ala Ile Pro Leu Val Leu		
85	90	95
Ala Val Arg Trp Thr Glu Ala Trp Leu Leu Gly Pro Val Ala Cys His		
100	105	110
Leu Leu Phe Tyr Val Met Thr Leu Ser Gly Ser Val Thr Ile Leu Thr		
115	120	125
Leu Ala Ala Val Ser Leu Glu Arg Met Val Cys Ile Val His Leu Gln		
130	135	140
Arg Gly Val Arg Gly Pro Gly Arg Arg Ala Arg Ala Val Leu Leu Ala		
145	150	155
Leu Ile Trp Gly Tyr Ser Ala Val Ala Ala Leu Pro Leu Cys Val Phe		
165	170	175
Phe Arg Val Val Pro Gln Arg Leu Pro Gly Ala Asp Gln Glu Ile Ser		
180	185	190
Ile Cys Thr Leu Ile Trp Pro Thr Ile Pro Gly Glu Ile Ser Trp Asp		
195	200	205
Val Ser Phe Val Thr Leu Asn Phe Leu Val Pro Gly Leu Val Ile Val		
210	215	220
Ile Ser Tyr Ser Lys Ile Leu Gln Ile Thr Lys Ala Ser Arg Lys Arg		
225	230	235
Leu Thr Val Ser Leu Ala Tyr Ser Glu Ser His Gln Ile Arg Val Ser		
245	250	255
Gln Gln Asp Phe Arg Leu Phe Arg Thr Leu Phe Leu Leu Met Val Ser		
260	265	270

37/518

Phe Phe Ile Met Trp Ser Pro Ile Ile Ile Thr Ile Leu Leu Ile Leu
 275 280 285
 Ile Gln Asn Phe Lys Gln Asp Leu Val Ile Trp Pro Ser Leu Phe Phe
 290 295 300
 Trp Val Val Ala Phe Thr Phe Ala Asn Ser Ala Leu Asn Pro Ile Leu
 305 310 315 320
 Tyr Asn Met Thr Leu Cys Arg Asn Glu Trp Lys Lys Ile Phe Cys Cys
 325 330 335
 Phe Trp Phe Pro Glu Lys Gly Ala Ile Leu Thr Asp Thr Ser Val Lys
 340 345 350
 Arg Asn Asp Leu Ser Ile Ile Ser Gly Ala Ser Lys Gly Glu Glu Leu
 355 360 365
 Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn
 370 375 380
 Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr
 385 390 395 400
 Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
 405 410 415
 Pro Trp Pro Thr Leu Val Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe
 420 425 430
 Ser Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala
 435 440 445
 Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
 450 455 460
 Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
 465 470 475 480
 Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
 485 490 495
 Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr

38/518

500 505 510
 Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr
 515 520 525
 Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
 530 535 540
 Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
 545 550 555 560
 Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
 565 570 575
 Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His
 580 585 590
 Gly Met Asp Glu Leu Tyr Asn
 595

<210> 33

<211> 890

<212> PRT

<213> Human

<400> 33

Met Gln Gly Pro Leu Leu Leu Pro Gly Leu Cys Phe Leu Leu Ser Leu
 5 10 15
 Phe Gly Ala Val Thr Gln Lys Thr Lys Thr Ser Cys Ala Lys Cys Pro
 20 25 30
 Pro Asn Ala Ser Cys Val Asn Asn Thr His Cys Thr Cys Asn His Gly
 35 40 45
 Tyr Thr Ser Gly Ser Gly Gln Lys Leu Phe Thr Phe Pro Leu Glu Thr
 50 55 60
 Cys Asn Asp Ile Asn Glu Cys Thr Pro Pro Tyr Ser Val Tyr Cys Gly

39/518

65	70	75	80
Phe Asn Ala Val Cys Tyr Asn Val Glu Gly Ser Phe Tyr Cys Gln Cys			
85	90	95	
Val Pro Gly Tyr Arg Leu His Ser Gly Asn Glu Gln Phe Ser Asn Ser			
100	105	110	
Asn Glu Asn Thr Cys Gln Asp Thr Thr Ser Ser Lys Thr Thr Gln Gly			
115	120	125	
Arg Lys Glu Leu Gln Lys Ile Val Asp Lys Phe Glu Ser Leu Leu Thr			
130	135	140	
Asn Gln Thr Leu Trp Arg Thr Glu Gly Arg Gln Glu Ile Ser Ser Thr			
145	150	155	160
Ala Thr Thr Ile Leu Arg Asp Val Glu Ser Lys Val Leu Glu Thr Ala			
165	170	175	
Leu Lys Asp Pro Glu Gln Lys Val Leu Lys Ile Gln Asn Asp Ser Val			
180	185	190	
Ala Ile Glu Thr Gln Ala Ile Thr Asp Asn Cys Ser Glu Glu Arg Lys			
195	200	205	
Thr Phe Asn Leu Asn Val Gln Met Asn Ser Met Asp Ile Arg Cys Ser			
210	215	220	
Asp Ile Ile Gln Gly Asp Thr Gln Gly Pro Ser Ala Ile Ala Phe Ile			
225	230	235	240
Ser Tyr Ser Ser Leu Gly Asn Ile Ile Asn Ala Thr Phe Phe Glu Glu			
245	250	255	
Met Asp Lys Lys Asp Gln Val Tyr Leu Asn Ser Gln Val Val Ser Ala			
260	265	270	
Ala Ile Gly Pro Lys Arg Asn Val Ser Leu Ser Lys Ser Val Thr Leu			
275	280	285	
Thr Phe Gln His Val Lys Met Thr Pro Ser Thr Lys Lys Val Phe Cys			
290	295	300	

40/518

Val Tyr Trp Lys Ser Thr Gly Gln Gly Ser Gln Trp Ser Arg Asp Gly
 305 310 315 320
 Cys Phe Leu Ile His Val Asn Lys Ser His Thr Met Cys Asn Cys Ser
 325 330 335
 His Leu Ser Ser Phe Ala Val Leu Met Ala Leu Thr Ser Gln Glu Glu
 340 345 350
 Asp Pro Val Leu Thr Val Ile Thr Tyr Val Gly Leu Ser Val Ser Leu
 355 360 365
 Leu Cys Leu Leu Leu Ala Ala Leu Thr Phe Leu Leu Cys Lys Ala Ile
 370 375 380
 Gln Asn Thr Ser Thr Ser Leu His Leu Gln Leu Ser Leu Cys Leu Phe
 385 390 395 400
 Leu Ala His Leu Leu Phe Leu Val Gly Ile Asp Arg Thr Glu Pro Lys
 405 410 415
 Val Leu Cys Ser Ile Ile Ala Gly Ala Leu His Tyr Leu Tyr Leu Ala
 420 425 430
 Ala Phe Thr Trp Met Leu Leu Glu Gly Val His Leu Phe Leu Thr Ala
 435 440 445
 Arg Asn Leu Thr Val Val Asn Tyr Ser Ser Ile Asn Arg Leu Met Lys
 450 455 460
 Trp Ile Met Phe Pro Val Gly Tyr Gly Val Pro Ala Val Thr Val Ala
 465 470 475 480
 Ile Ser Ala Ala Ser Trp Pro His Leu Tyr Gly Thr Ala Asp Arg Cys
 485 490 495
 Trp Leu His Leu Asp Gln Gly Phe Met Trp Ser Phe Leu Gly Pro Val
 500 505 510
 Cys Ala Ile Phe Ser Ala Asn Leu Val Leu Phe Ile Leu Val Phe Trp
 515 520 525
 Ile Leu Lys Arg Lys Leu Ser Ser Leu Asn Ser Glu Val Ser Thr Ile

41/518

530	535	540	
Gln Asn Thr Arg Met Leu Ala Phe Lys Ala Thr Ala Gln Leu Phe Ile			
545	550	555	560
Leu Gly Cys Thr Trp Cys Leu Gly Leu Leu Gln Val Gly Pro Ala Ala			
565	570	575	
Gln Val Met Ala Tyr Leu Phe Thr Ile Ile Asn Ser Leu Gln Gly Phe			
580	585	590	
Phe Ile Phe Leu Val Tyr Cys Leu Leu Ser Gln Gln Val Gln Lys Gln			
595	600	605	
Tyr Gln Lys Trp Phe Arg Glu Ile Val Lys Ser Lys Ser Glu Ser Glu			
610	615	620	
Thr Tyr Thr Leu Ser Ser Lys Met Gly Pro Asp Ser Lys Pro Ser Glu			
625	630	635	640
Gly Asp Val Phe Pro Gly Gln Val Lys Arg Lys Tyr Ala Ser Lys Gly			
645	650	655	
Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly			
660	665	670	
Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp			
675	680	685	
Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys			
690	695	700	
Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Cys Tyr Gly Val			
705	710	715	720
Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe			
725	730	735	
Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe			
740	745	750	
Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly			
755	760	765	

42/518

Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
 770 775 780
 Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His
 785 790 795 800
 Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn
 805 810 815
 Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp
 820 825 830
 His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro
 835 840 845
 Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn
 850 855 860
 Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly
 865 870 875 880
 Ile Thr His Gly Met Asp Glu Leu Tyr Asn
 885 890

<210> 34

<211> 598

<212> PRT

<213> Human

<400> 34

Met Asp Pro Glu Glu Thr Ser Val Tyr Leu Asp Tyr Tyr Tyr Ala Thr
 5 10 15
 Ser Pro Asn Ser Asp Ile Arg Glu Thr His Ser His Val Pro Tyr Thr
 20 25 30
 Ser Val Phe Leu Pro Val Phe Tyr Thr Ala Val Phe Leu Thr Gly Val
 35 40 45

43/518

Leu Gly Asn Leu Val Leu Met Gly Ala Leu His Phe Lys Pro Gly Ser
 50 55 60
 Arg Arg Leu Ile Asp Ile Phe Ile Ile Asn Leu Ala Ala Ser Asp Phe
 65 70 75 80
 Ile Phe Leu Val Thr Leu Pro Leu Trp Val Asp Lys Glu Ala Ser Leu
 85 90 95
 Gly Leu Trp Arg Thr Gly Ser Phe Leu Cys Lys Gly Ser Ser Tyr Met
 100 105 110
 Ile Ser Val Asn Met His Cys Ser Val Leu Leu Leu Thr Cys Met Ser
 115 120 125
 Val Asp Arg Tyr Leu Ala Ile Val Trp Pro Val Val Ser Arg Lys Phe
 130 135 140
 Arg Arg Thr Asp Cys Ala Tyr Val Val Cys Ala Ser Ile Trp Phe Ile
 145 150 155 160
 Ser Cys Leu Leu Gly Leu Pro Thr Leu Leu Ser Arg Glu Leu Thr Leu
 165 170 175
 Ile Asp Asp Lys Pro Tyr Cys Ala Glu Lys Lys Ala Thr Pro Ile Lys
 180 185 190
 Leu Ile Trp Ser Leu Val Ala Leu Ile Phe Thr Phe Phe Val Pro Leu
 195 200 205
 Leu Ser Ile Val Thr Cys Tyr Cys Cys Ile Ala Arg Lys Leu Cys Ala
 210 215 220
 His Tyr Gln Gln Ser Gly Lys His Asn Lys Lys Leu Lys Lys Ser Ile
 225 230 235 240
 Lys Ile Ile Phe Ile Val Val Ala Ala Phe Leu Val Ser Trp Leu Pro
 245 250 255
 Phe Asn Thr Phe Lys Phe Leu Ala Ile Val Ser Gly Leu Arg Gln Glu
 260 265 270
 His Tyr Leu Pro Ser Ala Ile Leu Gln Leu Gly Met Glu Val Ser Gly

44/518

275	280	285
Pro Leu Ala Phe Ala Asn Ser Cys Val Asn Pro Phe Ile Tyr Tyr Ile		
290	295	300
Phe Asp Ser Tyr Ile Arg Arg Ala Ile Val His Cys Leu Cys Pro Cys		
305	310	315
Leu Lys Asn Tyr Asp Phe Gly Ser Ser Thr Glu Thr Ser Asp Ser His		
325	330	335
Leu Thr Lys Ala Leu Ser Thr Phe Ile His Ala Glu Asp Phe Ala Arg		
340	345	350
Arg Arg Lys Arg Ser Val Ser Leu Ala Ser Lys Gly Glu Glu Leu Phe		
355	360	365
Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly		
370	375	380
His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly		
385	390	395
Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro		
405	410	415
Trp Pro Thr Leu Val Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe Ser		
420	425	430
Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met		
435	440	445
Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly		
450	455	460
Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val		
465	470	475
Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile		
485	490	495
Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile		
500	505	510

45/518

Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr Arg
 515 520 525
 His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln
 530 535 540
 Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr
 545 550 555 560
 Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp
 565 570 575
 His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly
 580 585 590
 Met Asp Glu Leu Tyr Asn
 595

<210> 35

<211> 557

<212> PRT

<213> Human

<400> 35

Met Pro Phe Pro Asn Cys Ser Ala Pro Ser Thr Val Val Ala Thr Ala
 5 10 15
 Val Gly Val Leu Leu Gly Leu Glu Cys Gly Leu Gly Leu Leu Gly Asn
 20 25 30
 Ala Val Ala Leu Trp Thr Phe Leu Phe Arg Val Arg Val Trp Lys Pro
 35 40 45
 Tyr Ala Val Tyr Leu Leu Asn Leu Ala Leu Ala Asp Leu Leu Leu Ala
 50 55 60
 Ala Cys Leu Pro Phe Leu Ala Ala Phe Tyr Leu Ser Leu Gln Ala Trp
 65 70 75 80

46/518

His Leu Gly Arg Val Gly Cys Trp Ala Leu Arg Phe Leu Leu Asp Leu
 85 90 95
 Ser Arg Ser Val Gly Met Ala Phe Leu Ala Ala Val Ala Leu Asp Arg
 100 105 110
 Tyr Leu Arg Val Val His Pro Arg Leu Lys Val Asn Leu Leu Ser Pro
 115 120 125
 Gln Ala Ala Leu Gly Val Ser Gly Leu Val Trp Leu Leu Met Val Ala
 130 135 140
 Leu Thr Cys Pro Gly Leu Leu Ile Ser Glu Ala Ala Gln Asn Ser Thr
 145 150 155 160
 Arg Cys His Ser Phe Tyr Ser Arg Ala Asp Gly Ser Phe Ser Ile Ile
 165 170 175
 Trp Gln Glu Ala Leu Ser Cys Leu Gln Phe Val Leu Pro Phe Gly Leu
 180 185 190
 Ile Val Phe Cys Asn Ala Gly Ile Ile Arg Ala Leu Gln Lys Arg Leu
 195 200 205
 Arg Glu Pro Glu Lys Gln Pro Lys Leu Gln Arg Ala Gln Ala Leu Val
 210 215 220
 Thr Leu Val Val Val Leu Phe Ala Leu Cys Phe Leu Pro Cys Phe Leu
 225 230 235 240
 Ala Arg Val Leu Met His Ile Phe Gln Asn Leu Gly Ser Cys Arg Ala
 245 250 255
 Leu Cys Ala Val Ala His Thr Ser Asp Val Thr Gly Ser Leu Thr Tyr
 260 265 270
 Leu His Ser Val Leu Asn Pro Val Val Tyr Cys Phe Ser Ser Pro Thr
 275 280 285
 Phe Arg Ser Ser Tyr Arg Arg Val Phe His Thr Leu Arg Gly Lys Gly
 290 295 300
 Gln Ala Ala Glu Pro Pro Asp Phe Asn Pro Arg Asp Ser Tyr Ser Ala

47/518

305	310	315	320
Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu			
	325	330	335
Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly			
	340	345	350
Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr			
	355	360	365
Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Cys			
	370	375	380
Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg His			
385	390	395	400
Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr			
	405	410	415
Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys			
	420	425	430
Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp			
	435	440	445
Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr			
	450	455	460
Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile			
465	470	475	480
Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser Val Gln			
	485	490	495
Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val			
	500	505	510
Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys			
	515	520	525
Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr			
	530	535	540

48/518

Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn

545

550

555

<210> 36

<211> 641

<212> PRT

<213> Human

<400> 36

Met Phe Val Ala Ser Glu Arg Lys Met Arg Ala His Gln Val Leu Thr

5

10

15

Phe Leu Leu Leu Phe Val Ile Thr Ser Val Ala Ser Glu Asn Ala Ser

20

25

30

Thr Ser Arg Gly Cys Gly Leu Asp Leu Leu Pro Gln Tyr Val Ser Leu

35

40

45

Cys Asp Leu Asp Ala Ile Trp Gly Ile Val Val Glu Ala Val Ala Gly

50

55

60

Ala Gly Ala Leu Ile Thr Leu Leu Leu Met Leu Ile Leu Leu Val Arg

65

70

75

80

Leu Pro Phe Ile Lys Glu Lys Glu Lys Lys Ser Pro Val Gly Leu His

85

90

95

Phe Leu Phe Leu Leu Gly Thr Leu Gly Leu Phe Gly Leu Thr Phe Ala

100

105

110

Phe Ile Ile Gln Glu Asp Glu Thr Ile Cys Ser Val Arg Arg Phe Leu

115

120

125

Trp Gly Val Leu Phe Ala Leu Cys Phe Ser Cys Leu Leu Ser Gln Ala

130

135

140

Trp Arg Val Arg Arg Leu Val Arg His Gly Thr Gly Pro Ala Gly Trp

145

150

155

160

49/518

Gln Leu Val Gly Leu Ala Leu Cys Leu Met Leu Val Gln Val Ile Ile
 165 170 175
 Ala Val Glu Trp Leu Val Leu Thr Val Leu Arg Asp Thr Arg Pro Ala
 180 185 190
 Cys Ala Tyr Glu Pro Met Asp Phe Val Met Ala Leu Ile Tyr Asp Met
 195 200 205
 Val Leu Leu Val Val Thr Leu Gly Leu Ala Leu Phe Thr Leu Cys Gly
 210 215 220
 Lys Phe Lys Arg Trp Lys Leu Asn Gly Ala Phe Leu Leu Ile Thr Ala
 225 230 235 240
 Phe Leu Ser Val Leu Ile Trp Val Ala Trp Met Thr Met Tyr Leu Phe
 245 250 255
 Gly Asn Val Lys Leu Gln Gln Gly Asp Ala Trp Asn Asp Pro Thr Leu
 260 265 270
 Ala Ile Thr Leu Ala Ala Ser Gly Trp Val Phe Val Ile Phe His Ala
 275 280 285
 Ile Pro Glu Ile His Cys Thr Leu Leu Pro Ala Leu Gln Glu Asn Thr
 290 295 300
 Pro Asn Tyr Phe Asp Thr Ser Gln Pro Arg Met Arg Glu Thr Ala Phe
 305 310 315 320
 Glu Glu Asp Val Gln Leu Pro Arg Ala Tyr Met Glu Asn Lys Ala Phe
 325 330 335
 Ser Met Asp Glu His Asn Ala Ala Leu Arg Thr Ala Gly Phe Pro Asn
 340 345 350
 Gly Ser Leu Gly Lys Arg Pro Ser Gly Ser Leu Gly Lys Arg Pro Ser
 355 360 365
 Ala Pro Phe Arg Ser Asn Val Tyr Gln Pro Thr Glu Met Ala Val Val
 370 375 380
 Leu Asn Gly Gly Thr Ile Pro Thr Ala Pro Pro Ser His Thr Gly Arg

50/518

385	390	395	400
His Leu Trp Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro			
	405	410	415
Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val			
	420	425	430
Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys			
	435	440	445
Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val			
	450	455	460
Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His			
465	470	475	480
Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val			
	485	490	495
Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg			
	500	505	510
Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu			
	515	520	525
Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu			
	530	535	540
Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln			
545	550	555	560
Lys Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp			
	565	570	575
Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly			
	580	585	590
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser			
	595	600	605
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu			
	610	615	620

51/518

Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr
625 630 635 640
Asn

<210> 37

<211> 581

<212> PRT

<213> Human

<400> 37

Met	Ala	Gly	Asn	Cys	Ser	Trp	Glu	Ala	His	Pro	Gly	Asn	Arg	Asn	Arg
				5					10					15	
Met	Cys	Pro	Gly	Leu	Ser	Glu	Ala	Pro	Glu	Leu	Tyr	Ser	Arg	Gly	Phe
			20					25					30		
Leu	Thr	Ile	Glu	Gln	Ile	Ala	Met	Leu	Pro	Pro	Pro	Ala	Val	Met	Asn
			35					40					45		
Tyr	Ile	Phe	Leu	Leu	Leu	Cys	Leu	Cys	Gly	Leu	Val	Gly	Asn	Gly	Leu
	50					55					60				
Val	Leu	Trp	Phe	Phe	Gly	Phe	Ser	Ile	Lys	Arg	Asn	Pro	Phe	Ser	Ile
65					70					75					80
Tyr	Phe	Leu	His	Leu	Ala	Ser	Ala	Asp	Val	Gly	Tyr	Leu	Phe	Ser	Lys
				85					90					95	
Ala	Val	Phe	Ser	Ile	Leu	Asn	Thr	Gly	Gly	Phe	Leu	Gly	Thr	Phe	Ala
			100					105					110		
Asp	Tyr	Ile	Arg	Ser	Val	Cys	Arg	Val	Leu	Gly	Leu	Cys	Met	Phe	Leu
		115						120				125			
Thr	Gly	Val	Ser	Leu	Leu	Pro	Ala	Val	Ser	Ala	Glu	Arg	Cys	Ala	Ser
	130					135					140				
Val	Ile	Phe	Pro	Ala	Trp	Tyr	Trp	Arg	Arg	Arg	Pro	Lys	Arg	Leu	Ser

52/518

145	150	155	160
Ala Val Val Cys	Ala Leu Leu Trp Val Leu Ser Leu Leu Val Thr Cys		
165	170	175	
Leu His Asn Tyr Phe Cys Val Phe Leu Gly Arg Gly Ala Pro Gly Ala			
180	185	190	
Ala Cys Arg His Met Asp Ile Phe Leu Gly Ile Leu Leu Phe Leu Leu			
195	200	205	
Cys Cys Pro Leu Met Val Leu Pro Cys Leu Ala Leu Ile Leu His Val			
210	215	220	
Glu Cys Arg Ala Arg Arg Arg Gln Arg Ser Ala Lys Leu Asn His Val			
225	230	235	240
Ile Leu Ala Met Val Ser Val Phe Leu Val Ser Ser Ile Tyr Leu Gly			
245	250	255	
Ile Asp Trp Phe Leu Phe Trp Val Phe Gln Ile Pro Ala Pro Phe Pro			
260	265	270	
Glu Tyr Val Thr Asp Leu Cys Ile Cys Ile Asn Ser Ser Ala Lys Pro			
275	280	285	
Ile Val Tyr Phe Leu Ala Gly Arg Asp Lys Ser Gln Arg Leu Trp Glu			
290	295	300	
Pro Leu Arg Val Val Phe Gln Arg Ala Leu Arg Asp Gly Ala Glu Leu			
305	310	315	320
Gly Glu Ala Gly Gly Ser Thr Pro Asn Thr Val Thr Met Glu Met Gln			
325	330	335	
Cys Pro Pro Gly Asn Ala Ser Ala Ser Lys Gly Glu Glu Leu Phe Thr			
340	345	350	
Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His			
355	360	365	
Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys			
370	375	380	

53/518

Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp
 385 390 395 400
 Pro Thr Leu Val Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg
 405 410 415
 Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro
 420 425 430
 Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn
 435 440 445
 Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn
 450 455 460
 Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu
 465 470 475 480
 Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met
 485 490 495
 Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His
 500 505 510
 Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn
 515 520 525
 Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu
 530 535 540
 Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His
 545 550 555 560
 Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met
 565 570 575
 Asp Glu Leu Tyr Asn
 580

<210> 38

<211> 1252

54/518

<212> PRT

<213> Human

<400> 38

Met Val Phe Ser Val Arg Gln Cys Gly His Val Gly Arg Thr Glu Glu

5 10 15

Val Leu Leu Thr Phe Lys Ile Phe Leu Val Ile Ile Cys Leu His Val

20 25 30

Val Leu Val Thr Ser Leu Glu Glu Asp Thr Asp Asn Ser Ser Leu Ser

35 40 45

Pro Pro Pro Ala Lys Leu Ser Val Val Ser Phe Ala Pro Ser Ser Asn

50 55 60

Glu Val Glu Thr Thr Ser Leu Asn Asp Val Thr Leu Ser Leu Leu Pro

65 70 75 80

Ser Asn Glu Thr Glu Lys Thr Lys Ile Thr Ile Val Lys Thr Phe Asn

85 90 95

Ala Ser Gly Val Lys Pro Gln Arg Asn Ile Cys Asn Leu Ser Ser Ile

100 105 110

Cys Asn Asp Ser Ala Phe Phe Arg Gly Glu Ile Met Phe Gln Tyr Asp

115 120 125

Lys Glu Ser Thr Val Pro Gln Asn Gln His Ile Thr Asn Gly Thr Leu

130 135 140

Thr Gly Val Leu Ser Leu Ser Glu Leu Lys Arg Ser Glu Leu Asn Lys

145 150 155 160

Thr Leu Gln Thr Leu Ser Glu Thr Tyr Phe Ile Met Cys Ala Thr Ala

165 170 175

Glu Ala Gln Ser Thr Leu Asn Cys Thr Phe Thr Ile Lys Leu Asn Asn

180 185 190

Thr Met Asn Ala Cys Ala Val Ile Ala Ala Leu Glu Arg Val Lys Ile

55/518

195	200	205
Arg Pro Met Glu His Cys Cys Cys Ser Val Arg Ile Pro Cys Pro Ser		
210	215	220
Ser Pro Glu Glu Leu Glu Lys Leu Gln Cys Asp Leu Gln Asp Pro Ile		
225	230	235
Val Cys Leu Ala Asp His Pro Arg Gly Pro Pro Phe Ser Ser Ser Gln		
245	250	255
Ser Ile Pro Val Val Pro Arg Ala Thr Val Leu Ser Gln Val Pro Lys		
260	265	270
Ala Thr Ser Phe Ala Glu Pro Pro Asp Tyr Ser Pro Val Thr His Asn		
275	280	285
Val Pro Ser Pro Ile Gly Glu Ile Gln Pro Leu Ser Pro Gln Pro Ser		
290	295	300
Ala Pro Ile Ala Ser Ser Pro Ala Ile Asp Met Pro Pro Gln Ser Glu		
305	310	315
Thr Ile Ser Ser Pro Met Pro Gln Thr His Val Ser Gly Thr Pro Pro		
325	330	335
Pro Val Lys Ala Ser Phe Ser Ser Pro Thr Val Ser Ala Pro Ala Asn		
340	345	350
Val Asn Thr Thr Ser Ala Pro Pro Val Gln Thr Asp Ile Val Asn Thr		
355	360	365
Ser Ser Ile Ser Asp Leu Glu Asn Gln Val Leu Gln Met Glu Lys Ala		
370	375	380
Leu Ser Leu Gly Ser Leu Glu Pro Asn Leu Ala Gly Glu Met Ile Asn		
385	390	395
Gln Val Ser Arg Leu Leu His Ser Pro Pro Asp Met Leu Ala Pro Leu		
405	410	415
Ala Gln Arg Leu Leu Lys Val Val Asp Asp Ile Gly Leu Gln Leu Asn		
420	425	430

56/518

Phe Ser Asn Thr Thr Ile Ser Leu Thr Ser Pro Ser Leu Ala Leu Ala
 435 440 445
 Val Ile Arg Val Asn Ala Ser Ser Phe Asn Thr Thr Thr Phe Val Ala
 450 455 460
 Gln Asp Pro Ala Asn Leu Gln Val Ser Leu Glu Thr Gln Ala Pro Glu
 465 470 475 480
 Asn Ser Ile Gly Thr Ile Thr Leu Pro Ser Ser Leu Met Asn Asn Leu
 485 490 495
 Pro Ala His Asp Met Glu Leu Ala Ser Arg Val Gln Phe Asn Phe Phe
 500 505 510
 Glu Thr Pro Ala Leu Phe Gln Asp Pro Ser Leu Glu Asn Leu Ser Leu
 515 520 525
 Ile Ser Tyr Val Ile Ser Ser Ser Val Ala Asn Leu Thr Val Arg Asn
 530 535 540
 Leu Thr Arg Asn Val Thr Val Thr Leu Lys His Ile Asn Pro Ser Gln
 545 550 555 560
 Asp Glu Leu Thr Val Arg Cys Val Phe Trp Asp Leu Gly Arg Asn Gly
 565 570 575
 Gly Arg Gly Gly Trp Ser Asp Asn Gly Cys Ser Val Lys Asp Arg Arg
 580 585 590
 Leu Asn Glu Thr Ile Cys Thr Cys Ser His Leu Thr Ser Phe Gly Val
 595 600 605
 Leu Leu Asp Leu Ser Arg Thr Ser Val Leu Pro Ala Gln Met Met Ala
 610 615 620
 Leu Thr Phe Ile Thr Tyr Ile Gly Cys Gly Leu Ser Ser Ile Phe Leu
 625 630 635 640
 Ser Val Thr Leu Val Thr Tyr Ile Ala Phe Glu Lys Ile Arg Arg Asp
 645 650 655
 Tyr Pro Ser Lys Ile Leu Ile Gln Leu Cys Ala Ala Leu Leu Leu Leu

57/518

660	665	670	
Asn Leu Val Phe Leu Leu Asp Ser Trp Ile Ala Leu Tyr Lys Met Gln			
675	680	685	
Gly Leu Cys Ile Ser Val Ala Val Phe Leu His Tyr Phe Leu Leu Val			
690	695	700	
Ser Phe Thr Trp Met Gly Leu Glu Ala Phe His Met Tyr Leu Ala Leu			
705	710	715	720
Val Lys Val Phe Asn Thr Tyr Ile Arg Lys Tyr Ile Leu Lys Phe Cys			
725	730	735	
Ile Val Gly Trp Gly Val Pro Ala Val Val Val Thr Ile Ile Leu Thr			
740	745	750	
Ile Ser Pro Asp Asn Tyr Gly Leu Gly Ser Tyr Gly Lys Phe Pro Asn			
755	760	765	
Gly Ser Pro Asp Asp Phe Cys Trp Ile Asn Asn Asn Ala Val Phe Tyr			
770	775	780	
Ile Thr Val Val Gly Tyr Phe Cys Val Ile Phe Leu Leu Asn Val Ser			
785	790	795	800
Met Phe Ile Val Val Leu Val Gln Leu Cys Arg Ile Lys Lys Lys Lys			
805	810	815	
Gln Leu Gly Ala Gln Arg Lys Thr Ser Ile Gln Asp Leu Arg Ser Ile			
820	825	830	
Ala Gly Leu Thr Phe Leu Leu Gly Ile Thr Trp Gly Phe Ala Phe Phe			
835	840	845	
Ala Trp Gly Pro Val Asn Val Thr Phe Met Tyr Leu Phe Ala Ile Phe			
850	855	860	
Asn Thr Leu Gln Gly Phe Phe Ile Phe Ile Phe Tyr Cys Val Ala Lys			
865	870	875	880
Glu Asn Val Arg Lys Gln Trp Arg Arg Tyr Leu Cys Cys Gly Lys Leu			
885	890	895	

58/518

Arg Leu Ala Glu Asn Ser Asp Trp Ser Lys Thr Ala Thr Asn Gly Leu

900

905

910

Lys Lys Gln Thr Val Asn Gln Gly Val Ser Ser Ser Ser Asn Ser Leu

915

920

925

Gln Ser Ser Ser Asn Ser Thr Asn Ser Thr Thr Leu Leu Val Asn Asn

930

935

940

Asp Cys Ser Val His Ala Ser Gly Asn Gly Asn Ala Ser Thr Glu Arg

945

950

955

960

Asn Gly Val Ser Phe Ser Val Gln Asn Gly Asp Val Cys Leu His Asp

965

970

975

Phe Thr Gly Lys Gln His Met Phe Asn Glu Lys Glu Asp Ser Cys Asn

980

985

990

Gly Lys Gly Arg Met Ala Leu Arg Arg Thr Ser Lys Arg Gly Ser Leu

995

1000

1005

His Phe Ile Glu Gln Met Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly

1010

1015

1020

Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys

1025

1030

1035

1040

Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu

1045

1050

1055

Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro

1060

1065

1070

Thr Leu Val Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr

1075

1080

1085

Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu

1090

1095

1100

Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr

1105

1110

1115

1120

Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg

59/518

1125	1130	1135	
Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly			
1140	1145	1150	
His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala			
1155	1160	1165	
Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn			
1170	1175	1180	
Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr			
1185	1190	1195	1200
Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser			
1205	1210	1215	
Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met			
1220	1225	1230	
Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp			
1235	1240	1245	
Glu Leu Tyr Asn			
1250			

<210> 39

<211> 655

<212> PRT

<213> Human

<400> 39

Met Glu Ser Ser Pro Ile Pro Gln Ser Ser Gly Asn Ser Ser Thr Leu		
5	10	15
Gly Arg Val Pro Gln Thr Pro Gly Pro Ser Thr Ala Ser Gly Val Pro		
20	25	30
Glu Val Gly Leu Arg Asp Val Ala Ser Glu Ser Val Ala Leu Phe Phe		

60/518

35	40	45
Met Leu Leu Leu Asp Leu Thr Ala Val Ala Gly Asn Ala Ala Val Met		
50	55	60
Ala Val Ile Ala Lys Thr Pro Ala Leu Arg Lys Phe Val Phe Val Phe		
65	70	75
His Leu Cys Leu Val Asp Leu Leu Ala Ala Leu Thr Leu Met Pro Leu		
85	90	95
Ala Met Leu Ser Ser Ser Ala Leu Phe Asp His Ala Leu Phe Gly Glu		
100	105	110
Val Ala Cys Arg Leu Tyr Leu Phe Leu Ser Val Cys Phe Val Ser Leu		
115	120	125
Ala Ile Leu Ser Val Ser Ala Ile Asn Val Glu Arg Tyr Tyr Tyr Val		
130	135	140
Val His Pro Met Arg Tyr Glu Val Arg Met Thr Leu Gly Leu Val Ala		
145	150	155
Ser Val Leu Val Gly Val Trp Val Lys Ala Leu Ala Met Ala Ser Val		
165	170	175
Pro Val Leu Gly Arg Val Ser Trp Glu Glu Gly Ala Pro Ser Val Pro		
180	185	190
Pro Gly Cys Ser Leu Gln Trp Ser His Ser Ala Tyr Cys Gln Leu Phe		
195	200	205
Val Val Val Phe Ala Val Leu Tyr Phe Leu Leu Pro Leu Leu Leu Ile		
210	215	220
Leu Val Val Tyr Cys Ser Met Phe Arg Val Ala Arg Val Ala Ala Met		
225	230	235
Gln His Gly Pro Leu Pro Thr Trp Met Glu Thr Pro Arg Gln Arg Ser		
245	250	255
Glu Ser Leu Ser Ser Arg Ser Thr Met Val Thr Ser Ser Gly Ala Pro		
260	265	270

61/518

Gln Thr Thr Pro His Arg Thr Phe Gly Gly Gly Lys Ala Ala Val Val
 275 280 285
 Leu Leu Ala Val Gly Gly Gln Phe Leu Leu Cys Trp Leu Pro Tyr Phe
 290 295 300
 Ser Phe His Leu Tyr Val Ala Leu Ser Ala Gln Pro Ile Ser Thr Gly
 305 310 315 320
 Gln Val Glu Ser Val Val Thr Trp Ile Gly Tyr Phe Cys Phe Thr Ser
 325 330 335
 Asn Pro Phe Phe Tyr Gly Cys Leu Asn Arg Gln Ile Arg Gly Glu Leu
 340 345 350
 Ser Lys Gln Phe Val Cys Phe Phe Lys Pro Ala Pro Glu Glu Glu Leu
 355 360 365
 Arg Leu Pro Ser Arg Glu Gly Ser Ile Glu Glu Asn Phe Leu Gln Phe
 370 375 380
 Leu Gln Gly Thr Gly Cys Pro Ser Glu Ser Trp Val Ser Arg Pro Leu
 385 390 395 400
 Pro Ser Pro Lys Gln Glu Pro Pro Ala Val Asp Phe Arg Ile Gln Ala
 405 410 415
 Arg Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 420 425 430
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 435 440 445
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 450 455 460
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 465 470 475 480
 Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 485 490 495
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu

62/518

500	505	510
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu		
515	520	525
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly		
530	535	540
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr		
545	550	555
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn		
565	570	575
Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser		
580	585	590
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly		
595	600	605
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu		
610	615	620
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe		
625	630	635
Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn		
645	650	655

<210> 40

<211> 573

<212> PRT

<213> Human

<400> 40

Met Gln Pro Ser Pro Pro Pro Thr Glu Leu Val Pro Ser Glu Arg Ala
5 10 15
Val Val Leu Leu Ser Cys Ala Leu Ser Ala Leu Gly Ser Gly Leu Leu

63/518

	20	25	30
Val	Ala	Thr	His
Ala	Leu	Trp	Pro
Asp	Leu	Arg	Ser
Arg	Ala	Arg	Arg
	35	40	45
Leu	Leu	Leu	Phe
Leu	Ser	Leu	Ala
Asp	Leu	Leu	Ser
Ala	Ala	Ser	Tyr
	50	55	60
Phe	Tyr	Gly	Val
Leu	Gln	Asn	Phe
Ala	Gly	Pro	Ser
Trp	Asp	Cys	Val
	65	70	75
Leu	Gln	Gly	Ala
Leu	Ser	Thr	Phe
Ala	Asn	Thr	Ser
Ser	Ser	Phe	Phe
Trp			
	85	90	95
Thr	Val	Ala	Ile
Ala	Leu	Tyr	Leu
Tyr	Leu	Ser	Ile
Val	Arg	Ala	Ala
	100	105	110
Arg	Gly	Pro	Arg
Thr	Asp	Arg	Leu
Leu	Trp	Ala	Phe
His	Val	Val	Ser
	115	120	125
Trp	Gly	Val	Pro
Leu	Val	Ile	Thr
Val	Ala	Ala	Val
Ala	Leu	Lys	Lys
	130	135	140
Ile	Gly	Tyr	Asp
Ala	Ser	Asp	Val
Ser	Val	Gly	Trp
Cys	Trp	Ile	Asp
	145	150	155
Leu	Glu	Ala	Lys
Asp	His	Val	Leu
Trp	Met	Leu	Leu
Thr	Gly	Lys	Leu
	165	170	175
Trp	Glu	Met	Leu
Ala	Tyr	Val	Leu
Leu	Pro	Leu	Leu
Tyr	Leu	Leu	Val
	180	185	190
Arg	Lys	His	Ile
Asn	Arg	Ala	His
Thr	Ala	Leu	Ser
Glu	Tyr	Arg	Pro
	195	200	205
Ile	Leu	Ser	Gln
Glu	His	Arg	Leu
Leu	Arg	His	Ser
Ser	Ser	Met	Ala
Asp			
	210	215	220
Lys	Lys	Leu	Val
Leu	Ile	Pro	Leu
Ile	Phe	Ile	Gly
Leu	Arg	Val	Trp
	225	230	235
Ser	Thr	Val	Arg
Phe	Val	Leu	Thr
Leu	Cys	Gly	Ser
Pro	Ala	Val	Gln
	245	250	255

64/518

Thr Pro Val Leu Val Val Leu His Gly Ile Gly Asn Thr Phe Gln Gly
 260 265 270
 Gly Ala Asn Cys Ile Met Phe Val Leu Cys Thr Arg Ala Val Arg Thr
 275 280 285
 Arg Leu Phe Ser Leu Cys Cys Cys Cys Cys Ser Ser Gln Pro Pro Thr
 290 295 300
 Lys Ser Pro Ala Gly Thr Pro Lys Ala Pro Ala Pro Ser Lys Pro Gly
 305 310 315 320
 Glu Ser Gln Glu Ser Gln Gly Thr Pro Gly Glu Leu Pro Ser Thr Ala
 325 330 335
 Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu
 340 345 350
 Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly
 355 360 365
 Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr
 370 375 380
 Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Cys
 385 390 395 400
 Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg His
 405 410 415
 Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr
 420 425 430
 Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys
 435 440 445
 Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp
 450 455 460
 Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr
 465 470 475 480
 Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile

65/518

	485	490	495
Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser Val Gln			
	500	505	510
Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val			
	515	520	525
Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys			
	530	535	540
Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr			
545	550	555	560
Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn			
	565	570	

<210> 41

<211> 920

<212> PRT

<213> Human

<400> 41

Met Ala Val Arg Leu Cys Ser Leu Ser Leu Tyr Gly Glu Ile Glu Leu			
	5	10	15
Gln Lys Val Thr Ile Gly Asn Cys Asn Glu Asn Leu Glu Thr Leu Glu			
	20	25	30
Lys Gln Val Lys Asp Val Thr Ala Pro Leu Asn Asn Ile Ser Ser Glu			
	35	40	45
Val Gln Ile Leu Thr Ser Asp Ala Asn Lys Leu Thr Ala Glu Asn Ile			
	50	55	60
Thr Ser Ala Thr Arg Val Val Gly Gln Ile Phe Asn Thr Ser Arg Asn			
65	70	75	80
Ala Ser Pro Glu Ala Lys Lys Val Ala Ile Val Thr Val Ser Gln Leu			

66/518

	85	90	95
Leu Asp Ala Ser Glu Asp Ala Phe Gln Arg Val Ala Ala Thr Ala Asn			
100	105	110	
Asp Asp Ala Leu Thr Thr Leu Ile Glu Gln Met Glu Thr Tyr Ser Leu			
115	120	125	
Ser Leu Gly Asn Gln Ser Val Val Glu Pro Asn Ile Ala Ile Gln Ser			
130	135	140	
Ala Asn Phe Ser Ser Glu Asn Ala Val Gly Pro Ser Asn Val Arg Phe			
145	150	155	160
Ser Val Gln Lys Gly Ala Ser Ser Ser Leu Val Ser Ser Ser Thr Phe			
165	170	175	
Ile His Thr Asn Val Asp Gly Leu Asn Pro Asp Ala Gln Thr Glu Leu			
180	185	190	
Gln Val Leu Leu Asn Met Thr Lys Asn Tyr Thr Lys Thr Cys Gly Phe			
195	200	205	
Val Val Tyr Gln Asn Asp Lys Leu Phe Gln Ser Lys Thr Phe Thr Ala			
210	215	220	
Lys Ser Asp Phe Ser Gln Lys Ile Ile Ser Ser Lys Thr Asp Glu Asn			
225	230	235	240
Glu Gln Asp Gln Ser Ala Ser Val Asp Met Val Phe Ser Pro Lys Tyr			
245	250	255	
Asn Gln Lys Glu Phe Gln Leu Tyr Ser Tyr Ala Cys Val Tyr Trp Asn			
260	265	270	
Leu Ser Ala Lys Asp Trp Asp Thr Tyr Gly Cys Gln Lys Asp Lys Gly			
275	280	285	
Thr Asp Gly Phe Leu Arg Cys Arg Cys Asn His Thr Thr Asn Phe Ala			
290	295	300	
Val Leu Met Thr Phe Lys Lys Asp Tyr Gln Tyr Pro Lys Ser Leu Asp			
305	310	315	320

67/518

Ile Leu Ser Asn Val Gly Cys Ala Leu Ser Val Thr Gly Leu Ala Leu
 325 330 335
 Thr Val Ile Phe Gln Ile Val Thr Arg Lys Val Arg Lys Thr Ser Val
 340 345 350
 Thr Trp Val Leu Val Asn Leu Cys Ile Ser Met Leu Ile Phe Asn Leu
 355 360 365
 Leu Phe Val Phe Gly Ile Glu Asn Ser Asn Lys Asn Leu Gln Thr Ser
 370 375 380
 Asp Gly Asp Ile Asn Asn Ile Asp Phe Asp Asn Asn Asp Ile Pro Arg
 385 390 395 400
 Thr Asp Thr Ile Asn Ile Pro Asn Pro Met Cys Thr Ala Ile Ala Ala
 405 410 415
 Leu Leu His Tyr Phe Leu Leu Val Thr Phe Thr Trp Asn Ala Leu Ser
 420 425 430
 Ala Ala Gln Leu Tyr Tyr Leu Leu Ile Arg Thr Met Lys Pro Leu Pro
 435 440 445
 Arg His Phe Ile Leu Phe Ile Ser Leu Ile Gly Trp Gly Val Pro Ala
 450 455 460
 Ile Val Val Ala Ile Thr Val Gly Val Ile Tyr Ser Gln Asn Gly Asn
 465 470 475 480
 Asn Pro Gln Trp Glu Leu Asp Tyr Arg Gln Glu Lys Ile Cys Trp Leu
 485 490 495
 Ala Ile Pro Glu Pro Asn Gly Val Ile Lys Ser Pro Leu Leu Trp Ser
 500 505 510
 Phe Ile Val Pro Val Thr Ile Ile Leu Ile Ser Asn Val Val Met Phe
 515 520 525
 Ile Thr Ile Ser Ile Lys Val Leu Trp Lys Asn Asn Gln Asn Leu Thr
 530 535 540
 Ser Thr Lys Lys Val Ser Ser Met Lys Lys Ile Val Ser Thr Leu Ser

68/518

545	550	555	560
Val Ala Val Val Phe Gly Ile Thr Trp Ile Leu Ala Tyr Leu Met Leu			
565	570	575	
Val Asn Asp Asp Ser Ile Arg Ile Val Phe Ser Tyr Ile Phe Cys Leu			
580	585	590	
Phe Asn Thr Thr Gln Gly Leu Gln Ile Phe Ile Leu Tyr Thr Val Arg			
595	600	605	
Thr Lys Val Phe Gln Ser Glu Ala Ser Lys Val Leu Met Leu Leu Ser			
610	615	620	
Ser Ile Gly Arg Arg Lys Ser Leu Pro Ser Val Thr Arg Pro Arg Leu			
625	630	635	640
Arg Val Lys Met Tyr Asn Phe Leu Arg Ser Leu Pro Thr Leu His Glu			
645	650	655	
Arg Phe Arg Leu Leu Glu Thr Ser Pro Ser Thr Glu Glu Ile Thr Leu			
660	665	670	
Ser Glu Ser Asp Asn Ala Lys Glu Ser Ile Ala Ser Lys Gly Glu Glu			
675	680	685	
Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val			
690	695	700	
Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr			
705	710	715	720
Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro			
725	730	735	
Val Pro Trp Pro Thr Leu Val Thr Thr Leu Cys Tyr Gly Val Gln Cys			
740	745	750	
Phe Ser Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser			
755	760	765	
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp			
770	775	780	

69/518

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
 785 790 795 800
 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
 805 810 815
 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
 820 825 830
 Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
 835 840 845
 Thr Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
 850 855 860
 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
 865 870 875 880
 His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
 885 890 895
 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
 900 905 910
 His Gly Met Asp Glu Leu Tyr Asn
 915 920

<210> 42

<211> 766

<212> PRT

<213> Human

<400> 42

Met Asp His Cys Gly Ala Leu Phe Leu Cys Leu Cys Leu Leu Thr Leu
 5 10 15
 Gln Asn Ala Thr Thr Glu Thr Trp Glu Glu Leu Leu Ser Tyr Met Glu
 20 25 30

70/518

Asn Met Gln Val Ser Arg Gly Arg Ser Ser Val Phe Ser Ser Arg Gln
 35 40 45
 Leu His Gln Leu Glu Gln Met Leu Leu Asn Thr Ser Phe Pro Gly Tyr
 50 55 60
 Asn Leu Thr Leu Gln Thr Pro Thr Ile Gln Ser Leu Ala Phe Lys Leu
 65 70 75 80
 Ser Cys Asp Phe Ser Gly Leu Ser Leu Thr Ser Ala Thr Leu Lys Arg
 85 90 95
 Val Pro Gln Ala Gly Gly Gln His Ala Arg Gly Gln His Ala Met Gln
 100 105 110
 Phe Pro Ala Glu Leu Thr Arg Asp Ala Cys Lys Thr Arg Pro Arg Glu
 115 120 125
 Leu Arg Leu Ile Cys Ile Tyr Phe Ser Asn Thr His Phe Phe Lys Asp
 130 135 140
 Glu Asn Asn Ser Ser Leu Leu Asn Asn Tyr Val Leu Gly Ala Gln Leu
 145 150 155 160
 Ser His Gly His Val Asn Asn Leu Arg Asp Pro Val Asn Ile Ser Phe
 165 170 175
 Trp His Asn Gln Ser Leu Glu Gly Tyr Thr Leu Thr Cys Val Phe Trp
 180 185 190
 Lys Glu Gly Ala Arg Lys Gln Pro Trp Gly Gly Trp Ser Pro Glu Gly
 195 200 205
 Cys Arg Thr Glu Gln Pro Ser His Ser Gln Val Leu Cys Arg Cys Asn
 210 215 220
 His Leu Thr Tyr Phe Ala Val Leu Met Gln Leu Ser Pro Ala Leu Val
 225 230 235 240
 Pro Ala Glu Leu Leu Ala Pro Leu Thr Tyr Ile Ser Leu Val Gly Cys
 245 250 255
 Ser Ile Ser Ile Val Ala Ser Leu Ile Thr Val Leu Leu His Phe His

71/518

260	265	270
Phe Arg Lys Gln Ser Asp Ser Leu Thr Arg Ile His Met Asn Leu His		
275	280	285
Ala Ser Val Leu Leu Leu Asn Ile Ala Phe Leu Leu Ser Pro Ala Phe		
290	295	300
Ala Met Ser Pro Val Pro Gly Ser Ala Cys Thr Ala Leu Ala Ala Ala		
305	310	315
Leu His Tyr Ala Leu Leu Ser Cys Leu Thr Trp Met Ala Ile Glu Gly		
325	330	335
Phe Asn Leu Tyr Leu Leu Leu Gly Arg Val Tyr Asn Ile Tyr Ile Arg		
340	345	350
Arg Tyr Val Phe Lys Leu Gly Val Leu Gly Trp Gly Ala Pro Ala Leu		
355	360	365
Leu Val Leu Leu Ser Leu Ser Val Lys Ser Ser Val Tyr Gly Pro Cys		
370	375	380
Thr Ile Pro Val Phe Asp Ser Trp Glu Asn Gly Thr Gly Phe Gln Asn		
385	390	395
Met Ser Ile Cys Trp Val Arg Ser Pro Val Val His Ser Val Leu Val		
405	410	415
Met Gly Tyr Gly Gly Leu Thr Ser Leu Phe Asn Leu Val Val Leu Ala		
420	425	430
Trp Ala Leu Trp Thr Leu Arg Arg Leu Arg Glu Arg Ala Asp Ala Pro		
435	440	445
Ser Val Arg Ala Cys His Asp Thr Val Thr Val Leu Gly Leu Thr Val		
450	455	460
Leu Leu Gly Thr Thr Trp Ala Leu Ala Phe Phe Ser Phe Gly Val Phe		
465	470	475
Leu Leu Pro Gln Leu Phe Leu Phe Thr Ile Leu Asn Ser Leu Tyr Gly		
485	490	495

72/518

Phe Phe Leu Phe Leu Trp Phe Cys Ser Gln Arg Cys Arg Ser Glu Ala
 500 505 510
 Glu Ala Lys Ala Gln Ile Glu Ala Phe Ser Ser Ser Gln Thr Thr Gln
 515 520 525
 Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 530 535 540
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 545 550 555 560
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 565 570 575
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
 580 585 590
 Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg
 595 600 605
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 610 615 620
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 625 630 635 640
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 645 650 655
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 660 665 670
 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 675 680 685
 Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser Val
 690 695 700
 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
 705 710 715 720
 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser

73/518

	725		730		735										
Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val
	740		745		750										
Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	Leu	Tyr	Asn		
	755		760		765										

<210> 43

<211> 1124

<212> PRT

<213> Human

<400> 43

Met	Arg	Gly	Phe	Asn	Leu	Leu	Leu	Phe	Trp	Gly	Cys	Cys	Val	Met	His
				5					10					15	
Ser	Trp	Glu	Gly	His	Ile	Arg	Pro	Thr	Arg	Lys	Pro	Asn	Thr	Lys	Gly
			20					25					30		
Asn	Asn	Cys	Arg	Asp	Ser	Thr	Leu	Cys	Pro	Ala	Tyr	Ala	Thr	Cys	Thr
		35					40					45			
Asn	Thr	Val	Asp	Ser	Tyr	Tyr	Cys	Thr	Cys	Lys	Gln	Gly	Phe	Leu	Ser
	50						55					60			
Ser	Asn	Gly	Gln	Asn	His	Phe	Lys	Asp	Pro	Gly	Val	Arg	Cys	Lys	Asp
	65				70				75					80	
Ile	Asp	Glu	Cys	Ser	Gln	Ser	Pro	Gln	Pro	Cys	Gly	Pro	Asn	Ser	Ser
				85					90					95	
Cys	Lys	Asn	Leu	Ser	Gly	Arg	Tyr	Lys	Cys	Ser	Cys	Leu	Asp	Gly	Phe
		100						105					110		
Ser	Ser	Pro	Thr	Gly	Asn	Asp	Trp	Val	Pro	Gly	Lys	Pro	Gly	Asn	Phe
		115					120						125		
Ser	Cys	Thr	Asp	Ile	Asn	Glu	Cys	Leu	Thr	Ser	Arg	Val	Cys	Pro	Glu

74/518

130	135	140	
His Ser Asp Cys Val Asn Ser Met Gly Ser Tyr Ser Cys Ser Cys Gln			
145	150	155	160
Val Gly Phe Ile Ser Arg Asn Ser Thr Cys Glu Asp Val Asn Glu Cys			
	165	170	175
Ala Asp Pro Arg Ala Cys Pro Glu His Ala Thr Cys Asn Asn Thr Val			
	180	185	190
Gly Asn Tyr Ser Cys Phe Cys Asn Pro Gly Phe Glu Ser Ser Ser Gly			
	195	200	205
His Leu Ser Phe Gln Gly Leu Lys Ala Ser Cys Glu Asp Ile Asp Glu			
	210	215	220
Cys Thr Glu Met Cys Pro Ile Asn Ser Thr Cys Thr Asn Thr Pro Gly			
225	230	235	240
Ser Tyr Phe Cys Thr Cys His Pro Gly Phe Ala Pro Ser Ser Gly Gln			
	245	250	255
Leu Asn Phe Thr Asp Gln Gly Val Glu Cys Arg Asp Ile Asp Glu Cys			
	260	265	270
Arg Gln Asp Pro Ser Thr Cys Gly Pro Asn Ser Ile Cys Thr Asn Ala			
	275	280	285
Leu Gly Ser Tyr Ser Cys Gly Cys Ile Val Gly Phe His Pro Asn Pro			
	290	295	300
Glu Gly Ser Gln Lys Asp Gly Asn Phe Ser Cys Gln Arg Val Leu Phe			
305	310	315	320
Lys Cys Lys Glu Asp Val Ile Pro Asp Asn Lys Gln Ile Gln Gln Cys			
	325	330	335
Gln Glu Gly Thr Ala Val Lys Pro Ala Tyr Val Ser Phe Cys Ala Gln			
	340	345	350
Ile Asn Asn Ile Phe Ser Val Leu Asp Lys Val Cys Glu Asn Lys Thr			
	355	360	365

75/518

Thr Val Val Ser Leu Lys Asn Thr Thr Glu Ser Phe Val Pro Val Leu
 370 375 380
 Lys Gln Ile Ser Thr Trp Thr Lys Phe Thr Lys Glu Glu Thr Ser Ser
 385 390 395 400
 Leu Ala Thr Val Phe Leu Glu Ser Val Glu Ser Met Thr Leu Ala Ser
 405 410 415
 Phe Trp Lys Pro Ser Ala Asn Val Thr Pro Ala Val Arg Thr Glu Tyr
 420 425 430
 Leu Asp Ile Glu Ser Lys Val Ile Asn Lys Glu Cys Ser Glu Glu Asn
 435 440 445
 Val Thr Leu Asp Leu Val Ala Lys Gly Asp Lys Met Lys Ile Gly Cys
 450 455 460
 Ser Thr Ile Glu Glu Ser Glu Ser Thr Glu Thr Thr Gly Val Ala Phe
 465 470 475 480
 Val Ser Phe Val Gly Met Glu Ser Val Leu Asn Glu Arg Phe Phe Gln
 485 490 495
 Asp His Gln Ala Pro Leu Thr Thr Ser Glu Ile Lys Leu Lys Met Asn
 500 505 510
 Ser Arg Val Val Gly Gly Ile Met Thr Gly Glu Lys Lys Asp Gly Phe
 515 520 525
 Ser Asp Pro Ile Ile Tyr Thr Leu Glu Asn Val Gln Pro Lys Gln Lys
 530 535 540
 Phe Glu Arg Pro Ile Cys Val Ser Trp Ser Thr Asp Val Lys Gly Gly
 545 550 555 560
 Arg Trp Thr Ser Phe Gly Cys Val Ile Leu Glu Ala Ser Glu Thr Tyr
 565 570 575
 Thr Ile Cys Ser Cys Asn Gln Met Ala Asn Leu Ala Val Ile Met Ala
 580 585 590
 Ser Gly Glu Leu Thr Met Asp Phe Ser Leu Tyr Ile Ile Ser His Val

76/518

595	600	605
Gly Ile Ile Ile Ser Leu Val Cys Leu Val Leu Ala Ile Ala Thr Phe		
610	615	620
Leu Leu Cys Arg Ser Ile Arg Asn His Asn Thr Tyr Leu His Leu His		
625	630	635
Leu Cys Val Cys Leu Leu Ala Lys Thr Leu Phe Leu Ala Gly Ile		
645	650	655
His Lys Thr Asp Asn Lys Thr Gly Cys Ala Ile Ile Ala Gly Phe Leu		
660	665	670
His Tyr Leu Phe Leu Ala Cys Phe Phe Trp Met Leu Val Glu Ala Val		
675	680	685
Ile Leu Phe Leu Met Val Arg Asn Leu Lys Val Val Asn Tyr Phe Ser		
690	695	700
Ser Arg Asn Ile Lys Met Leu His Ile Cys Ala Phe Gly Tyr Gly Leu		
705	710	715
Pro Met Leu Val Val Val Ile Ser Ala Ser Val Gln Pro Gln Gly Tyr		
725	730	735
Gly Met His Asn Arg Cys Trp Leu Asn Thr Glu Thr Gly Phe Ile Trp		
740	745	750
Ser Phe Leu Gly Pro Val Cys Thr Val Ile Val Ile Asn Ser Leu Leu		
755	760	765
Leu Thr Trp Thr Leu Trp Ile Leu Arg Gln Arg Leu Ser Ser Val Asn		
770	775	780
Ala Glu Val Ser Thr Leu Lys Asp Thr Arg Leu Leu Thr Phe Lys Ala		
785	790	795
Phe Ala Gln Leu Phe Ile Leu Gly Cys Ser Trp Val Leu Gly Ile Phe		
805	810	815
Gln Ile Gly Pro Val Ala Gly Val Met Ala Tyr Leu Phe Thr Ile Ile		
820	825	830

77/518

Asn Ser Leu Gln Gly Ala Phe Ile Phe Leu Ile His Cys Leu Leu Asn
 835 840 845
 Gly Gln Val Arg Glu Glu Tyr Lys Arg Trp Ile Thr Gly Lys Thr Lys
 850 855 860
 Pro Ser Ser Gln Ser Gln Thr Ser Arg Ile Leu Leu Ser Ser Met Pro
 865 870 875 880
 Ser Ala Ser Lys Thr Gly Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly
 885 890 895
 Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys
 900 905 910
 Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu
 915 920 925
 Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro
 930 935 940
 Thr Leu Val Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr
 945 950 955 960
 Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu
 965 970 975
 Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr
 980 985 990
 Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg
 995 1000 1005
 Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly
 1010 1015 1020
 His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala
 1025 1030 1035 1040
 Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn
 1045 1050 1055
 Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr

78/518

1060	1065	1070	
Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser			
1075	1080	1085	
Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met			
1090	1095	1100	
Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp			
1105	1110	1115	1120
Glu Leu Tyr Asn			

<210> 44

<211> 599

<212> PRT

<213> Human

<400> 44

Met Ala Pro Thr Glu Pro Trp Ser Pro Ser Pro Gly Ser Ala Pro Trp			
5	10	15	
Asp Tyr Ser Gly Leu Asp Gly Leu Glu Glu Leu Glu Leu Cys Pro Ala			
20	25	30	
Gly Asp Leu Pro Tyr Gly Tyr Val Tyr Ile Pro Ala Leu Tyr Leu Ala			
35	40	45	
Ala Phe Ala Val Gly Leu Leu Gly Asn Ala Phe Val Val Trp Leu Leu			
50	55	60	
Ala Gly Arg Arg Gly Pro Arg Arg Leu Val Asp Thr Phe Val Leu His			
65	70	75	80
Leu Ala Ala Ala Asp Leu Gly Phe Val Leu Thr Leu Pro Leu Trp Ala			
85	90	95	
Ala Ala Ala Ala Leu Gly Gly Arg Trp Pro Phe Gly Asp Gly Leu Cys			
100	105	110	

79/518

Lys Leu Ser Ser Phe Ala Leu Ala Gly Thr Arg Cys Ala Gly Ala Leu
 115 120 125
 Leu Leu Ala Gly Met Ser Val Asp Arg Tyr Leu Ala Val Val Lys Leu
 130 135 140
 Leu Glu Ala Arg Pro Leu Arg Thr Pro Arg Cys Ala Leu Ala Ser Cys
 145 150 155 160
 Cys Gly Val Trp Ala Val Ala Leu Leu Ala Gly Leu Pro Ser Leu Val
 165 170 175
 Tyr Arg Gly Leu Gln Pro Leu Pro Gly Gly Gln Asp Ser Gln Cys Gly
 180 185 190
 Glu Glu Pro Ser His Ala Phe Gln Gly Leu Ser Leu Leu Leu Leu Leu
 195 200 205
 Leu Thr Phe Val Leu Pro Leu Val Val Thr Leu Phe Cys Tyr Cys Arg
 210 215 220
 Ile Ser Arg Arg Leu Arg Arg Pro Pro His Val Gly Arg Ala Arg Arg
 225 230 235 240
 Asn Ser Leu Arg Ile Ile Phe Ala Ile Glu Ser Thr Phe Val Gly Ser
 245 250 255
 Trp Leu Pro Phe Ser Ala Leu Arg Ala Val Phe His Leu Ala Arg Leu
 260 265 270
 Gly Ala Leu Pro Leu Pro Cys Pro Leu Leu Leu Ala Leu Arg Trp Gly
 275 280 285
 Leu Thr Ile Ala Thr Cys Leu Ala Phe Val Asn Ser Cys Ala Asn Pro
 290 295 300
 Leu Ile Tyr Leu Leu Leu Asp Arg Ser Phe Arg Ala Arg Ala Leu Asp
 305 310 315 320
 Gly Ala Cys Gly Arg Thr Gly Arg Leu Ala Arg Arg Ile Ser Ser Ala
 325 330 335
 Ser Ser Leu Ser Arg Asp Asp Ser Ser Val Phe Arg Cys Arg Ala Gln

80/518

340	345	350	
Ala Ala Asn Thr Ala Ser Ala Ser Trp Ala Ser Lys Gly Glu Glu Leu			
355	360	365	
Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn			
370	375	380	
Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr			
385	390	395	400
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val			
405	410	415	
Pro Trp Pro Thr Leu Val Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe			
420	425	430	
Ser Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala			
435	440	445	
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp			
450	455	460	
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu			
465	470	475	480
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn			
485	490	495	
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr			
500	505	510	
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr			
515	520	525	
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln			
530	535	540	
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His			
545	550	555	560
Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg			
565	570	575	

81/518

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His

580

585

590

Gly Met Asp Glu Leu Tyr Asn

595

<210> 45

<211> 557

<212> PRT

<213> Human

<400> 45

Met Ser Gln Gln Asn Thr Ser Gly Asp Cys Leu Phe Asp Gly Val Asn

5

10

15

Glu Leu Met Lys Thr Leu Gln Phe Ala Val His Ile Pro Thr Phe Val

20

25

30

Leu Gly Leu Leu Leu Asn Leu Leu Ala Ile His Gly Phe Ser Thr Phe

35

40

45

Leu Lys Asn Arg Trp Pro Asp Tyr Ala Ala Thr Ser Ile Tyr Met Ile

50

55

60

Asn Leu Ala Val Phe Asp Leu Leu Leu Val Leu Ser Leu Pro Phe Lys

65

70

75

80

Met Val Leu Ser Gln Val Gln Ser Pro Phe Pro Ser Leu Cys Thr Leu

85

90

95

Val Glu Cys Leu Tyr Phe Val Ser Met Tyr Gly Ser Val Phe Thr Ile

100

105

110

Cys Phe Ile Ser Met Asp Arg Phe Leu Ala Ile Arg Tyr Pro Leu Leu

115

120

125

Val Ser His Leu Arg Ser Pro Arg Lys Ile Phe Gly Ile Cys Cys Thr

130

135

140

82/518

Ile Trp Val Leu Val Trp Thr Gly Ser Ile Pro Ile Tyr Ser Phe His
 145 150 155 160
 Gly Lys Val Glu Lys Tyr Met Cys Phe His Asn Met Ser Asp Asp Thr
 165 170 175
 Trp Ser Ala Lys Val Phe Phe Pro Leu Glu Val Phe Gly Phe Leu Leu
 180 185 190
 Pro Met Gly Ile Met Gly Phe Cys Cys Ser Arg Ser Ile His Ile Leu
 195 200 205
 Leu Gly Arg Arg Asp His Thr Gln Asp Trp Val Gln Gln Lys Ala Cys
 210 215 220
 Ile Tyr Ser Ile Ala Ala Ser Leu Ala Val Phe Val Val Ser Phe Leu
 225 230 235 240
 Pro Val His Leu Gly Phe Phe Leu Gln Phe Leu Val Arg Asn Ser Phe
 245 250 255
 Ile Val Glu Cys Arg Ala Lys Gln Ser Ile Ser Phe Phe Leu Gln Leu
 260 265 270
 Ser Met Cys Phe Ser Asn Val Asn Cys Cys Leu Asp Val Phe Cys Tyr
 275 280 285
 Tyr Phe Val Ile Lys Glu Phe Arg Met Asn Ile Arg Ala His Arg Pro
 290 295 300
 Ser Arg Val Gln Leu Val Leu Gln Asp Thr Thr Ile Ser Arg Gly Ala
 305 310 315 320
 Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu
 325 330 335
 Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly
 340 345 350
 Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr
 355 360 365
 Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Cys

83/518

370	375	380	
Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg His			
385	390	395	400
Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr			
	405	410	415
Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys			
	420	425	430
Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp			
	435	440	445
Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr			
	450	455	460
Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile			
465	470	475	480
Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser Val Gln			
	485	490	495
Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val			
	500	505	510
Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys			
	515	520	525
Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr			
	530	535	540
Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn			
545	550	555	

<210> 46

<211> 708

<212> PRT

<213> Human

84/518

<400> 46

Met Asp Thr Thr Met Glu Ala Asp Leu Gly Ala Thr Gly His Arg Pro			
	5	10	15
Arg Thr Glu Leu Asp Asp Glu Asp Ser Tyr Pro Gln Gly Gly Trp Asp			
	20	25	30
Thr Val Phe Leu Val Ala Leu Leu Leu Gly Leu Pro Ala Asn Gly			
	35	40	45
Leu Met Ala Trp Leu Ala Gly Ser Gln Ala Arg His Gly Ala Gly Thr			
	50	55	60
Arg Leu Ala Leu Leu Leu Ser Leu Ala Leu Ser Asp Phe Leu Phe			
	65	70	75
Leu Ala Ala Ala Ala Phe Gln Ile Leu Glu Ile Arg His Gly Gly His			
	85	90	95
Trp Pro Leu Gly Thr Ala Ala Cys Arg Phe Tyr Tyr Phe Leu Trp Gly			
	100	105	110
Val Ser Tyr Ser Ser Gly Leu Phe Leu Leu Ala Ala Leu Ser Leu Asp			
	115	120	125
Arg Cys Leu Leu Ala Leu Cys Pro His Trp Tyr Pro Gly His Arg Pro			
	130	135	140
Val Arg Leu Pro Leu Trp Val Cys Ala Gly Val Trp Val Leu Ala Thr			
	145	150	155
Leu Phe Ser Val Pro Trp Leu Val Phe Pro Glu Ala Ala Val Trp Trp			
	165	170	175
Tyr Asp Leu Val Ile Cys Leu Asp Phe Trp Asp Ser Glu Glu Leu Ser			
	180	185	190
Leu Arg Met Leu Glu Val Leu Gly Gly Phe Leu Pro Phe Leu Leu Leu			
	195	200	205
Leu Val Cys His Val Leu Thr Gln Ala Thr Ala Cys Arg Thr Cys His			
	210	215	220

85/518

Arg Gln Gln Gln Pro Ala Ala Cys Arg Gly Phe Ala Arg Val Ala Arg
 225 230 235 240
 Thr Ile Leu Ser Ala Tyr Val Val Leu Arg Leu Pro Tyr Gln Leu Ala
 245 250 255
 Gln Leu Leu Tyr Leu Ala Phe Leu Trp Asp Val Tyr Ser Gly Tyr Leu
 260 265 270
 Leu Trp Glu Ala Leu Val Tyr Ser Asp Tyr Leu Ile Leu Leu Asn Ser
 275 280 285
 Cys Leu Ser Pro Phe Leu Cys Leu Met Ala Ser Ala Asp Leu Arg Thr
 290 295 300
 Leu Leu Arg Ser Val Leu Ser Ser Phe Ala Ala Ala Leu Cys Glu Glu
 305 310 315 320
 Arg Pro Gly Ser Phe Thr Pro Thr Glu Pro Gln Thr Gln Leu Asp Ser
 325 330 335
 Glu Gly Pro Thr Leu Pro Glu Pro Met Ala Glu Ala Gln Ser Gln Met
 340 345 350
 Asp Pro Val Ala Gln Pro Gln Val Asn Pro Thr Leu Gln Pro Arg Ser
 355 360 365
 Asp Pro Thr Ala Gln Pro Gln Leu Asn Pro Thr Ala Gln Pro Gln Ser
 370 375 380
 Asp Pro Thr Ala Gln Pro Gln Leu Asn Leu Met Ala Gln Pro Gln Ser
 385 390 395 400
 Asp Ser Val Ala Gln Pro Gln Ala Asp Thr Asn Val Gln Thr Pro Ala
 405 410 415
 Pro Ala Ala Ser Ser Val Pro Ser Pro Cys Asp Glu Ala Ser Pro Thr
 420 425 430
 Pro Ser Ser His Pro Thr Pro Gly Ala Leu Glu Asp Pro Ala Thr Pro
 435 440 445
 Pro Ala Ser Glu Gly Glu Ser Pro Ser Ser Thr Pro Pro Glu Ala Ala

86/518

450	455	460
Pro Gly Ala Gly Pro Thr Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly		
465	470	475 480
Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys		
485	490	495
Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu		
500	505	510
Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro		
515	520	525
Thr Leu Val Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr		
530	535	540
Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu		
545	550	555 560
Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr		
565	570	575
Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg		
580	585	590
Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly		
595	600	605
His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala		
610	615	620
Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn		
625	630	635 640
Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr		
645	650	655
Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser		
660	665	670
Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met		
675	680	685

87/518

Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp

690

695

700

Glu Leu Tyr Asn

705

<210> 47

<211> 637

<212> PRT

<213> Human

<400> 47

Met Arg Pro Glu Arg Pro Arg Pro Arg Gly Ser Ala Pro Gly Pro Met

5

10

15

Glu Thr Pro Pro Trp Asp Pro Ala Arg Asn Asp Ser Leu Pro Pro Thr

20

25

30

Leu Thr Pro Ala Val Pro Pro Tyr Val Lys Leu Gly Leu Thr Val Val

35

40

45

Tyr Thr Val Phe Tyr Ala Leu Leu Phe Val Phe Ile Tyr Val Gln Leu

50

55

60

Trp Leu Val Leu Arg Tyr Arg His Lys Arg Leu Ser Tyr Gln Ser Val

65

70

75

80

Phe Leu Phe Leu Cys Leu Phe Trp Ala Ser Leu Arg Thr Val Leu Phe

85

90

95

Ser Phe Tyr Phe Lys Asp Phe Val Ala Ala Asn Ser Leu Ser Pro Phe

100

105

110

Val Phe Trp Leu Leu Tyr Cys Phe Pro Val Cys Leu Gln Phe Phe Thr

115

120

125

Leu Thr Leu Met Asn Leu Tyr Phe Thr Gln Val Ile Phe Lys Ala Lys

130

135

140

88/518

Ser Lys Tyr Ser Pro Glu Leu Leu Lys Tyr Arg Leu Pro Leu Tyr Leu
 145 150 155 160
 Ala Ser Leu Phe Ile Ser Leu Val Phe Leu Leu Val Asn Leu Thr Cys
 165 170 175
 Ala Val Leu Val Lys Thr Gly Asn Trp Glu Arg Lys Val Ile Val Ser
 180 185 190
 Val Arg Val Ala Ile Asn Asp Thr Leu Phe Val Leu Cys Ala Val Ser
 195 200 205
 Leu Ser Ile Cys Leu Tyr Lys Ile Ser Lys Met Ser Leu Ala Asn Ile
 210 215 220
 Tyr Leu Glu Ser Lys Gly Ser Ser Val Cys Gln Val Thr Ala Ile Gly
 225 230 235 240
 Val Thr Val Ile Leu Leu Tyr Thr Ser Arg Ala Cys Tyr Asn Leu Phe
 245 250 255
 Ile Leu Ser Phe Ser Gln Asn Lys Ser Val His Ser Phe Asp Tyr Asp
 260 265 270
 Trp Tyr Asn Val Ser Asp Gln Ala Asp Leu Lys Asn Gln Leu Gly Asp
 275 280 285
 Ala Gly Tyr Val Leu Phe Gly Val Val Leu Phe Val Trp Glu Leu Leu
 290 295 300
 Pro Thr Thr Leu Val Val Tyr Phe Phe Arg Val Arg Asn Pro Thr Lys
 305 310 315 320
 Asp Leu Thr Asn Pro Gly Met Val Pro Ser His Gly Phe Ser Pro Arg
 325 330 335
 Ser Tyr Phe Phe Asp Asn Pro Arg Arg Tyr Asp Ser Asp Asp Asp Leu
 340 345 350
 Ala Trp Asn Ile Ala Pro Gln Gly Leu Gln Gly Gly Phe Ala Pro Asp
 355 360 365
 Tyr Tyr Asp Trp Gly Gln Gln Thr Asn Ser Phe Leu Ala Gln Ala Gly

89/518

370	375	380	
Thr Leu Gln Asp Ser Thr Leu Asp Pro Asp Lys Pro Ser Leu Gly Ala			
385	390	395	400
Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu			
405	410	415	
Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly			
420	425	430	
Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr			
435	440	445	
Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Cys			
450	455	460	
Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg His			
465	470	475	480
Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr			
485	490	495	
Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys			
500	505	510	
Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp			
515	520	525	
Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr			
530	535	540	
Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile			
545	550	555	560
Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser Val Gln			
565	570	575	
Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val			
580	585	590	
Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys			
595	600	605	

90/518

Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr

610

615

620

Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn

625

630

635

<210> 48

<211> 657

<212> PRT

<213> Human

<400> 48

Met Val Phe Ser Ala Val Leu Thr Ala Phe His Thr Gly Thr Ser Asn

5

10

15

Thr Thr Phe Val Val Tyr Glu Asn Thr Tyr Met Asn Ile Thr Leu Pro

20

25

30

Pro Pro Phe Gln His Pro Asp Leu Ser Pro Leu Leu Arg Tyr Ser Phe

35

40

45

Glu Thr Met Ala Pro Thr Gly Leu Ser Ser Leu Thr Val Asn Ser Thr

50

55

60

Ala Val Pro Thr Thr Pro Ala Ala Phe Lys Ser Leu Asn Leu Pro Leu

65

70

75

80

Gln Ile Thr Leu Ser Ala Ile Met Ile Phe Ile Leu Phe Val Ser Phe

85

90

95

Leu Gly Asn Leu Val Val Cys Leu Met Val Tyr Gln Lys Ala Ala Met

100

105

110

Arg Ser Ala Ile Asn Ile Leu Leu Ala Ser Leu Ala Phe Ala Asp Met

115

120

125

Leu Leu Ala Val Leu Asn Met Pro Phe Ala Leu Val Thr Ile Leu Thr

130

135

140

91/518

Thr Arg Trp Ile Phe Gly Lys Phe Phe Cys Arg Val Ser Ala Met Phe
 145 150 155 160
 Phe Trp Leu Phe Val Ile Glu Gly Val Ala Ile Leu Leu Ile Ile Ser
 165 170 175
 Ile Asp Arg Phe Leu Ile Ile Val Gln Arg Gln Asp Lys Leu Asn Pro
 180 185 190
 Tyr Arg Ala Lys Val Leu Ile Ala Val Ser Trp Ala Thr Ser Phe Cys
 195 200 205
 Val Ala Phe Pro Leu Ala Val Gly Asn Pro Asp Leu Gln Ile Pro Ser
 210 215 220
 Arg Ala Pro Gln Cys Val Phe Gly Tyr Thr Thr Asn Pro Gly Tyr Gln
 225 230 235 240
 Ala Tyr Val Ile Leu Ile Ser Leu Ile Ser Phe Phe Ile Pro Phe Leu
 245 250 255
 Val Ile Leu Tyr Ser Phe Met Gly Ile Leu Asn Thr Leu Arg His Asn
 260 265 270
 Ala Leu Arg Ile His Ser Tyr Pro Glu Gly Ile Cys Leu Ser Gln Ala
 275 280 285
 Ser Lys Leu Gly Leu Met Ser Leu Gln Arg Pro Phe Gln Met Ser Ile
 290 295 300
 Asp Met Gly Phe Lys Thr Arg Ala Phe Thr Thr Ile Leu Ile Leu Phe
 305 310 315 320
 Ala Val Phe Ile Val Cys Trp Ala Pro Phe Thr Thr Tyr Ser Leu Val
 325 330 335
 Ala Thr Phe Ser Lys His Phe Tyr Tyr Gln His Asn Phe Phe Glu Ile
 340 345 350
 Ser Thr Trp Leu Leu Trp Leu Cys Tyr Leu Lys Ser Ala Leu Asn Pro
 355 360 365
 Leu Ile Tyr Tyr Trp Arg Ile Lys Lys Phe His Asp Ala Cys Leu Asp

92/518

370	375	380	
Met Met Pro Lys Ser Phe Lys Phe Leu Pro Gln Leu Pro Gly His Thr			
385	390	395	400
Lys Arg Arg Ile Arg Pro Ser Ala Val Tyr Val Cys Gly Glu His Arg			
405	410	415	
Thr Val Val Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro			
420	425	430	
Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val			
435	440	445	
Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys			
450	455	460	
Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val			
465	470	475	480
Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His			
485	490	495	
Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val			
500	505	510	
Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg			
515	520	525	
Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu			
530	535	540	
Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu			
545	550	555	560
Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln			
565	570	575	
Lys Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp			
580	585	590	
Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly			
595	600	605	

93/518

Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser

610

615

620

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu

625

630

635

640

Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr

645

650

655

Asn

<210> 49

<211> 611

<212> PRT

<213> Human

<400> 49

Met Ala Asn Thr Thr Gly Glu Pro Glu Glu Val Ser Gly Ala Leu Ser

5

10

15

Pro Pro Ser Ala Ser Ala Tyr Val Lys Leu Val Leu Leu Gly Leu Ile

20

25

30

Met Cys Val Ser Leu Ala Gly Asn Ala Ile Leu Ser Leu Leu Val Leu

35

40

45

Lys Glu Arg Ala Leu His Lys Ala Pro Tyr Tyr Phe Leu Leu Asp Leu

50

55

60

Cys Leu Ala Asp Gly Ile Arg Ser Ala Val Cys Phe Pro Phe Val Leu

65

70

75

80

Ala Ser Val Arg His Gly Ser Ser Trp Thr Phe Ser Ala Leu Ser Cys

85

90

95

Lys Ile Val Ala Phe Met Ala Val Leu Phe Cys Phe His Ala Ala Phe

100

105

110

Met Leu Phe Cys Ile Ser Val Thr Arg Tyr Met Ala Ile Ala His His

94/518

115	120	125
Arg Phe Tyr Ala Lys Arg Met Thr Leu Trp Thr Cys Ala Ala Val Ile		
130	135	140
Cys Met Ala Trp Thr Leu Ser Val Ala Met Ala Phe Pro Pro Val Phe		
145	150	155
Asp Val Gly Thr Tyr Lys Phe Ile Arg Glu Glu Asp Gln Cys Ile Phe		
165	170	175
Glu His Arg Tyr Phe Lys Ala Asn Asp Thr Leu Gly Phe Met Leu Met		
180	185	190
Leu Ala Val Leu Met Ala Ala Thr His Ala Val Tyr Gly Lys Leu Leu		
195	200	205
Leu Phe Glu Tyr Arg His Arg Lys Met Lys Pro Val Gln Met Val Pro		
210	215	220
Ala Ile Ser Gln Asn Trp Thr Phe His Gly Pro Gly Ala Thr Gly Gln		
225	230	235
Ala Ala Ala Asn Trp Ile Ala Gly Phe Gly Arg Gly Pro Met Pro Pro		
245	250	255
Thr Leu Leu Gly Ile Arg Gln Asn Gly His Ala Ala Ser Arg Arg Leu		
260	265	270
Leu Gly Met Asp Glu Val Lys Gly Glu Lys Gln Leu Gly Arg Met Phe		
275	280	285
Tyr Ala Ile Thr Leu Leu Phe Leu Leu Leu Trp Ser Pro Tyr Ile Val		
290	295	300
Ala Cys Tyr Trp Arg Val Phe Val Lys Ala Cys Ala Val Pro His Arg		
305	310	315
Tyr Leu Ala Thr Ala Val Trp Met Ser Phe Ala Gln Ala Ala Val Asn		
325	330	335
Pro Ile Val Cys Phe Leu Leu Asn Lys Asp Leu Lys Lys Cys Leu Arg		
340	345	350

95/518

Thr His Ala Pro Cys Trp Gly Thr Gly Gly Ala Pro Ala Pro Arg Glu
 355 360 365
 Pro Tyr Cys Val Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 370 375 380
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 385 390 395 400
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 405 410 415
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 420 425 430
 Leu Val Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 435 440 445
 Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 450 455 460
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 465 470 475 480
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 485 490 495
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 500 505 510
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 515 520 525
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile
 530 535 540
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 545 550 555 560
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 565 570 575
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val

96/518

580	585	590
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu		
595	600	605
Leu Tyr Asn		
610		

<210> 50
 <211> 798
 <212> PRT
 <213> Human

```

<400> 50
Met Asp Leu Lys Thr Val Leu Ser Leu Pro Arg Tyr Pro Gly Glu Phe
      5                      10                      15
Leu His Pro Val Val Tyr Ala Cys Thr Ala Val Met Leu Leu Cys Leu
      20                      25                      30
Leu Ala Ser Phe Val Thr Tyr Ile Val His Gln Ser Ala Ile Arg Ile
      35                      40                      45
Ser Arg Lys Gly Arg His Thr Leu Leu Asn Phe Cys Phe His Ala Ala
      50                      55                      60
Leu Thr Phe Thr Val Phe Ala Gly Gly Ile Asn Arg Thr Lys Tyr Pro
      65                      70                      75                      80
Ile Leu Cys Gln Ala Val Gly Ile Val Leu His Tyr Ser Thr Leu Ser
      85                      90                      95
Thr Met Leu Trp Ile Gly Val Thr Ala Arg Asn Ile Tyr Lys Gln Val
      100                     105                     110
Thr Lys Lys Ala Pro Leu Cys Leu Asp Thr Asp Gln Pro Pro Tyr Pro
      115                     120                     125
Arg Gln Pro Leu Leu Arg Phe Tyr Leu Val Ser Gly Gly Val Pro Phe

```

97/518

130	135	140	
Ile Ile Cys Gly Val Thr Ala Ala Thr Asn Ile Arg Asn Tyr Gly Thr			
145	150	155	160
Glu Asp Glu Asp Thr Ala Tyr Cys Trp Met Ala Trp Glu Pro Ser Leu			
	165	170	175
Gly Ala Phe Tyr Gly Pro Ala Ala Ile Ile Thr Leu Val Thr Cys Val			
	180	185	190
Tyr Phe Leu Gly Thr Tyr Val Gln Leu Arg Arg His Pro Gly Arg Arg			
	195	200	205
Tyr Glu Leu Arg Thr Gln Pro Glu Glu Gln Arg Arg Leu Ala Thr Pro			
	210	215	220
Glu Gly Gly Arg Gly Ile Arg Pro Gly Thr Pro Pro Ala His Asp Ala			
225	230	235	240
Pro Gly Ala Ser Val Leu Gln Asn Glu His Ser Phe Gln Ala Gln Leu			
	245	250	255
Arg Ala Ala Ala Phe Thr Leu Phe Leu Phe Thr Ala Thr Trp Ala Phe			
	260	265	270
Gly Ala Leu Ala Val Ser Gln Gly His Phe Leu Asp Met Val Phe Ser			
	275	280	285
Cys Leu Tyr Gly Ala Phe Cys Val Thr Leu Gly Leu Phe Val Leu Ile			
	290	295	300
His His Cys Ala Lys Arg Glu Asp Val Trp Gln Cys Trp Trp Ala Cys			
305	310	315	320
Cys Pro Pro Arg Lys Asp Ala His Pro Ala Leu Asp Ala Asn Gly Ala			
	325	330	335
Ala Leu Gly Arg Ala Ala Cys Leu His Ser Pro Gly Leu Gly Gln Pro			
	340	345	350
Arg Gly Phe Ala His Pro Pro Gly Pro Cys Lys Met Thr Asn Leu Gln			
	355	360	365

98/518

Ala Ala Gln Gly His Ala Ser Cys Leu Ser Pro Ala Thr Pro Cys Cys
 370 375 380
 Ala Lys Met His Cys Glu Pro Leu Thr Ala Asp Glu Ala His Val His
 385 390 395 400
 Leu Gln Glu Glu Gly Ala Phe Gly His Asp Pro His Leu His Gly Cys
 405 410 415
 Leu Gln Gly Arg Thr Lys Pro Pro Tyr Phe Ser Arg His Pro Ala Glu
 420 425 430
 Glu Pro Glu Tyr Ala Tyr His Ile Pro Ser Ser Leu Asp Gly Ser Pro
 435 440 445
 Arg Ser Ser Arg Thr Asp Ser Pro Pro Ser Ser Leu Asp Gly Pro Ala
 450 455 460
 Gly Thr His Thr Leu Ala Cys Cys Thr Gln Gly Asp Pro Phe Pro Met
 465 470 475 480
 Val Thr Gln Pro Glu Gly Ser Asp Gly Ser Pro Ala Leu Tyr Ser Cys
 485 490 495
 Pro Thr Gln Pro Gly Arg Glu Ala Ala Leu Gly Pro Gly His Leu Glu
 500 505 510
 Met Leu Arg Arg Thr Gln Ser Leu Pro Phe Gly Gly Pro Ser Gln Asn
 515 520 525
 Gly Leu Pro Lys Gly Lys Leu Leu Glu Gly Leu Pro Phe Gly Thr Asp
 530 535 540
 Gly Thr Gly Asn Ile Arg Thr Gly Pro Trp Lys Asn Glu Thr Thr Val
 545 550 555 560
 Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 565 570 575
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 580 585 590
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys

99/518

595	600	605
Thr Thr Gly Lys Leu Pro Val	Pro Trp Pro Thr Leu Val	Thr Thr Leu
610	615	620
Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg		
625	630	635
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg		
645	650	655
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val		
660	665	670
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile		
675	680	685
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn		
690	695	700
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly		
705	710	715
Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser Val		
725	730	735
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro		
740	745	750
Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser		
755	760	765
Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val		
770	775	780
Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn		
785	790	795

<210> 51

<211> 557

<212> PRT

100/518

<213> Human

<400> 51

Met Thr Asn Ser Ser Phe Phe Cys Pro Val Tyr Lys Asp Leu Glu Pro
5 10 15
Phe Thr Tyr Phe Phe Tyr Leu Val Phe Leu Val Gly Ile Ile Gly Ser
20 25 30
Cys Phe Ala Thr Trp Ala Phe Ile Gln Lys Asn Thr Asn His Arg Cys
35 40 45
Val Ser Ile Tyr Leu Ile Asn Leu Leu Thr Ala Asp Phe Leu Leu Thr
50 55 60
Leu Ala Leu Pro Val Lys Ile Val Val Asp Leu Gly Val Ala Pro Trp
65 70 75 80
Lys Leu Lys Ile Phe His Cys Gln Val Thr Ala Cys Leu Ile Tyr Ile
85 90 95
Asn Met Tyr Leu Ser Ile Ile Phe Leu Ala Phe Val Ser Ile Asp Arg
100 105 110
Cys Leu Gln Leu Thr His Ser Cys Lys Ile Tyr Arg Ile Gln Glu Pro
115 120 125
Gly Phe Ala Lys Met Ile Ser Thr Val Val Trp Leu Met Val Leu Leu
130 135 140
Ile Met Val Pro Asn Met Met Ile Pro Ile Lys Asp Ile Lys Glu Lys
145 150 155 160
Ser Asn Val Gly Cys Met Glu Phe Lys Lys Glu Phe Gly Arg Asn Trp
165 170 175
His Leu Leu Thr Asn Phe Ile Cys Val Ala Ile Phe Leu Asn Phe Ser
180 185 190
Ala Ile Ile Leu Ile Ser Asn Cys Leu Val Ile Arg Gln Leu Tyr Arg
195 200 205

101/518

Asn Lys Asp Asn Glu Asn Tyr Pro Asn Val Lys Lys Ala Leu Ile Asn
 210 215 220
 Ile Leu Leu Val Thr Thr Gly Tyr Ile Ile Cys Phe Val Pro Tyr His
 225 230 235 240
 Ile Val Arg Ile Pro Tyr Thr Leu Ser Gln Thr Glu Val Ile Thr Asp
 245 250 255
 Cys Ser Thr Arg Ile Ser Leu Phe Lys Ala Lys Glu Ala Thr Leu Leu
 260 265 270
 Leu Ala Val Ser Asn Leu Cys Phe Asp Pro Ile Leu Tyr Tyr His Leu
 275 280 285
 Ser Lys Ala Phe Arg Ser Lys Val Thr Glu Thr Phe Ala Ser Pro Lys
 290 295 300
 Glu Thr Lys Ala Gln Lys Glu Lys Leu Arg Cys Glu Asn Asn Ala Ala
 305 310 315 320
 Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu
 325 330 335
 Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly
 340 345 350
 Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr
 355 360 365
 Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Cys
 370 375 380
 Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg His
 385 390 395 400
 Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr
 405 410 415
 Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys
 420 425 430
 Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp

102/518

435 440 445
 Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr
 450 455 460
 Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile
 465 470 475 480
 Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser Val Gln
 485 490 495
 Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val
 500 505 510
 Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys
 515 520 525
 Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr
 530 535 540
 Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn
 545 550 555

<210> 52

<211> 596

<212> PRT

<213> Human

<400> 52

Met Gly Phe Asn Leu Thr Leu Ala Lys Leu Pro Asn Asn Glu Leu His
 5 10 15
 Gly Gln Glu Ser His Asn Ser Gly Asn Arg Ser Asp Gly Pro Gly Lys
 20 25 30
 Asn Thr Thr Leu His Asn Glu Phe Asp Thr Ile Val Leu Pro Val Leu
 35 40 45
 Tyr Leu Ile Ile Phe Val Ala Ser Ile Leu Leu Asn Gly Leu Ala Val

103/518

50	55	60	
Trp Ile Phe Phe His Ile Arg Asn Lys Thr Ser Phe Ile Phe Tyr Leu			
65	70	75	80
Lys Asn Ile Val Val Ala Asp Leu Ile Met Thr Leu Thr Phe Pro Phe			
85	90	95	
Arg Ile Val His Asp Ala Gly Phe Gly Pro Trp Tyr Phe Lys Phe Ile			
100	105	110	
Leu Cys Arg Tyr Thr Ser Val Leu Phe Tyr Ala Asn Met Tyr Thr Ser			
115	120	125	
Ile Val Phe Leu Gly Leu Ile Ser Ile Asp Arg Tyr Leu Lys Val Val			
130	135	140	
Lys Pro Phe Gly Asp Ser Arg Met Tyr Ser Ile Thr Phe Thr Lys Val			
145	150	155	160
Leu Ser Val Cys Val Trp Val Ile Met Ala Val Leu Ser Leu Pro Asn			
165	170	175	
Ile Ile Leu Thr Asn Gly Gln Pro Thr Glu Asp Asn Ile His Asp Cys			
180	185	190	
Ser Lys Leu Lys Ser Pro Leu Gly Val Lys Trp His Thr Ala Val Thr			
195	200	205	
Tyr Val Asn Ser Cys Leu Phe Val Ala Val Leu Val Ile Leu Ile Gly			
210	215	220	
Cys Tyr Ile Ala Ile Ser Arg Tyr Ile His Lys Ser Ser Arg Gln Phe			
225	230	235	240
Ile Ser Gln Ser Ser Arg Lys Arg Lys His Asn Gln Ser Ile Arg Val			
245	250	255	
Val Val Ala Val Phe Phe Thr Cys Phe Leu Pro Tyr His Leu Cys Arg			
260	265	270	
Ile Pro Phe Thr Phe Ser His Leu Asp Arg Leu Leu Asp Glu Ser Ala			
275	280	285	

104/518

Gln Lys Ile Leu Tyr Tyr Cys Lys Glu Ile Thr Leu Phe Leu Ser Ala
 290 295 300
 Cys Asn Val Cys Leu Asp Pro Ile Ile Tyr Phe Phe Met Cys Arg Ser
 305 310 315 320
 Phe Ser Arg Arg Leu Phe Lys Lys Ser Asn Ile Arg Thr Arg Ser Glu
 325 330 335
 Ser Ile Arg Ser Leu Gln Ser Val Arg Arg Ser Glu Val Arg Ile Tyr
 340 345 350
 Tyr Asp Tyr Thr Asp Val Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly
 355 360 365
 Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys
 370 375 380
 Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu
 385 390 395 400
 Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro
 405 410 415
 Thr Leu Val Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr
 420 425 430
 Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu
 435 440 445
 Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr
 450 455 460
 Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg
 465 470 475 480
 Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly
 485 490 495
 His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala
 500 505 510
 Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn

105/518

515 520 525
 Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr
 530 535 540
 Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser
 545 550 555 560
 Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met
 565 570 575
 Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp
 580 585 590
 Glu Leu Tyr Asn
 595

<210> 53

<211> 572

<212> PRT

<213> Human

<400> 53

Met Leu Gly Ile Met Ala Trp Asn Ala Thr Cys Lys Asn Trp Leu Ala
 5 10 15
 Ala Glu Ala Ala Leu Glu Lys Tyr Tyr Leu Ser Ile Phe Tyr Gly Ile
 20 25 30
 Glu Phe Val Val Gly Val Leu Gly Asn Thr Ile Val Val Tyr Gly Tyr
 35 40 45
 Ile Phe Ser Leu Lys Asn Trp Asn Ser Ser Asn Ile Tyr Leu Phe Asn
 50 55 60
 Leu Ser Val Ser Asp Leu Ala Phe Leu Cys Thr Leu Pro Met Leu Ile
 65 70 75 80
 Arg Ser Tyr Ala Asn Gly Asn Trp Ile Tyr Gly Asp Val Leu Cys Ile

106/518

	85		90		95
Ser Asn Arg Tyr Val Leu His Ala Asn Leu Tyr Thr Ser Ile Leu Phe					
	100		105		110
Leu Thr Phe Ile Ser Ile Asp Arg Tyr Leu Ile Ile Lys Tyr Pro Phe					
	115		120		125
Arg Glu His Leu Leu Gln Lys Lys Glu Phe Ala Ile Leu Ile Ser Leu					
	130		135		140
Ala Ile Trp Val Leu Val Thr Leu Glu Leu Leu Pro Ile Leu Pro Leu					
	145		150		155
Ile Asn Pro Val Ile Thr Asp Asn Gly Thr Thr Cys Asn Asp Phe Ala					
	165		170		175
Ser Ser Gly Asp Pro Asn Tyr Asn Leu Ile Tyr Ser Met Cys Leu Thr					
	180		185		190
Leu Leu Gly Phe Leu Ile Pro Leu Phe Val Met Cys Phe Phe Tyr Tyr					
	195		200		205
Lys Ile Ala Leu Phe Leu Lys Gln Arg Asn Arg Gln Val Ala Thr Ala					
	210		215		220
Leu Pro Leu Glu Lys Pro Leu Asn Leu Val Ile Met Ala Val Val Ile					
	225		230		235
Phe Ser Val Pro Phe Thr Pro Tyr His Val Met Arg Asn Val Arg Ile					
	245		250		255
Ala Ser Arg Leu Gly Ser Trp Lys Gln Tyr Gln Cys Thr Gln Val Val					
	260		265		270
Ile Asn Ser Phe Tyr Ile Val Thr Arg Pro Leu Ala Phe Leu Asn Ser					
	275		280		285
Val Ile Asn Pro Val Phe Tyr Phe Leu Leu Gly Asp His Phe Arg Asp					
	290		295		300
Met Leu Met Asn Gln Leu Arg His Asn Phe Lys Ser Leu Thr Ser Phe					
	305		310		315
					320

107/518

Ser Arg Trp Ala His Glu Leu Leu Leu Ser Phe Arg Glu Lys Ala Ser
 325 330 335
 Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu
 340 345 350
 Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu
 355 360 365
 Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr
 370 375 380
 Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Cys Tyr
 385 390 395 400
 Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg His Asp
 405 410 415
 Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile
 420 425 430
 Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe
 435 440 445
 Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe
 450 455 460
 Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn
 465 470 475 480
 Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys
 485 490 495
 Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu
 500 505 510
 Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu
 515 520 525
 Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp
 530 535 540
 Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala

108/518

545 550 555 560
 Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn
 565 570

<210> 54

<211> 575

<212> PRT

<213> Human

<400> 54

Met Arg Ala Val Phe Ile Gln Gly Ala Glu Glu His Pro Ala Ala Phe
 5 10 15
 Cys Tyr Gln Val Asn Gly Ser Cys Pro Arg Thr Val His Thr Leu Gly
 20 25 30
 Ile Gln Leu Val Ile Tyr Leu Ala Cys Ala Ala Gly Met Leu Ile Ile
 35 40 45
 Val Leu Gly Asn Val Phe Val Ala Phe Ala Val Ser Tyr Phe Lys Ala
 50 55 60
 Leu His Thr Pro Thr Asn Phe Leu Leu Leu Ser Leu Ala Leu Ala Asp
 65 70 75 80
 Met Phe Leu Gly Leu Leu Val Leu Pro Leu Ser Thr Ile Arg Ser Val
 85 90 95
 Glu Ser Cys Trp Phe Phe Gly Asp Phe Leu Cys Arg Leu His Thr Tyr
 100 105 110
 Leu Asp Thr Leu Phe Cys Leu Thr Ser Ile Phe His Leu Cys Phe Ile
 115 120 125
 Ser Ile Asp Arg His Cys Ala Ile Cys Asp Pro Leu Leu Tyr Pro Ser
 130 135 140
 Lys Phe Thr Val Arg Val Ala Leu Arg Tyr Ile Leu Ala Gly Trp Gly

109/518

145	150	155	160
Val Pro Ala Ala Tyr Thr Ser Leu Phe Leu Tyr Thr Asp Val Val Glu			
	165	170	175
Thr Arg Leu Ser Gln Trp Leu Glu Glu Met Pro Cys Val Gly Ser Cys			
	180	185	190
Gln Leu Leu Leu Asn Lys Phe Trp Gly Trp Leu Asn Phe Pro Leu Phe			
	195	200	205
Phe Val Pro Cys Leu Ile Met Ile Ser Leu Tyr Val Lys Ile Phe Val			
	210	215	220
Val Ala Thr Arg Gln Ala Gln Gln Ile Thr Thr Leu Ser Lys Ser Leu			
225	230	235	240
Ala Gly Ala Ala Lys His Glu Arg Lys Ala Ala Lys Thr Leu Gly Ile			
	245	250	255
Ala Val Gly Ile Tyr Leu Leu Cys Trp Leu Pro Phe Thr Ile Asp Thr			
	260	265	270
Met Val Asp Ser Leu Leu His Phe Ile Thr Pro Pro Leu Val Phe Asp			
	275	280	285
Ile Phe Ile Trp Phe Ala Tyr Phe Asn Ser Ala Cys Asn Pro Ile Ile			
	290	295	300
Tyr Val Phe Ser Tyr Gln Trp Phe Arg Lys Ala Leu Lys Leu Thr Leu			
305	310	315	320
Ser Gln Lys Val Phe Ser Pro Gln Thr Arg Thr Val Asp Leu Tyr Gln			
	325	330	335
Glu Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu			
	340	345	350
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly			
	355	360	365
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile			
	370	375	380

110/518

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 385 390 395 400
 Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 405 410 415
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 420 425 430
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 435 440 445
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 450 455 460
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 465 470 475 480
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 485 490 495
 Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser
 500 505 510
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 515 520 525
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 530 535 540
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 545 550 555 560
 Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn
 565 570 575

<210> 55

<211> 580

<212> PRT

<213> Human

111/518

<400> 55

Met Thr Ser Asn Phe Ser Gln Pro Val Val Gln Leu Cys Tyr Glu Asp
 5 10 15
 Val Asn Gly Ser Cys Ile Glu Thr Pro Tyr Ser Pro Gly Ser Arg Val
 20 25 30
 Ile Leu Tyr Thr Ala Phe Ser Phe Gly Ser Leu Leu Ala Val Phe Gly
 35 40 45
 Asn Leu Leu Val Met Thr Ser Val Leu His Phe Lys Gln Leu His Ser
 50 55 60
 Pro Thr Asn Phe Leu Ile Ala Ser Leu Ala Cys Ala Asp Phe Leu Val
 65 70 75 80
 Gly Val Thr Val Met Leu Phe Ser Met Val Arg Thr Val Glu Ser Cys
 85 90 95
 Trp Tyr Phe Gly Ala Lys Phe Cys Thr Leu His Ser Cys Cys Asp Val
 100 105 110
 Ala Phe Cys Tyr Ser Ser Val Leu His Leu Cys Phe Ile Cys Ile Asp
 115 120 125
 Arg Tyr Ile Val Val Thr Asp Pro Leu Val Tyr Ala Thr Lys Phe Thr
 130 135 140
 Val Ser Val Ser Gly Ile Cys Ile Ser Val Ser Trp Ile Leu Pro Leu
 145 150 155 160
 Thr Tyr Ser Gly Ala Val Phe Tyr Thr Gly Val Asn Asp Asp Gly Leu
 165 170 175
 Glu Glu Leu Val Ser Ala Leu Asn Cys Val Gly Gly Cys Gln Ile Ile
 180 185 190
 Val Ser Gln Gly Trp Val Leu Ile Asp Phe Leu Leu Phe Phe Ile Pro
 195 200 205
 Thr Leu Val Met Ile Ile Leu Tyr Ser Lys Ile Phe Leu Ile Ala Lys

112/518

210	215	220
Gln Gln Ala Ile Lys Ile Glu Thr Thr Ser Ser Lys Val Glu Ser Ser		
225	230	235
Ser Glu Ser Tyr Lys Ile Arg Val Ala Lys Arg Glu Arg Lys Ala Ala		240
245	250	255
Lys Thr Leu Gly Val Thr Val Leu Ala Phe Val Ile Ser Trp Leu Pro		
260	265	270
Tyr Thr Val Asp Ile Leu Ile Asp Ala Phe Met Gly Phe Leu Thr Pro		
275	280	285
Ala Tyr Ile Tyr Glu Ile Cys Cys Trp Ser Ala Tyr Tyr Asn Ser Ala		
290	295	300
Met Asn Pro Leu Ile Tyr Ala Leu Phe Tyr Pro Trp Phe Arg Lys Ala		
305	310	315
Ile Lys Leu Ile Leu Ser Gly Asp Val Leu Lys Ala Ser Ser Ser Thr		320
325	330	335
Ile Ser Leu Phe Leu Glu Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly		
340	345	350
Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys		
355	360	365
Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu		
370	375	380
Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro		
385	390	395
Thr Leu Val Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr		400
405	410	415
Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu		
420	425	430
Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr		
435	440	445

113/518

Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg
 450 455 460
 Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly
 465 470 475 480
 His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala
 485 490 495
 Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn
 500 505 510
 Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr
 515 520 525
 Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser
 530 535 540
 Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met
 545 550 555 560
 Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp
 565 570 575
 Glu Leu Tyr Asn
 580

<210> 56

<211> 583

<212> PRT

<213> Human

<400> 56

Met Ser Ser Asn Ser Ser Leu Leu Val Ala Val Gln Leu Cys Tyr Ala
 5 10 15
 Asn Val Asn Gly Ser Cys Val Lys Ile Pro Phe Ser Pro Gly Ser Arg
 20 25 30

114/518

Val Ile Leu Tyr Ile Val Phe Gly Phe Gly Ala Val Leu Ala Val Phe
 35 40 45
 Gly Asn Leu Leu Val Met Ile Ser Ile Leu His Phe Lys Gln Leu His
 50 55 60
 Ser Pro Thr Asn Phe Leu Val Ala Ser Leu Ala Cys Ala Asp Phe Leu
 65 70 75 80
 Val Gly Val Thr Val Met Pro Phe Ser Met Val Arg Thr Val Glu Ser
 85 90 95
 Cys Trp Tyr Phe Gly Arg Ser Phe Cys Thr Phe His Thr Cys Cys Asp
 100 105 110
 Val Ala Phe Cys Tyr Ser Ser Leu Phe His Leu Cys Phe Ile Ser Ile
 115 120 125
 Asp Arg Tyr Ile Ala Val Thr Asp Pro Leu Val Tyr Pro Thr Lys Phe
 130 135 140
 Thr Val Ser Val Ser Gly Ile Cys Ile Ser Val Ser Trp Ile Leu Pro
 145 150 155 160
 Leu Met Tyr Ser Gly Ala Val Phe Tyr Thr Gly Val Tyr Asp Asp Gly
 165 170 175
 Leu Glu Glu Leu Ser Asp Ala Leu Asn Cys Ile Gly Gly Cys Gln Thr
 180 185 190
 Val Val Asn Gln Asn Trp Val Leu Thr Asp Phe Leu Ser Phe Phe Ile
 195 200 205
 Pro Thr Phe Ile Met Ile Ile Leu Tyr Gly Asn Ile Phe Leu Val Ala
 210 215 220
 Arg Arg Gln Ala Lys Lys Ile Glu Asn Thr Gly Ser Lys Thr Glu Ser
 225 230 235 240
 Ser Ser Glu Ser Tyr Lys Ala Arg Val Ala Arg Arg Glu Arg Lys Ala
 245 250 255
 Ala Lys Thr Leu Gly Val Thr Val Val Ala Phe Met Ile Ser Trp Leu

115/518

260	265	270
Pro Tyr Ser Ile Asp Ser Leu Ile Asp Ala Phe Met Gly Phe Ile Thr		
275	280	285
Pro Ala Cys Ile Tyr Glu Ile Cys Cys Trp Cys Ala Tyr Tyr Asn Ser		
290	295	300
Ala Met Asn Pro Leu Ile Tyr Ala Leu Phe Tyr Pro Trp Phe Arg Lys		
305	310	315
Ala Ile Lys Val Ile Val Thr Gly Gln Val Leu Lys Asn Ser Ser Ala		
325	330	335
Thr Met Asn Leu Phe Ser Glu His Ile Ala Ser Lys Gly Glu Glu Leu		
340	345	350
Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn		
355	360	365
Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr		
370	375	380
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val		
385	390	395
Pro Trp Pro Thr Leu Val Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe		
405	410	415
Ser Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala		
420	425	430
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp		
435	440	445
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu		
450	455	460
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn		
465	470	475
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr		
485	490	495

116/518

Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr
 500 505 510
 Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
 515 520 525
 Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
 530 535 540
 Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
 545 550 555 560
 Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His
 565 570 575
 Gly Met Asp Glu Leu Tyr Asn
 580

<210> 57

<211> 851

<212> PRT

<213> Human

<400> 57

Met Gly Pro Thr Leu Ala Val Pro Thr Pro Tyr Gly Cys Ile Gly Cys
 5 10 15
 Lys Leu Pro Gln Pro Glu Tyr Pro Pro Ala Leu Ile Ile Phe Met Phe
 20 25 30
 Cys Ala Met Val Ile Thr Ile Val Val Asp Leu Ile Gly Asn Ser Met
 35 40 45
 Val Ile Leu Ala Val Thr Lys Asn Lys Lys Leu Arg Asn Ser Gly Asn
 50 55 60
 Ile Phe Val Val Ser Leu Ser Val Ala Asp Met Leu Val Ala Ile Tyr
 65 70 75 80

117/518

Pro Tyr Pro Leu Met Leu His Ala Met Ser Ile Gly Gly Trp Asp Leu
 85 90 95
 Ser Gln Leu Gln Cys Gln Met Val Gly Phe Ile Thr Gly Leu Ser Val
 100 105 110
 Val Gly Ser Ile Phe Asn Ile Val Ala Ile Ala Ile Asn Arg Tyr Cys
 115 120 125
 Tyr Ile Cys His Ser Leu Gln Tyr Glu Arg Ile Phe Ser Val Arg Asn
 130 135 140
 Thr Cys Ile Tyr Leu Val Ile Thr Trp Ile Met Thr Val Leu Ala Val
 145 150 155 160
 Leu Pro Asn Met Tyr Ile Gly Thr Ile Glu Tyr Asp Pro Arg Thr Tyr
 165 170 175
 Thr Cys Ile Phe Asn Tyr Leu Asn Asn Pro Val Phe Thr Val Thr Ile
 180 185 190
 Val Cys Ile His Phe Val Leu Pro Leu Leu Ile Val Gly Phe Cys Tyr
 195 200 205
 Val Arg Ile Trp Thr Lys Val Leu Ala Ala Arg Asp Pro Ala Gly Gln
 210 215 220
 Asn Pro Asp Asn Gln Leu Ala Glu Val Arg Asn Phe Leu Thr Met Phe
 225 230 235 240
 Val Ile Phe Leu Leu Phe Ala Val Cys Trp Cys Pro Ile Asn Val Leu
 245 250 255
 Thr Val Leu Val Ala Val Ser Pro Lys Glu Met Ala Gly Lys Ile Pro
 260 265 270
 Asn Trp Leu Tyr Leu Ala Ala Tyr Phe Ile Ala Tyr Phe Asn Ser Cys
 275 280 285
 Leu Asn Ala Val Ile Tyr Gly Leu Leu Asn Glu Asn Phe Arg Arg Glu
 290 295 300
 Tyr Trp Thr Ile Phe His Ala Met Arg His Pro Ile Ile Phe Phe Pro

118/518

305	310	315	320
Gly Leu Ile Ser Asp Ile Arg Glu Met Gln Glu Ala Arg Thr Leu Ala			
325	330	335	
Arg Ala Arg Ala His Ala Arg Asp Gln Ala Arg Glu Gln Asp Arg Ala			
340	345	350	
His Ala Cys Pro Ala Val Glu Glu Thr Pro Met Asn Val Arg Asn Val			
355	360	365	
Pro Leu Pro Gly Asp Ala Ala Ala Gly His Pro Asp Arg Ala Ser Gly			
370	375	380	
His Pro Lys Pro His Ser Arg Ser Ser Ser Ala Tyr Arg Lys Ser Ala			
385	390	395	400
Ser Thr His His Lys Ser Val Phe Ser His Ser Lys Ala Ala Ser Gly			
405	410	415	
His Leu Lys Pro Val Ser Gly His Ser Lys Pro Ala Ser Gly His Pro			
420	425	430	
Lys Ser Ala Thr Val Tyr Pro Lys Pro Ala Ser Val His Phe Lys Gly			
435	440	445	
Asp Ser Val His Phe Lys Gly Asp Ser Val His Phe Lys Pro Asp Ser			
450	455	460	
Val His Phe Lys Pro Ala Ser Ser Asn Pro Lys Pro Ile Thr Gly His			
465	470	475	480
His Val Ser Ala Gly Ser His Ser Lys Ser Ala Phe Ser Ala Ala Thr			
485	490	495	
Ser His Pro Lys Pro Ile Lys Pro Ala Thr Ser His Ala Glu Pro Thr			
500	505	510	
Thr Ala Asp Tyr Pro Lys Pro Ala Thr Thr Ser His Pro Lys Pro Ala			
515	520	525	
Ala Ala Asp Asn Pro Glu Leu Ser Ala Ser His Cys Pro Glu Ile Pro			
530	535	540	

119/518

Ala Ile Ala His Pro Val Ser Asp Asp Ser Asp Leu Pro Glu Ser Ala
545 550 555 560
Ser Ser Pro Ala Ala Gly Pro Thr Lys Pro Ala Ala Ser Gln Leu Glu
565 570 575
Ser Asp Thr Ile Ala Asp Leu Pro Asp Pro Thr Val Val Thr Thr Ser
580 585 590
Thr Asn Asp Tyr His Asp Val Val Val Asp Val Glu Asp Asp Pro
595 600 605
Asp Glu Met Ala Val Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
610 615 620
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
625 630 635 640
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
645 650 655
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
660 665 670
Leu Val Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
675 680 685
Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
690 695 700
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
705 710 715 720
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
725 730 735
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
740 745 750
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
755 760 765
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile

120/518

770 775 780
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 785 790 795 800
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 805 810 815
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 820 825 830
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 835 840 845
 Leu Tyr Asn
 850

<210> 58

<211> 895

<212> PRT

<213> Human

<400> 58

Met Lys Met Lys Ser Gln Ala Thr Met Ile Cys Cys Leu Val Phe Phe
 5 10 15
 Leu Ser Thr Glu Cys Ser His Tyr Arg Ser Lys Ile His Leu Lys Ala
 20 25 30
 Gly Asp Lys Leu Gln Ser Pro Glu Gly Lys Pro Lys Thr Gly Arg Ile
 35 40 45
 Gln Glu Lys Cys Glu Gly Pro Cys Ile Ser Ser Ser Asn Cys Ser Gln
 50 55 60
 Pro Cys Ala Lys Asp Phe His Gly Glu Ile Gly Phe Thr Cys Asn Gln
 65 70 75 80
 Lys Lys Trp Gln Lys Ser Ala Glu Thr Cys Thr Ser Leu Ser Val Glu

121/518

	85	90	95
Lys Leu Phe Lys Asp Ser Thr Gly Ala Ser Arg Leu Ser Val Ala Ala			
100	105	110	
Pro Ser Ile Pro Leu His Ile Leu Asp Phe Arg Ala Pro Glu Thr Ile			
115	120	125	
Glu Ser Val Ala Gln Gly Ile Arg Lys Asn Cys Pro Phe Asp Tyr Ala			
130	135	140	
Cys Ile Thr Asp Met Val Lys Ser Ser Glu Thr Thr Ser Gly Asn Ile			
145	150	155	160
Ala Phe Ile Val Glu Leu Leu Lys Asn Ile Ser Thr Asp Leu Ser Asp			
165	170	175	
Asn Val Thr Arg Glu Lys Met Lys Ser Tyr Ser Glu Val Ala Asn His			
180	185	190	
Ile Leu Asp Thr Ala Ala Ile Ser Asn Trp Ala Phe Ile Pro Asn Lys			
195	200	205	
Asn Ala Ser Ser Asp Leu Leu Gln Ser Val Asn Leu Phe Ala Arg Gln			
210	215	220	
Leu His Ile His Asn Asn Ser Glu Asn Ile Val Asn Glu Leu Phe Ile			
225	230	235	240
Gln Thr Lys Gly Phe His Ile Asn His Asn Thr Ser Glu Lys Ser Leu			
245	250	255	
Asn Phe Ser Met Ser Met Asn Asn Thr Thr Glu Asp Ile Leu Gly Met			
260	265	270	
Val Gln Ile Pro Arg Gln Glu Leu Arg Lys Leu Trp Pro Asn Ala Ser			
275	280	285	
Gln Ala Ile Ser Ile Ala Phe Pro Thr Leu Gly Ala Ile Leu Arg Glu			
290	295	300	
Ala His Leu Gln Asn Val Ser Leu Pro Arg Gln Val Asn Gly Leu Val			
305	310	315	320

122/518

Leu Ser Val Val Leu Pro Glu Arg Leu Gln Glu Ile Ile Leu Thr Phe
 325 330 335
 Glu Lys Ile Asn Lys Thr Arg Asn Ala Arg Ala Gln Cys Val Gly Trp
 340 345 350
 His Ser Lys Lys Arg Arg Trp Asp Glu Lys Ala Cys Gln Met Met Leu
 355 360 365
 Asp Ile Arg Asn Glu Val Lys Cys Arg Cys Asn Tyr Thr Ser Val Val
 370 375 380
 Met Ser Phe Ser Ile Leu Met Ser Ser Lys Ser Met Thr Asp Lys Val
 385 390 395 400
 Leu Asp Tyr Ile Thr Cys Ile Gly Leu Ser Val Ser Ile Leu Ser Leu
 405 410 415
 Val Leu Cys Leu Ile Ile Glu Ala Thr Val Trp Ser Arg Val Val Val
 420 425 430
 Thr Glu Ile Ser Tyr Met Arg His Val Cys Ile Val Asn Ile Ala Val
 435 440 445
 Ser Leu Leu Thr Ala Asn Val Trp Phe Ile Ile Gly Ser His Phe Asn
 450 455 460
 Ile Lys Ala Gln Asp Tyr Asn Met Cys Val Ala Val Thr Phe Phe Ser
 465 470 475 480
 His Phe Phe Tyr Leu Ser Leu Phe Phe Trp Met Leu Phe Lys Ala Leu
 485 490 495
 Leu Ile Ile Tyr Gly Ile Leu Val Ile Phe Arg Arg Met Met Lys Ser
 500 505 510
 Arg Met Met Val Ile Gly Phe Ala Ile Gly Tyr Gly Cys Pro Leu Ile
 515 520 525
 Ile Ala Val Thr Thr Val Ala Ile Thr Glu Pro Glu Asn Gly Tyr Met
 530 535 540
 Arg Pro Glu Ala Cys Trp Leu Asn Trp Asp Asn Thr Lys Ala Leu Leu

123/518

545	550	555	560
Ala Phe Ala Ile Pro Ala Phe Val Ile Val Ala Val Asn Leu Ile Val			
	565	570	575
Val Leu Val Val Ala Val Asn Thr Gln Arg Pro Ser Ile Gly Ser Ser			
	580	585	590
Lys Ser Gln Asp Val Val Ile Ile Met Arg Ile Ser Lys Asn Val Ala			
	595	600	605
Ile Leu Thr Pro Leu Leu Gly Leu Thr Trp Gly Phe Gly Ile Ala Thr			
	610	615	620
Leu Ile Glu Gly Thr Ser Leu Thr Phe His Ile Ile Phe Ala Leu Leu			
	625	630	635
Asn Ala Phe Gln Val Ser Ser Lys Arg Glu Thr Phe Leu Cys Tyr Ser			
	645	650	655
Asp Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu			
	660	665	670
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly			
	675	680	685
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile			
	690	695	700
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr			
	705	710	715
Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys			
	725	730	735
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu			
	740	745	750
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu			
	755	760	765
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly			
	770	775	780

124/518

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 785 790 795 800
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 805 810 815
 Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser
 820 825 830
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 835 840 845
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 850 855 860
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 865 870 875 880
 Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn
 885 890 895

<210> 59

<211> 1148

<212> PRT

<213> Human

<400> 59

Met Lys Val Gly Val Leu Trp Leu Ile Ser Phe Phe Thr Phe Thr Asp
 5 10 15
 Gly His Gly Gly Phe Leu Gly Lys Asn Asp Gly Ile Lys Thr Lys Lys
 20 25 30
 Glu Leu Ile Val Asn Lys Lys Lys His Leu Gly Pro Val Glu Glu Tyr
 35 40 45
 Gln Leu Leu Leu Gln Val Thr Tyr Arg Asp Ser Lys Glu Lys Arg Asp
 50 55 60

125/518

Leu	Arg	Asn	Phe	Leu	Lys	Leu	Leu	Lys	Pro	Pro	Leu	Leu	Trp	Ser	His
65					70					75					80
Gly	Leu	Ile	Arg	Ile	Ile	Arg	Ala	Lys	Ala	Thr	Thr	Asp	Cys	Asn	Ser
				85					90					95	
Leu	Asn	Gly	Val	Leu	Gln	Cys	Thr	Cys	Glu	Asp	Ser	Tyr	Thr	Trp	Phe
				100					105					110	
Pro	Pro	Ser	Cys	Leu	Asp	Pro	Gln	Asn	Cys	Tyr	Leu	His	Thr	Ala	Gly
				115				120						125	
Ala	Leu	Pro	Ser	Cys	Glu	Cys	His	Leu	Asn	Asn	Leu	Ser	Gln	Ser	Val
				130				135						140	
Asn	Phe	Cys	Glu	Arg	Thr	Lys	Ile	Trp	Gly	Thr	Phe	Lys	Ile	Asn	Glu
145						150					155				160
Arg	Phe	Thr	Asn	Asp	Leu	Leu	Asn	Ser	Ser	Ser	Ala	Ile	Tyr	Ser	Lys
				165					170						175
Tyr	Ala	Asn	Gly	Ile	Glu	Ile	Gln	Leu	Lys	Lys	Ala	Tyr	Glu	Arg	Ile
				180					185					190	
Gln	Gly	Phe	Glu	Ser	Val	Gln	Val	Thr	Gln	Phe	Arg	Asn	Gly	Ser	Ile
				195					200					205	
Val	Ala	Gly	Tyr	Glu	Val	Val	Gly	Ser	Ser	Ser	Ala	Ser	Glu	Leu	Leu
				210					215					220	
Ser	Ala	Ile	Glu	His	Val	Ala	Glu	Lys	Ala	Lys	Thr	Ala	Leu	His	Lys
225						230					235				240
Leu	Phe	Pro	Leu	Glu	Asp	Gly	Ser	Phe	Arg	Val	Phe	Gly	Lys	Ala	Gln
				245					250						255
Cys	Asn	Asp	Ile	Val	Phe	Gly	Phe	Gly	Ser	Lys	Asp	Asp	Glu	Tyr	Thr
				260					265					270	
Leu	Pro	Cys	Ser	Ser	Gly	Tyr	Arg	Gly	Asn	Ile	Thr	Ala	Lys	Cys	Glu
				275					280					285	
Ser	Ser	Gly	Trp	Gln	Val	Ile	Arg	Glu	Thr	Cys	Val	Leu	Ser	Leu	Leu

126/518

290	295	300
Glu Glu Leu Asn Lys Asn Phe Ser Met Ile Val Gly Asn Ala Thr Glu		
305	310	315
Ala Ala Val Ser Ser Phe Val Gln Asn Leu Ser Val Ile Ile Arg Gln		
325	330	335
Asn Pro Ser Thr Thr Val Gly Asn Leu Ala Ser Val Val Ser Ile Leu		
340	345	350
Ser Asn Ile Ser Ser Leu Ser Leu Ala Ser His Phe Arg Val Ser Asn		
355	360	365
Ser Thr Met Glu Asp Val Ile Ser Ile Ala Asp Asn Ile Leu Asn Ser		
370	375	380
Ala Ser Val Thr Asn Trp Thr Val Leu Leu Arg Glu Glu Lys Tyr Ala		
385	390	395
Ser Ser Arg Leu Leu Glu Thr Leu Glu Asn Ile Ser Thr Leu Val Pro		
405	410	415
Pro Thr Ala Leu Pro Leu Asn Phe Ser Arg Lys Phe Ile Asp Trp Lys		
420	425	430
Gly Ile Pro Val Asn Lys Ser Gln Leu Lys Arg Gly Tyr Ser Tyr Gln		
435	440	445
Ile Lys Met Cys Pro Gln Asn Thr Ser Ile Pro Ile Arg Gly Arg Val		
450	455	460
Leu Ile Gly Ser Asp Gln Phe Gln Arg Ser Leu Pro Glu Thr Ile Ile		
465	470	475
Ser Met Ala Ser Leu Thr Leu Gly Asn Ile Leu Pro Val Ser Lys Asn		
485	490	495
Gly Asn Ala Gln Val Asn Gly Pro Val Ile Ser Thr Val Ile Gln Asn		
500	505	510
Tyr Ser Ile Asn Glu Val Phe Leu Phe Phe Ser Lys Ile Glu Ser Asn		
515	520	525

127/518

Leu Ser Gln Pro His Cys Val Phe Trp Asp Phe Ser His Leu Gln Trp
 530 535 540
 Asn Asp Ala Gly Cys His Leu Val Asn Glu Thr Gln Asp Ile Val Thr
 545 550 555 560
 Cys Gln Cys Thr His Leu Thr Ser Phe Ser Ile Leu Met Ser Pro Phe
 565 570 575
 Val Pro Ser Thr Ile Phe Pro Val Val Lys Trp Ile Thr Tyr Val Gly
 580 585 590
 Leu Gly Ile Ser Ile Gly Ser Leu Ile Leu Cys Leu Ile Ile Glu Ala
 595 600 605
 Leu Phe Trp Lys Gln Ile Lys Lys Ser Gln Thr Ser His Thr Arg Arg
 610 615 620
 Ile Cys Met Val Asn Ile Ala Leu Ser Leu Leu Ile Ala Asp Val Trp
 625 630 635 640
 Phe Ile Val Gly Ala Thr Val Asp Thr Thr Val Asn Pro Ser Gly Val
 645 650 655
 Cys Thr Ala Ala Val Phe Phe Thr His Phe Phe Tyr Leu Ser Leu Phe
 660 665 670
 Phe Trp Met Leu Met Leu Gly Ile Leu Leu Ala Tyr Arg Ile Ile Leu
 675 680 685
 Val Phe His His Met Ala Gln His Leu Met Met Ala Val Gly Phe Cys
 690 695 700
 Leu Gly Tyr Gly Cys Pro Leu Ile Ile Ser Val Ile Thr Ile Ala Val
 705 710 715 720
 Thr Gln Pro Ser Asn Thr Tyr Lys Arg Lys Asp Val Cys Trp Leu Asn
 725 730 735
 Trp Ser Asn Gly Ser Lys Pro Leu Leu Ala Phe Val Val Pro Ala Leu
 740 745 750
 Ala Ile Val Ala Val Asn Phe Val Val Val Leu Leu Val Leu Thr Lys

128/518

755	760	765
Leu Trp Arg Pro Thr Val Gly Glu Arg Leu Ser Arg Asp Asp Lys Ala		
770	775	780
Thr Ile Ile Arg Val Gly Lys Ser Leu Leu Ile Leu Thr Pro Leu Leu		
785	790	795
Gly Leu Thr Trp Gly Phe Gly Ile Gly Thr Ile Val Asp Ser Gln Asn		
805	810	815
Leu Ala Trp His Val Ile Phe Ala Leu Leu Asn Ala Phe Gln Gly Phe		
820	825	830
Phe Ile Leu Cys Phe Gly Ile Leu Leu Asp Ser Lys Leu Arg Gln Leu		
835	840	845
Leu Phe Asn Lys Leu Ser Ala Leu Ser Ser Trp Lys Gln Thr Glu Lys		
850	855	860
Gln Asn Ser Ser Asp Leu Ser Ala Lys Pro Lys Phe Ser Lys Pro Phe		
865	870	875
Asn Pro Leu Gln Asn Lys Gly His Tyr Ala Phe Ser His Thr Gly Asp		
885	890	895
Ser Ser Asp Asn Ile Met Leu Thr Gln Phe Val Ser Asn Glu Ala Ser		
900	905	910
Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu		
915	920	925
Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu		
930	935	940
Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr		
945	950	955
Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Cys Tyr		
965	970	975
Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg His Asp		
980	985	990

129/518

Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile
 995 1000 1005

Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe
 1010 1015 1020

Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe
 1025 1030 1035 1040

Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn
 1045 1050 1055

Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys
 1060 1065 1070

Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu
 1075 1080 1085

Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu
 1090 1095 1100

Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp
 1105 1110 1115 1120

Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala
 1125 1130 1135

Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn
 1140 1145

<210> 60

<211> 642

<212> PRT

<213> Human

<400> 60

Met Ser Val Lys Pro Ser Trp Gly Pro Gly Pro Ser Glu Gly Val Thr
 5 10 15

130/518

Ala Val Pro Thr Ser Asp Leu Gly Glu Ile His Asn Trp Thr Glu Leu
 20 25 30
 Leu Asp Leu Phe Asn His Thr Leu Ser Glu Cys His Val Glu Leu Ser
 35 40 45
 Gln Ser Thr Lys Arg Val Val Leu Phe Ala Leu Tyr Leu Ala Met Phe
 50 55 60
 Val Val Gly Leu Val Glu Asn Leu Leu Val Ile Cys Val Asn Trp Arg
 65 70 75 80
 Gly Ser Gly Arg Ala Gly Leu Met Asn Leu Tyr Ile Leu Asn Met Ala
 85 90 95
 Ile Ala Asp Leu Gly Ile Val Leu Ser Leu Pro Val Trp Met Leu Glu
 100 105 110
 Val Thr Leu Asp Tyr Thr Trp Leu Trp Gly Ser Phe Ser Cys Arg Phe
 115 120 125
 Thr His Tyr Phe Tyr Phe Val Asn Met Tyr Ser Ser Ile Phe Phe Leu
 130 135 140
 Val Cys Leu Ser Val Asp Arg Tyr Ala Thr Leu Thr Ser Ala Ser Pro
 145 150 155 160
 Ser Trp Gln Arg Tyr Gln His Arg Val Arg Arg Ala Met Cys Ala Gly
 165 170 175
 Ile Trp Val Leu Ser Ala Ile Ile Pro Leu Pro Glu Val Val His Ile
 180 185 190
 Gln Leu Val Glu Gly Pro Glu Pro Met Cys Leu Phe Met Ala Pro Phe
 195 200 205
 Glu Thr Tyr Ser Thr Trp Ala Leu Ala Val Ala Leu Ser Thr Thr Ile
 210 215 220
 Leu Gly Phe Leu Leu Pro Phe Pro Leu Ile Thr Val Phe Asn Val Leu
 225 230 235 240
 Thr Ala Cys Arg Leu Arg Gln Pro Gly Gln Pro Lys Ser Arg Arg His

131/518

	245		250		255										
Cys	Leu	Leu	Leu	Cys	Ala	Tyr	Val	Ala	Val	Phe	Val	Met	Cys	Trp	Leu
	260		265		270										
Pro	Tyr	His	Val	Thr	Leu	Leu	Leu	Leu	Thr	Leu	His	Gly	Thr	His	Ile
	275		280		285										
Ser	Leu	His	Cys	His	Leu	Val	His	Leu	Leu	Tyr	Phe	Phe	Tyr	Asp	Val
	290		295		300										
Ile	Asp	Cys	Phe	Ser	Met	Leu	His	Cys	Val	Ile	Asn	Pro	Ile	Leu	Tyr
305			310						315					320	
Asn	Phe	Leu	Ser	Pro	His	Phe	Arg	Gly	Arg	Leu	Leu	Asn	Ala	Val	Val
			325						330					335	
His	Tyr	Leu	Pro	Lys	Asp	Gln	Thr	Lys	Ala	Gly	Thr	Cys	Ala	Ser	Ser
	340							345						350	
Ser	Ser	Cys	Ser	Thr	Gln	His	Ser	Ile	Ile	Ile	Thr	Lys	Gly	Asp	Ser
	355						360						365		
Gln	Pro	Ala	Ala	Ala	Ala	Pro	His	Pro	Glu	Pro	Ser	Leu	Ser	Phe	Gln
	370					375						380			
Ala	His	His	Leu	Leu	Pro	Asn	Thr	Ser	Pro	Ile	Ser	Pro	Thr	Gln	Pro
385					390					395				400	
Leu	Thr	Pro	Ser	Ala	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val
			405						410					415	
Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser
	420							425					430		
Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu
	435						440						445		
Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu
	450					455							460		
Val	Thr	Thr	Leu	Cys	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp
465					470						475			480	

132/518

His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr

485

490

495

Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr

500

505

510

Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu

515

520

525

Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys

530

535

540

Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys

545

550

555

560

Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu

565

570

575

Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile

580

585

590

Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln

595

600

605

Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu

610

615

620

Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu

625

630

635

640

Tyr Asn

<210> 61

<211> 653

<212> PRT

<213> Human

<400> 61

Met Val Phe Ala His Arg Met Asp Asn Ser Lys Pro His Leu Ile Ile

133/518

	5		10		15										
Pro	Thr	Leu	Leu	Val	Pro	Leu	Gln	Asn	Arg	Ser	Cys	Thr	Glu	Thr	Ala
	20					25							30		
Thr	Pro	Leu	Pro	Ser	Gln	Tyr	Leu	Met	Glu	Leu	Ser	Glu	Glu	His	Ser
	35					40						45			
Trp	Met	Ser	Asn	Gln	Thr	Asp	Leu	His	Tyr	Val	Leu	Lys	Pro	Gly	Glu
	50					55						60			
Val	Ala	Thr	Ala	Ser	Ile	Phe	Phe	Gly	Ile	Leu	Trp	Leu	Phe	Ser	Ile
	65				70					75				80	
Phe	Gly	Asn	Ser	Leu	Val	Cys	Leu	Val	Ile	His	Arg	Ser	Arg	Arg	Thr
				85					90					95	
Gln	Ser	Thr	Thr	Asn	Tyr	Phe	Val	Val	Ser	Met	Ala	Cys	Ala	Asp	Leu
	100							105						110	
Leu	Ile	Ser	Val	Ala	Ser	Thr	Pro	Phe	Val	Leu	Leu	Gln	Phe	Thr	Thr
	115						120						125		
Gly	Arg	Trp	Thr	Leu	Gly	Ser	Ala	Thr	Cys	Lys	Val	Val	Arg	Tyr	Phe
	130					135							140		
Gln	Tyr	Leu	Thr	Pro	Gly	Val	Gln	Ile	Tyr	Val	Leu	Leu	Ser	Ile	Cys
	145					150				155				160	
Ile	Asp	Arg	Phe	Tyr	Thr	Ile	Val	Tyr	Pro	Leu	Ser	Phe	Lys	Val	Ser
				165					170					175	
Arg	Glu	Lys	Ala	Lys	Lys	Met	Ile	Ala	Ala	Ser	Trp	Ile	Phe	Asp	Ala
			180					185						190	
Gly	Phe	Val	Thr	Pro	Val	Leu	Phe	Phe	Tyr	Gly	Ser	Asn	Trp	Asp	Ser
	195						200						205		
His	Cys	Asn	Tyr	Phe	Leu	Pro	Ser	Ser	Trp	Glu	Gly	Thr	Ala	Tyr	Thr
	210						215						220		
Val	Ile	His	Phe	Leu	Val	Gly	Phe	Val	Ile	Pro	Ser	Val	Leu	Ile	Ile
	225					230				235				240	

134/518

Leu Phe Tyr Gln Lys Val Ile Lys Tyr Ile Trp Arg Ile Gly Thr Asp
 245 250 255
 Gly Arg Thr Val Arg Arg Thr Met Asn Ile Val Pro Arg Thr Lys Val
 260 265 270
 Lys Thr Ile Lys Met Phe Leu Ile Leu Asn Leu Leu Phe Leu Leu Ser
 275 280 285
 Trp Leu Pro Phe His Val Ala Gln Leu Trp His Pro His Glu Gln Asp
 290 295 300
 Tyr Lys Lys Ser Ser Leu Val Phe Thr Ala Ile Thr Trp Ile Ser Phe
 305 310 315 320
 Ser Ser Ser Ala Ser Lys Pro Thr Leu Tyr Ser Ile Tyr Asn Ala Asn
 325 330 335
 Phe Arg Arg Gly Met Lys Glu Thr Phe Cys Met Ser Ser Met Lys Cys
 340 345 350
 Tyr Arg Ser Asn Ala Tyr Thr Ile Thr Thr Ser Ser Arg Met Ala Lys
 355 360 365
 Lys Asn Tyr Val Gly Ile Ser Glu Ile Pro Ser Met Ala Lys Thr Ile
 370 375 380
 Thr Lys Asp Ser Ile Tyr Asp Ser Phe Asp Arg Glu Ala Lys Glu Lys
 385 390 395 400
 Lys Leu Ala Trp Pro Ile Asn Ser Asn Pro Pro Asn Thr Phe Val Ala
 405 410 415
 Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu
 420 425 430
 Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly
 435 440 445
 Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr
 450 455 460
 Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Cys

135/518

465 470 475 480
 Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg His
 485 490 495
 Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr
 500 505 510
 Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys
 515 520 525
 Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp
 530 535 540
 Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr
 545 550 555 560
 Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile
 565 570 575
 Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser Val Gln
 580 585 590
 Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val
 595 600 605
 Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys
 610 615 620
 Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr
 625 630 635 640
 Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn
 645 650

<210> 62

<211> 610

<212> PRT

<213> Human

<400> 62

Met	Ala	Cys	Asn	Ser	Thr	Ser	Leu	Glu	Ala	Tyr	Thr	Tyr	Leu	Leu	Leu	
				5					10					15		
Asn	Thr	Ser	Asn	Ala	Ser	Asp	Ser	Gly	Ser	Thr	Gln	Leu	Pro	Ala	Pro	
				20					25					30		
Leu	Arg	Ile	Ser	Leu	Ala	Ile	Val	Met	Leu	Leu	Met	Thr	Val	Val	Gly	
				35					40					45		
Phe	Leu	Gly	Asn	Thr	Val	Val	Cys	Ile	Ile	Val	Tyr	Gln	Arg	Pro	Ala	
				50					55					60		
Met	Arg	Ser	Ala	Ile	Asn	Leu	Leu	Leu	Ala	Thr	Leu	Ala	Phe	Ser	Asp	
				65					70					75		
Ile	Met	Leu	Ser	Leu	Cys	Cys	Met	Pro	Phe	Thr	Ala	Val	Thr	Leu	Ile	
				85					90					95		
Thr	Val	Arg	Trp	His	Phe	Gly	Asp	His	Phe	Cys	Arg	Leu	Ser	Ala	Thr	
				100					105					110		
Leu	Tyr	Trp	Phe	Phe	Val	Leu	Glu	Gly	Val	Ala	Ile	Leu	Leu	Ile	Ile	
				115					120					125		
Ser	Val	Asp	Arg	Phe	Leu	Ile	Ile	Val	Gln	Arg	Gln	Asp	Lys	Leu	Asn	
				130					135					140		
Pro	Arg	Arg	Ala	Lys	Val	Ile	Ile	Ala	Val	Ser	Trp	Val	Leu	Ser	Phe	
				145					150					155		
Cys	Ile	Ala	Gly	Pro	Ser	Leu	Thr	Gly	Trp	Thr	Leu	Val	Glu	Val	Pro	
				165					170					175		
Ala	Arg	Ala	Pro	Gln	Cys	Val	Leu	Gly	Tyr	Thr	Glu	Leu	Pro	Ala	Asp	
				180					185					190		
Arg	Ala	Tyr	Val	Val	Thr	Leu	Val	Val	Ala	Val	Phe	Phe	Ala	Pro	Phe	
				195					200					205		
Gly	Val	Met	Leu	Cys	Ala	Tyr	Met	Cys	Ile	Leu	Asn	Thr	Val	Arg	Lys	
				210					215					220		

137/518

Asn Ala Val Arg Val His Asn Gln Ser Asp Ser Leu Asp Leu Arg Gln
 225 230 235 240
 Leu Thr Arg Ala Gly Leu Arg Arg Leu Gln Arg Gln Gln Gln Val Ser
 245 250 255
 Val Asp Leu Ser Phe Lys Thr Lys Ala Phe Thr Thr Ile Leu Ile Leu
 260 265 270
 Phe Val Gly Phe Ser Leu Cys Trp Leu Pro His Ser Val Tyr Ser Leu
 275 280 285
 Leu Ser Val Phe Ser Gln Arg Phe Tyr Cys Gly Ser Ser Phe Tyr Ala
 290 295 300
 Thr Ser Thr Cys Val Leu Trp Leu Ser Tyr Leu Lys Ser Val Phe Asn
 305 310 315 320
 Pro Ile Val Tyr Cys Trp Arg Ile Lys Lys Phe Arg Glu Ala Cys Ile
 325 330 335
 Glu Leu Leu Pro Gln Thr Phe Gln Ile Leu Pro Lys Val Pro Glu Arg
 340 345 350
 Ile Arg Arg Arg Ile Gln Pro Ser Thr Val Tyr Val Cys Asn Glu Asn
 355 360 365
 Gln Ser Ala Val Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val
 370 375 380
 Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser
 385 390 395 400
 Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu
 405 410 415
 Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu
 420 425 430
 Val Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp
 435 440 445
 His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr

138/518

450	455	460
Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr		
465	470	475
Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu		
485	490	495
Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys		
500	505	510
Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys		
515	520	525
Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu		
530	535	540
Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile		
545	550	555
Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln		
565	570	575
Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu		
580	585	590
Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu		
595	600	605
Tyr Asn		
610		

<210> 63

<211> 583

<212> PRT

<213> Human

<400> 63

Met Tyr Lys Asp Cys Ile Glu Ser Thr Gly Asp Tyr Phe Leu Leu Cys

[illegible]

140/518

Val Val Cys Ile Ala Leu Val Thr Asn Ala Trp Val Phe Leu Leu Leu
 245 250 255
 Tyr Ile Val Pro Glu Leu Cys Ile Leu Tyr Arg Ser Cys Arg Gln Glu
 260 265 270
 Cys Pro Leu Gln Gly Asn Ala Cys Pro Val Thr Ala Tyr Gln His Ser
 275 280 285
 Phe Gln Val Glu Asn Gln Glu Leu Ser Arg Ala Arg Asp Ser Asp Gly
 290 295 300
 Ala Glu Glu Asp Val Ala Leu Thr Ser Tyr Gly Thr Pro Ile Gln Pro
 305 310 315 320
 Gln Thr Val Asp Pro Thr Gln Glu Cys Phe Ile Pro Gln Ala Lys Leu
 325 330 335
 Ser Pro Gln Gln Asp Ala Gly Gly Val Ala Ser Lys Gly Glu Glu Leu
 340 345 350
 Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn
 355 360 365
 Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr
 370 375 380
 Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
 385 390 395 400
 Pro Trp Pro Thr Leu Val Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe
 405 410 415
 Ser Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala
 420 425 430
 Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
 435 440 445
 Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
 450 455 460
 Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn

141/518

465 470 475 480
 Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr
 485 490 495
 Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr
 500 505 510
 Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
 515 520 525
 Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
 530 535 540
 Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
 545 550 555 560
 Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His
 565 570 575
 Gly Met Asp Glu Leu Tyr Asn
 580

<210> 64

<211> 1205

<212> PRT

<213> Human

<400> 64

Met Pro Ser Pro Pro Gly Leu Arg Ala Leu Trp Leu Cys Ala Ala Leu
 5 10 15
 Cys Ala Ser Arg Arg Ala Gly Gly Ala Pro Gln Pro Gly Pro Gly Pro
 20 25 30
 Thr Ala Cys Pro Ala Pro Cys His Cys Gln Glu Asp Gly Ile Met Leu
 35 40 45
 Ser Ala Asp Cys Ser Glu Leu Gly Leu Ser Ala Val Pro Gly Asp Leu

142/518

50	55	60
Asp Pro Leu Thr Ala Tyr Leu Asp Leu Ser Met Asn Asn Leu Thr Glu		
65	70	75
Leu Gln Pro Gly Leu Phe His His Leu Arg Phe Leu Glu Glu Leu Arg		80
	85	90
Leu Ser Gly Asn His Leu Ser His Ile Pro Gly Gln Ala Phe Ser Gly		95
	100	105
Leu Tyr Ser Leu Lys Ile Leu Met Leu Gln Asn Asn Gln Leu Gly Gly		110
	115	120
Ile Pro Ala Glu Ala Leu Trp Glu Leu Pro Ser Leu Gln Ser Leu Arg		125
	130	135
Leu Asp Ala Asn Leu Ile Ser Leu Val Pro Glu Arg Ser Phe Glu Gly		140
145	150	155
Leu Ser Ser Leu Arg His Leu Trp Leu Asp Asp Asn Ala Leu Thr Glu		160
	165	170
Ile Pro Val Arg Ala Leu Asn Asn Leu Pro Ala Leu Gln Ala Met Thr		175
	180	185
Leu Ala Leu Asn Arg Ile Ser His Ile Pro Asp Tyr Ala Phe Gln Asn		190
	195	200
Leu Thr Ser Leu Val Val Leu His Leu His Asn Asn Arg Ile Gln His		205
	210	215
Leu Gly Thr His Ser Phe Glu Gly Leu His Asn Leu Glu Thr Leu Asp		220
225	230	235
Leu Asn Tyr Asn Lys Leu Gln Glu Phe Pro Val Ala Ile Arg Thr Leu		240
	245	250
Gly Arg Leu Gln Glu Leu Gly Phe His Asn Asn Asn Ile Lys Ala Ile		255
	260	265
Pro Glu Lys Ala Phe Met Gly Asn Pro Leu Leu Gln Thr Ile His Phe		270
	275	280
		285

143/518

Tyr Asp Asn Pro Ile Gln Phe Val Gly Arg Ser Ala Phe Gln Tyr Leu
 290 295 300
 Pro Lys Leu His Thr Leu Ser Leu Asn Gly Ala Met Asp Ile Gln Glu
 305 310 315 320
 Phe Pro Asp Leu Lys Gly Thr Thr Ser Leu Glu Ile Leu Thr Leu Thr
 325 330 335
 Arg Ala Gly Ile Arg Leu Leu Pro Ser Gly Met Cys Gln Gln Leu Pro
 340 345 350
 Arg Leu Arg Val Leu Glu Leu Ser His Asn Gln Ile Glu Glu Leu Pro
 355 360 365
 Ser Leu His Arg Cys Gln Lys Leu Glu Glu Ile Gly Leu Gln His Asn
 370 375 380
 Arg Ile Trp Glu Ile Gly Ala Asp Thr Phe Ser Gln Leu Ser Ser Leu
 385 390 395 400
 Gln Ala Leu Asp Leu Ser Trp Asn Ala Ile Arg Ser Ile His Pro Glu
 405 410 415
 Ala Phe Ser Thr Leu His Ser Leu Val Lys Leu Asp Leu Thr Asp Asn
 420 425 430
 Gln Leu Thr Thr Leu Pro Leu Ala Gly Leu Gly Gly Leu Met His Leu
 435 440 445
 Lys Leu Lys Gly Asn Leu Ala Leu Ser Gln Ala Phe Ser Lys Asp Ser
 450 455 460
 Phe Pro Lys Leu Arg Ile Leu Glu Val Pro Tyr Ala Tyr Gln Cys Cys
 465 470 475 480
 Pro Tyr Gly Met Cys Ala Ser Phe Phe Lys Ala Ser Gly Gln Trp Glu
 485 490 495
 Ala Glu Asp Leu His Leu Asp Asp Glu Glu Ser Ser Lys Arg Pro Leu
 500 505 510
 Gly Leu Leu Ala Arg Gln Ala Glu Asn His Tyr Asp Gln Asp Leu Asp

144/518

515	520	525
Glu Leu Gln Leu Glu Met Glu Asp Ser Lys Pro His Pro Ser Val Gln		
530	535	540
Cys Ser Pro Thr Pro Gly Pro Phe Lys Pro Cys Glu Tyr Leu Phe Glu		
545	550	555
Ser Trp Gly Ile Arg Leu Ala Val Trp Ala Ile Val Leu Leu Ser Val		
565	570	575
Leu Cys Asn Gly Leu Val Leu Leu Thr Val Phe Ala Gly Gly Pro Val		
580	585	590
Pro Leu Pro Pro Val Lys Phe Val Val Gly Ala Ile Ala Gly Ala Asn		
595	600	605
Thr Leu Thr Gly Ile Ser Cys Gly Leu Leu Ala Ser Val Asp Ala Leu		
610	615	620
Thr Phe Gly Gln Phe Ser Glu Tyr Gly Ala Arg Trp Glu Thr Gly Leu		
625	630	635
Gly Cys Arg Ala Thr Gly Phe Leu Ala Val Leu Gly Ser Glu Ala Ser		
645	650	655
Val Leu Leu Leu Thr Leu Ala Ala Val Gln Cys Ser Val Ser Val Ser		
660	665	670
Cys Val Arg Ala Tyr Gly Lys Ser Pro Ser Leu Gly Ser Val Arg Ala		
675	680	685
Gly Val Leu Gly Cys Leu Ala Leu Ala Gly Leu Ala Ala Ala Leu Pro		
690	695	700
Leu Ala Ser Val Gly Glu Tyr Gly Ala Ser Pro Leu Cys Leu Pro Tyr		
705	710	715
Ala Pro Pro Glu Gly Gln Pro Ala Ala Leu Gly Phe Thr Val Ala Leu		
725	730	735
Val Met Met Asn Ser Phe Cys Phe Leu Val Val Ala Gly Ala Tyr Ile		
740	745	750

145/518

Lys Leu Tyr Cys Asp Leu Pro Arg Gly Asp Phe Glu Ala Val Trp Asp
 755 760 765
 Cys Ala Met Val Arg His Val Ala Trp Leu Ile Phe Ala Asp Gly Leu
 770 775 780
 Leu Tyr Cys Pro Val Ala Phe Leu Ser Phe Ala Ser Met Leu Gly Leu
 785 790 795 800
 Phe Pro Val Thr Pro Glu Ala Val Lys Ser Val Leu Leu Val Val Leu
 805 810 815
 Pro Leu Pro Ala Cys Leu Asn Pro Leu Leu Tyr Leu Leu Phe Asn Pro
 820 825 830
 His Phe Arg Asp Asp Leu Arg Arg Leu Arg Pro Arg Ala Gly Asp Ser
 835 840 845
 Gly Pro Leu Ala Tyr Ala Ala Ala Gly Glu Leu Glu Lys Ser Ser Cys
 850 855 860
 Asp Ser Thr Gln Ala Leu Val Ala Phe Ser Asp Val Asp Leu Ile Leu
 865 870 875 880
 Glu Ala Ser Glu Ala Gly Arg Pro Pro Gly Leu Glu Thr Tyr Gly Phe
 885 890 895
 Pro Ser Val Thr Leu Ile Ser Cys Gln Gln Pro Gly Ala Pro Arg Leu
 900 905 910
 Glu Gly Ser His Cys Val Glu Pro Glu Gly Asn His Phe Gly Asn Pro
 915 920 925
 Gln Pro Ser Met Asp Gly Glu Leu Leu Leu Arg Ala Glu Gly Ser Thr
 930 935 940
 Pro Ala Gly Gly Gly Leu Ser Gly Gly Gly Gly Phe Gln Pro Ser Gly
 945 950 955 960
 Leu Ala Phe Ala Ser His Val Ala Ser Lys Gly Glu Glu Leu Phe Thr
 965 970 975
 Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His

146/518

980	985	990
Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys		
995	1000	1005
Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp		
1010	1015	1020
Pro Thr Leu Val Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg		
1025	1030	1035
Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro		
1045	1050	1055
Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn		
1060	1065	1070
Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn		
1075	1080	1085
Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu		
1090	1095	1100
Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met		
1105	1110	1115
Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His		
1125	1130	1135
Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn		
1140	1145	1150
Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu		
1155	1160	1165
Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His		
1170	1175	1180
Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met		
1185	1190	1195
Asp Glu Leu Tyr Asn		1200
1205		

147/518

<210> 65

<211> 573

<212> PRT

<213> Human

<400> 65

Met Glu Ser Ser Phe Ser Phe Gly Val Ile Leu Ala Val Leu Ala Ser

5

10

15

Leu Ile Ile Ala Thr Asn Thr Leu Val Ala Val Ala Val Leu Leu Leu

20

25

30

Ile His Lys Asn Asp Gly Val Ser Leu Cys Phe Thr Leu Asn Leu Ala

35

40

45

Val Ala Asp Thr Leu Ile Gly Val Ala Ile Ser Gly Leu Leu Thr Asp

50

55

60

Gln Leu Ser Ser Pro Ser Arg Pro Thr Gln Lys Thr Leu Cys Ser Leu

65

70

75

80

Arg Met Ala Phe Val Thr Ser Ser Ala Ala Ala Ser Val Leu Thr Val

85

90

95

Met Leu Ile Thr Phe Asp Arg Tyr Leu Ala Ile Lys Gln Pro Phe Arg

100

105

110

Tyr Leu Lys Ile Met Ser Gly Phe Val Ala Gly Ala Cys Ile Ala Gly

115

120

125

Leu Trp Leu Val Ser Tyr Leu Ile Gly Phe Leu Pro Leu Gly Ile Pro

130

135

140

Met Phe Gln Gln Thr Ala Tyr Lys Gly Gln Cys Ser Phe Phe Ala Val

145

150

155

160

Phe His Pro His Phe Val Leu Thr Leu Ser Cys Val Gly Phe Phe Pro

165

170

175

148/518

Ala Met Leu Leu Phe Val Phe Phe Tyr Cys Asp Met Leu Lys Ile Ala
 180 185 190
 Ser Met His Ser Gln Gln Ile Arg Lys Met Glu His Ala Gly Ala Met
 195 200 205
 Ala Gly Gly Tyr Arg Ser Pro Arg Thr Pro Ser Asp Phe Lys Ala Leu
 210 215 220
 Arg Thr Val Ser Val Leu Ile Gly Ser Phe Ala Leu Ser Trp Thr Pro
 225 230 235 240
 Phe Leu Ile Thr Gly Ile Val Gln Val Ala Cys Gln Glu Cys His Leu
 245 250 255
 Tyr Leu Val Leu Glu Arg Tyr Leu Trp Leu Leu Gly Val Gly Asn Ser
 260 265 270
 Leu Leu Asn Pro Leu Ile Tyr Ala Tyr Trp Gln Lys Glu Val Arg Leu
 275 280 285
 Gln Leu Tyr His Met Ala Leu Gly Val Lys Lys Val Leu Thr Ser Phe
 290 295 300
 Leu Leu Phe Leu Ser Ala Arg Asn Cys Gly Pro Glu Arg Pro Arg Glu
 305 310 315 320
 Ser Ser Cys His Ile Val Thr Ile Ser Ser Ser Glu Phe Asp Gly Ala
 325 330 335
 Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu
 340 345 350
 Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly
 355 360 365
 Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr
 370 375 380
 Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Cys
 385 390 395 400
 Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg His

149/518

	405		410		415
Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr					
	420		425		430
Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys					
	435		440		445
Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp					
	450		455		460
Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr					
465		470		475	480
Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile					
	485		490		495
Lys. Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser Val Gln					
	500		505		510
Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val					
	515		520		525
Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys					
	530		535		540
Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr					
545		550		555	560
Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn					
	565		570		

<210> 66

<211> 612

<212> PRT

<213> Human

<400> 66

Met Leu Thr Gly Ser Cys Gly Asp Pro Gln Lys Lys Pro Gln Val Thr

150/518

	5	10	15
Gln Asp Ser Gly Pro Gln Ser Met Gly Leu Glu Gly Arg Glu Thr Ala			
	20	25	30
Gly Gln Pro Arg Val Thr Leu Leu Pro Thr Pro Asn Val Ser Gly Leu			
	35	40	45
Ser Gln Glu Phe Glu Ser His Trp Pro Glu Ile Ala Glu Arg Ser Pro			
	50	55	60
Cys Val Ala Gly Val Ile Pro Val Ile Tyr Tyr Ser Val Leu Leu Gly			
	65	70	75
Leu Gly Leu Pro Val Ser Leu Leu Thr Ala Val Ala Leu Ala Arg Leu			
	85	90	95
Ala Thr Arg Thr Arg Arg Pro Ser Tyr Tyr Tyr Leu Leu Ala Leu Thr			
	100	105	110
Ala Ser Asp Ile Ile Ile Gln Val Val Ile Val Phe Ala Gly Phe Leu			
	115	120	125
Leu Gln Gly Ala Val Leu Ala Arg Gln Val Pro Gln Ala Val Val Arg			
	130	135	140
Thr Ala Asn Ile Leu Glu Phe Ala Ala Asn His Ala Ser Val Trp Ile			
	145	150	155
Ala Ile Leu Leu Thr Val Asp Arg Tyr Thr Ala Leu Cys His Pro Leu			
	165	170	175
His His Arg Ala Ala Ser Ser Pro Gly Arg Thr Arg Arg Ala Ile Ala			
	180	185	190
Ala Val Leu Ser Ala Ala Leu Leu Thr Gly Ile Pro Phe Tyr Trp Trp			
	195	200	205
Leu Asp Met Trp Arg Asp Thr Asp Ser Pro Arg Thr Leu Asp Glu Val			
	210	215	220
Leu Lys Trp Ala His Cys Leu Thr Val Tyr Phe Ile Pro Cys Gly Val			
	225	230	235
			240

151/518

Phe Leu Val Thr Asn Ser Ala Ile Ile His Arg Leu Arg Arg Arg Gly
 245 250 255
 Arg Ser Gly Leu Gln Pro Arg Val Gly Lys Ser Thr Ala Ile Leu Leu
 260 265 270
 Gly Ile Thr Thr Leu Phe Thr Leu Leu Trp Ala Pro Arg Val Phe Val
 275 280 285
 Met Leu Tyr His Met Tyr Val Ala Pro Val His Arg Asp Trp Arg Val
 290 295 300
 His Leu Ala Leu Asp Val Ala Asn Met Val Ala Met Leu His Thr Ala
 305 310 315 320
 Ala Asn Phe Gly Leu Tyr Cys Phe Val Ser Lys Thr Phe Arg Ala Thr
 325 330 335
 Val Arg Gln Val Ile His Asp Ala Tyr Leu Pro Cys Thr Leu Ala Ser
 340 345 350
 Gln Pro Glu Gly Met Ala Ala Lys Pro Val Met Glu Pro Pro Gly Leu
 355 360 365
 Pro Thr Gly Ala Glu Val Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly
 370 375 380
 Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys
 385 390 395 400
 Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu
 405 410 415
 Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro
 420 425 430
 Thr Leu Val Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr
 435 440 445
 Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu
 450 455 460
 Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr

152/518

465 470 475 480
 Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg
 485 490 495
 Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly
 500 505 510
 His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala
 515 520 525
 Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn
 530 535 540
 Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr
 545 550 555 560
 Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser
 565 570 575
 Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met
 580 585 590
 Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp
 595 600 605
 Glu Leu Tyr Asn
 610

<210> 67

<211> 611

<212> PRT

<213> Human

<400> 67

Met Asp Thr Leu Glu Glu Val Thr Trp Ala Asn Gly Ser Thr Ala Leu
 5 10 15
 Pro Pro Pro Leu Ala Pro Asn Ile Ser Val Pro His Arg Cys Leu Leu

	20						25						30					
Leu	Leu	Tyr	Glu	Asp	Ile	Gly	Thr	Ser	Arg	Val	Arg	Tyr	Trp	Asp	Leu			
35						40						45						
Leu	Leu	Leu	Ile	Pro	Asn	Val	Leu	Phe	Leu	Ile	Phe	Leu	Leu	Trp	Lys			
50						55						60						
Leu	Pro	Ser	Ala	Arg	Ala	Lys	Ile	Arg	Ile	Thr	Ser	Ser	Pro	Ile	Phe			
65						70						75						
Ile	Thr	Phe	Tyr	Ile	Leu	Val	Phe	Val	Val	Ala	Leu	Val	Gly	Ile	Ala			
85						90						95						
Arg	Ala	Val	Val	Ser	Met	Thr	Val	Ser	Thr	Ser	Asn	Ala	Ala	Thr	Val			
100						105						110						
Ala	Asp	Lys	Ile	Leu	Trp	Glu	Ile	Thr	Arg	Phe	Phe	Leu	Leu	Ala	Ile			
115						120						125						
Glu	Leu	Ser	Val	Ile	Ile	Leu	Gly	Leu	Ala	Phe	Gly	His	Leu	Glu	Ser			
130						135						140						
Lys	Ser	Ser	Ile	Lys	Arg	Val	Leu	Ala	Ile	Thr	Thr	Val	Leu	Ser	Leu			
145						150						155						
Ala	Tyr	Ser	Val	Thr	Gln	Gly	Thr	Leu	Glu	Ile	Leu	Tyr	Pro	Asp	Ala			
165						170						175						
His	Leu	Ser	Ala	Glu	Asp	Phe	Asn	Ile	Tyr	Gly	His	Gly	Gly	Arg	Gln			
180						185						190						
Phe	Trp	Leu	Val	Ser	Ser	Cys	Phe	Phe	Phe	Leu	Val	Tyr	Ser	Leu	Val			
195						200						205						
Val	Ile	Leu	Pro	Lys	Thr	Pro	Leu	Lys	Glu	Arg	Ile	Ser	Leu	Pro	Ser			
210						215						220						
Arg	Arg	Ser	Phe	Tyr	Val	Tyr	Ala	Gly	Ile	Leu	Ala	Leu	Leu	Asn	Leu			
225						230						235						
Leu	Gln	Gly	Leu	Gly	Ser	Val	Leu	Leu	Cys	Phe	Asp	Ile	Ile	Glu	Gly			
245						250						255						

154/518

Leu Cys Cys Val Asp Ala Thr Thr Phe Leu Tyr Phe Ser Phe Phe Ala
 260 265 270
 Pro Leu Ile Tyr Val Ala Phe Leu Arg Gly Phe Phe Gly Ser Glu Pro
 275 280 285
 Lys Ile Leu Phe Ser Tyr Lys Cys Gln Val Asp Glu Thr Glu Glu Pro
 290 295 300
 Asp Val His Leu Pro Gln Pro Tyr Ala Val Ala Arg Arg Glu Gly Leu
 305 310 315 320
 Glu Ala Ala Gly Ala Ala Gly Ala Ser Ala Ala Ser Tyr Ser Ser Thr
 325 330 335
 Gln Phe Asp Ser Ala Gly Gly Val Ala Tyr Leu Asp Asp Ile Ala Ser
 340 345 350
 Met Pro Cys His Thr Gly Ser Ile Asn Ser Thr Asp Ser Glu Arg Trp
 355 360 365
 Lys Ala Ile Asn Ala Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 370 375 380
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 385 390 395 400
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 405 410 415
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 420 425 430
 Leu Val Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 435 440 445
 Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 450 455 460
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 465 470 475 480
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile

155/518

	485		490		495										
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His
	500		505		510										
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp
	515		520		525										
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Thr	Arg	His	Asn	Ile
	530		535		540										
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro
545			550		555								560		
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr
			565		570								575		
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val
			580		585								590		
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu
			595		600								605		
Leu	Tyr	Asn													
	610														

<210> 68

<211> 671

<212> PRT

<213> Human

<400> 68

Met	Cys	Phe	Ser	Pro	Ile	Leu	Glu	Ile	Asn	Met	Gln	Ser	Glu	Ser	Asn
			5						10					15	
Ile	Thr	Val	Arg	Asp	Asp	Ile	Asp	Asp	Ile	Asn	Thr	Asn	Met	Tyr	Gln
			20						25					30	
Pro	Leu	Ser	Tyr	Pro	Leu	Ser	Phe	Gln	Val	Ser	Leu	Thr	Gly	Phe	Leu

156/518

35	40	45
Met Leu Glu Ile Val Leu Gly Leu Gly Ser Asn Leu Thr Val Leu Val		
50	55	60
Leu Tyr Cys Met Lys Ser Asn Leu Ile Asn Ser Val Ser Asn Ile Ile		
65	70	75
Thr Met Asn Leu His Val Leu Asp Val Ile Ile Cys Val Gly Cys Ile		
85	90	95
Pro Leu Thr Ile Val Ile Leu Leu Leu Ser Leu Glu Ser Asn Thr Ala		
100	105	110
Leu Ile Cys Cys Phe His Glu Ala Cys Val Ser Phe Ala Ser Val Ser		
115	120	125
Thr Ala Ile Asn Val Phe Ala Ile Thr Leu Asp Arg Tyr Asp Ile Ser		
130	135	140
Val Lys Pro Ala Asn Arg Ile Leu Thr Met Gly Arg Ala Val Met Leu		
145	150	155
Met Ile Ser Ile Trp Ile Phe Ser Phe Phe Ser Phe Leu Ile Pro Phe		
165	170	175
Ile Glu Val Asn Phe Phe Ser Leu Gln Ser Gly Asn Thr Trp Glu Asn		
180	185	190
Lys Thr Leu Leu Cys Val Ser Thr Asn Glu Tyr Tyr Thr Glu Leu Gly		
195	200	205
Met Tyr Tyr His Leu Leu Val Gln Ile Pro Ile Phe Phe Phe Thr Val		
210	215	220
Val Val Met Leu Ile Thr Tyr Thr Lys Ile Leu Gln Ala Leu Asn Ile		
225	230	235
Arg Ile Gly Thr Arg Phe Ser Thr Gly Gln Lys Lys Lys Ala Arg Lys		
245	250	255
Lys Lys Thr Ile Ser Leu Thr Thr Gln His Glu Ala Thr Asp Met Ser		
260	265	270

157/518

Gln Ser Ser Gly Gly Arg Asn Val Val Phe Gly Val Arg Thr Ser Val
 275 280 285
 Ser Val Ile Ile Ala Leu Arg Arg Ala Val Lys Arg His Arg Glu Arg
 290 295 300
 Arg Glu Arg Gln Lys Arg Val Phe Arg Met Ser Leu Leu Ile Ile Ser
 305 310 315 320
 Thr Phe Leu Leu Cys Trp Thr Pro Ile Ser Val Leu Asn Thr Thr Ile
 325 330 335
 Leu Cys Leu Gly Pro Ser Asp Leu Leu Val Lys Leu Arg Leu Cys Phe
 340 345 350
 Leu Val Met Ala Tyr Gly Thr Thr Ile Phe His Pro Leu Leu Tyr Ala
 355 360 365
 Phe Thr Arg Gln Lys Phe Gln Lys Val Leu Lys Ser Lys Met Lys Lys
 370 375 380
 Arg Val Val Ser Ile Val Glu Ala Asp Pro Leu Pro Asn Asn Ala Val
 385 390 395 400
 Ile His Asn Ser Trp Ile Asp Pro Lys Arg Asn Lys Lys Ile Thr Phe
 405 410 415
 Glu Asp Ser Glu Ile Arg Glu Lys Cys Leu Val Pro Gln Val Val Thr
 420 425 430
 Asp Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 435 440 445
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 450 455 460
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 465 470 475 480
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 485 490 495
 Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys

158/518

500	505	510
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu		
515	520	525
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu		
530	535	540
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly		
545	550	555
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr		
565	570	575
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn		
580	585	590
Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser		
595	600	605
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly		
610	615	620
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu		
625	630	635
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe		
645	650	655
Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn		
660	665	670

<210> 69

<211> 599

<212> PRT

<213> Human

<400> 69

Met Asn Glu Ser Arg Trp Thr Glu Trp Arg Ile Leu Asn Met Ser Ser

				5					10					15			
Gly	Ile	Val	Asn	Val	Ser	Glu	Arg	His	Ser	Cys	Pro	Leu	Gly	Phe	Gly		
			20					25						30			
His	Tyr	Ser	Val	Val	Asp	Val	Cys	Ile	Phe	Glu	Thr	Val	Val	Ile	Val		
		35					40						45				
Leu	Leu	Thr	Phe	Leu	Ile	Ile	Ala	Gly	Asn	Leu	Thr	Val	Ile	Phe	Val		
		50					55					60					
Phe	His	Cys	Ala	Pro	Leu	Leu	His	His	Tyr	Thr	Thr	Ser	Tyr	Phe	Ile		
	65					70				75					80		
Gln	Thr	Met	Ala	Tyr	Ala	Asp	Leu	Phe	Val	Gly	Val	Ser	Cys	Leu	Val		
				85					90						95		
Pro	Thr	Leu	Ser	Leu	Leu	His	Tyr	Ser	Thr	Gly	Val	His	Glu	Ser	Leu		
			100					105						110			
Thr	Cys	Gln	Val	Phe	Gly	Tyr	Ile	Ile	Ser	Val	Leu	Lys	Ser	Val	Ser		
		115					120						125				
Met	Ala	Cys	Leu	Ala	Cys	Ile	Ser	Val	Asp	Arg	Tyr	Leu	Ala	Ile	Thr		
	130						135						140				
Lys	Pro	Leu	Ser	Tyr	Asn	Gln	Leu	Val	Thr	Pro	Cys	Arg	Leu	Arg	Ile		
	145					150					155				160		
Cys	Ile	Ile	Leu	Ile	Trp	Ile	Tyr	Ser	Cys	Leu	Ile	Phe	Leu	Pro	Ser		
				165					170						175		
Phe	Phe	Gly	Trp	Gly	Lys	Pro	Gly	Tyr	His	Gly	Asp	Ile	Phe	Glu	Trp		
			180					185						190			
Cys	Ala	Thr	Ser	Trp	Leu	Thr	Ser	Ala	Tyr	Phe	Thr	Gly	Phe	Ile	Val		
		195						200					205				
Cys	Leu	Leu	Tyr	Ala	Pro	Ala	Ala	Phe	Val	Val	Cys	Phe	Thr	Tyr	Phe		
		210					215					220					
His	Ile	Phe	Lys	Ile	Cys	Arg	Gln	His	Thr	Lys	Glu	Ile	Asn	Asp	Arg		
	225					230					235				240		

160/518

Arg Ala Arg Phe Pro Ser His Glu Val Asp Ser Ser Arg Glu Thr Gly
 245 250 255
 His Ser Pro Asp Arg Arg Tyr Ala Met Val Leu Phe Arg Ile Thr Ser
 260 265 270
 Val Phe Tyr Met Leu Trp Leu Pro Tyr Ile Ile Tyr Phe Leu Leu Glu
 275 280 285
 Ser Ser Arg Val Leu Asp Asn Pro Thr Leu Ser Phe Leu Thr Thr Trp
 290 295 300
 Leu Ala Ile Ser Asn Ser Phe Cys Asn Cys Val Ile Tyr Ser Leu Ser
 305 310 315 320
 Asn Ser Val Phe Arg Leu Gly Leu Arg Arg Leu Ser Glu Thr Met Cys
 325 330 335
 Thr Ser Cys Met Cys Val Lys Asp Gln Glu Ala Gln Glu Pro Lys Pro
 340 345 350
 Arg Lys Arg Ala Asn Ser Cys Ser Ile Ala Ser Lys Gly Glu Glu Leu
 355 360 365
 Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn
 370 375 380
 Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr
 385 390 395 400
 Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
 405 410 415
 Pro Trp Pro Thr Leu Val Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe
 420 425 430
 Ser Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala
 435 440 445
 Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
 450 455 460
 Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu

161/518

465 470 475 480
 Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
 485 490 495
 Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr
 500 505 510
 Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr
 515 520 525
 Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
 530 535 540
 Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
 545 550 555 560
 Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
 565 570 575
 Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His
 580 585 590
 Gly Met Asp Glu Leu Tyr Asn
 595

<210> 70

<211> 575

<212> PRT

<213> Human

<400> 70

Met Asn Ser Trp Asp Ala Gly Leu Ala Gly Leu Leu Val Gly Thr Met
 5 10 15
 Gly Val Ser Leu Leu Ser Asn Ala Leu Val Leu Leu Cys Leu Leu His
 20 25 30
 Ser Ala Asp Ile Arg Arg Gln Ala Pro Ala Leu Phe Thr Leu Asn Leu

162/518

35	40	45
Thr Cys Gly Asn Leu Leu Cys Thr Val Val Asn Met Pro Leu Thr Leu		
50	55	60
Ala Gly Val Val Ala Gln Arg Gln Pro Ala Gly Asp Arg Leu Cys Arg		
65	70	75
Leu Ala Ala Phe Leu Asp Thr Phe Leu Ala Ala Asn Ser Met Leu Ser		
85	90	95
Met Ala Ala Leu Ser Ile Asp Arg Trp Val Ala Val Val Phe Pro Leu		
100	105	110
Ser Tyr Arg Ala Lys Met Arg Leu Arg Asp Ala Ala Leu Met Val Ala		
115	120	125
Tyr Thr Trp Leu His Ala Leu Thr Phe Pro Ala Ala Ala Leu Ala Leu		
130	135	140
Ser Trp Leu Gly Phe His Gln Leu Tyr Ala Ser Cys Thr Leu Cys Ser		
145	150	155
Arg Arg Pro Asp Glu Arg Leu Arg Phe Ala Val Phe Thr Gly Ala Phe		
165	170	175
His Ala Leu Ser Phe Leu Leu Ser Phe Val Val Leu Cys Cys Thr Tyr		
180	185	190
Leu Lys Val Leu Lys Val Ala Arg Phe His Cys Lys Arg Ile Asp Val		
195	200	205
Ile Thr Met Gln Thr Leu Val Leu Leu Val Asp Leu His Pro Ser Val		
210	215	220
Arg Glu Arg Cys Leu Glu Glu Gln Lys Arg Arg Arg Gln Arg Ala Thr		
225	230	235
Lys Lys Ile Ser Thr Phe Ile Gly Thr Phe Leu Val Cys Phe Ala Pro		
245	250	255
Tyr Val Ile Thr Arg Leu Val Glu Leu Phe Ser Thr Val Pro Ile Gly		
260	265	270

163/518

Ser His Trp Gly Val Leu Ser Lys Cys Leu Ala Tyr Ser Lys Ala Ala
 275 280 285
 Ser Asp Pro Phe Val Tyr Ser Leu Leu Arg His Gln Tyr Arg Lys Ser
 290 295 300
 Cys Lys Glu Ile Leu Asn Arg Leu Leu His Arg Arg Ser Ile His Ser
 305 310 315 320
 Ser Gly Leu Thr Gly Asp Ser His Ser Gln Asn Ile Leu Pro Val Ser
 325 330 335
 Glu Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 340 345 350
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 355 360 365
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 370 375 380
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 385 390 395 400
 Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 405 410 415
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 420 425 430
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 435 440 445
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 450 455 460
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 465 470 475 480
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 485 490 495
 Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser

164/518

500 505 510
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 515 520 525
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 530 535 540
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 545 550 555 560
 Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn
 565 570 575

<210> 71

<211> 727

<212> PRT

<213> Human

<400> 71

Met Asn Pro Pro Ser Gly Pro Arg Val Leu Pro Ser Pro Thr Gln Glu
 5 10 15
 Pro Ser Cys Met Ala Thr Pro Ala Pro Pro Ser Trp Trp Asp Ser Ser
 20 25 30
 Gln Ser Ser Ile Ser Ser Leu Gly Arg Leu Pro Ser Ile Ser Pro Thr
 35 40 45
 Ala Pro Gly Thr Trp Ala Ala Ala Trp Val Pro Leu Pro Thr Val Asp
 50 55 60
 Val Pro Asp His Ala His Tyr Thr Leu Gly Thr Val Ile Leu Leu Val
 65 70 75 80
 Gly Leu Thr Gly Met Leu Gly Asn Leu Thr Val Ile Tyr Thr Phe Cys
 85 90 95
 Arg Ala Val Leu Arg Gly Val Thr Val Met Met Gln Ser Arg Ser Leu

165/518

100	105	110
Arg Thr Pro Ala Asn Met Phe Ile	Ile Asn Leu Ala Val Ser Asp Phe	
115	120	125
Leu Met Ser Phe Thr Gln Ala Pro Val Phe Phe Thr Ser Ser Leu Tyr		
130	135	140
Lys Gln Trp Leu Phe Gly Glu Thr Gly Cys Glu Phe Tyr Ala Phe Cys		
145	150	155
Gly Ala Leu Phe Gly Ile Ser Ser Met Ile Thr Leu Thr Ala Ile Ala		
165	170	175
Leu Asp Arg Tyr Leu Val Ile Thr Arg Pro Leu Ala Thr Phe Gly Val		
180	185	190
Ala Ser Lys Arg Arg Ala Ala Phe Val Leu Leu Gly Val Trp Leu Tyr		
195	200	205
Ala Leu Ala Trp Ser Leu Pro Pro Phe Phe Gly Trp Ser Ala Tyr Val		
210	215	220
Pro Glu Gly Leu Leu Thr Ser Cys Ser Trp Asp Tyr Met Ser Phe Thr		
225	230	235
Pro Ala Val Arg Ala Tyr Thr Met Leu Leu Cys Cys Phe Val Phe Phe		
245	250	255
Leu Pro Leu Leu Ile Ile Ile Tyr Cys Tyr Ile Phe Ile Phe Arg Ala		
260	265	270
Ile Arg Glu Thr Gly Arg Ala Leu Gln Thr Phe Gly Ala Cys Lys Gly		
275	280	285
Asn Gly Glu Ser Leu Trp Gln Arg Gln Arg Leu Gln Ser Glu Cys Lys		
290	295	300
Met Ala Lys Ile Met Leu Leu Val Ile Leu Leu Phe Val Leu Ser Trp		
305	310	315
Ala Pro Tyr Ser Ala Val Ala Leu Val Ala Phe Ala Gly Tyr Ala His		
325	330	335

166/518

Val Leu Thr Pro Tyr Met Ser Ser Val Pro Ala Val Ile Ala Lys Ala
 340 345 350
 Ser Ala Ile His Asn Pro Ile Ile Tyr Ala Ile Thr His Pro Lys Tyr
 355 360 365
 Arg Val Ala Ile Ala Gln His Leu Pro Cys Leu Gly Val Leu Leu Gly
 370 375 380
 Val Ser Arg Arg His Ser Arg Pro Tyr Pro Ser Tyr Arg Ser Thr His
 385 390 395 400
 Arg Ser Thr Leu Ile Ser His Thr Ser Asn Leu Ser Trp Ile Ser Ile
 405 410 415
 Arg Arg Arg Gln Glu Ser Leu Gly Ser Glu Ser Glu Val Gly Trp Thr
 420 425 430
 His Met Glu Ala Ala Ala Val Trp Gly Ala Ala Gln Gln Ala Asn Gly
 435 440 445
 Arg Ser Leu Tyr Gly Gln Gly Leu Glu Asp Leu Glu Ala Lys Ala Pro
 450 455 460
 Pro Arg Pro Gln Gly His Glu Ala Glu Thr Pro Gly Lys Thr Lys Gly
 465 470 475 480
 Leu Ile Pro Ser Gln Asp Pro Arg Met Ala Ser Lys Gly Glu Glu Leu
 485 490 495
 Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn
 500 505 510
 Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr
 515 520 525
 Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
 530 535 540
 Pro Trp Pro Thr Leu Val Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe
 545 550 555 560
 Ser Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala

167/518

	565		570		575										
Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp
	580		585		590										
Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu
	595		600		605										
Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn
	610		615		620										
Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr
625			630		635									640	
Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Thr
	645		650		655										
Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln
	660		665		670										
Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His
	675		680		685										
Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg
	690		695		700										
Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His
705			710		715									720	
Gly	Met	Asp	Glu	Leu	Tyr	Asn									
	725														

<210> 72

<211> 616

<212> PRT

<213> Human

<400> 72

Met Val Trp Gly Lys Ile Cys Trp Phe Ser Gln Arg Ala Gly Trp Thr

168/518

	5		10		15
Val	Phe	Ala	Glu	Ser	Gln
				Ile	Ser
				Leu	Ser
				Cys	Ser
				Leu	Cys
				Leu	His
	20		25		30
Ser	Gly	Asp	Gln	Glu	Ala
				Gln	Asn
				Pro	Asn
				Leu	Val
				Ser	Gln
				Leu	Cys
	35		40		45
Gly	Val	Phe	Leu	Gln	Asn
				Glu	Thr
				Asn	Glu
				Thr	Ile
				His	Met
				Gln	Met
	50		55		60
Ser	Met	Ala	Val	Gly	Gln
				Gln	Ala
				Leu	Pro
				Leu	Asn
				Ile	Ile
				Ala	Pro
	65		70		75
Lys	Ala	Val	Leu	Val	Ser
				Leu	Cys
				Gly	Val
				Leu	Leu
				Asn	Gly
				Thr	Val
	85		90		95
Phe	Trp	Leu	Leu	Cys	Cys
				Gly	Ala
				Thr	Asn
				Pro	Tyr
				Met	Val
				Tyr	Ile
	100		105		110
Leu	His	Leu	Val	Ala	Ala
				Asp	Val
				Ile	Tyr
				Leu	Cys
				Cys	Ser
				Ala	Val
	115		120		125
Gly	Phe	Leu	Gln	Val	Thr
				Leu	Leu
				Thr	Tyr
				His	Gly
				Val	Val
				Phe	Phe
	130		135		140
Ile	Pro	Asp	Phe	Leu	Ala
				Ile	Leu
				Ser	Pro
				Phe	Ser
				Phe	Glu
				Val	Cys
	145		150		155
Leu	Cys	Leu	Leu	Val	Ala
				Ile	Ser
				Thr	Glu
				Arg	Cys
				Val	Cys
				Val	Leu
	165		170		175
Phe	Pro	Ile	Trp	Tyr	Arg
				Cys	His
				Arg	Pro
				Lys	Tyr
				Thr	Ser
				Asn	Val
	180		185		190
Val	Cys	Thr	Leu	Ile	Trp
				Gly	Leu
				Pro	Phe
				Cys	Ile
				Asn	Ile
				Val	Lys
	195		200		205
Ser	Leu	Phe	Leu	Thr	Tyr
				Trp	Lys
				His	Val
				Lys	Ala
				Cys	Val
				Ile	Phe
	210		215		220
Leu	Lys	Leu	Ser	Gly	Leu
				Phe	His
				Ala	Ile
				Leu	Ser
				Leu	Val
				Met	Cys
	225		230		235
					240

169/518

Val Ser Ser Leu Thr Leu Leu Ile Arg Phe Leu Cys Cys Ser Gln Gln
 245 250 255
 Gln Lys Ala Thr Arg Val Tyr Ala Val Val Gln Ile Ser Ala Pro Met
 260 265 270
 Phe Leu Leu Trp Ala Leu Pro Leu Ser Val Ala Pro Leu Ile Thr Asp
 275 280 285
 Phe Lys Met Phe Val Thr Thr Ser Tyr Leu Ile Ser Leu Phe Leu Ile
 290 295 300
 Ile Asn Ser Ser Ala Asn Pro Ile Ile Tyr Phe Phe Val Gly Ser Leu
 305 310 315 320
 Arg Lys Lys Arg Leu Lys Glu Ser Leu Arg Val Ile Leu Gln Arg Ala
 325 330 335
 Leu Ala Asp Lys Pro Glu Val Gly Arg Asn Lys Lys Ala Ala Gly Ile
 340 345 350
 Asp Pro Met Glu Gln Pro His Ser Thr Gln His Val Glu Asn Leu Leu
 355 360 365
 Pro Arg Glu His Arg Val Asp Val Glu Thr Ala Ser Lys Gly Glu Glu
 370 375 380
 Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val
 385 390 395 400
 Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr
 405 410 415
 Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
 420 425 430
 Val Pro Trp Pro Thr Leu Val Thr Thr Leu Cys Tyr Gly Val Gln Cys
 435 440 445
 Phe Ser Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
 450 455 460
 Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp

170/518

465 470 475 480
 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
 485 490 495
 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
 500 505 510
 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
 515 520 525
 Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
 530 535 540
 Thr Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
 545 550 555 560
 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
 565 570 575
 His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
 580 585 590
 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
 595 600 605
 His Gly Met Asp Glu Leu Tyr Asn
 610 615

<210> 73

<211> 608

<212> PRT

<213> Human

<400> 73

Met Ala Asn Tyr Ser His Ala Ala Asp Asn Ile Leu Gln Asn Leu Ser
 5 10 15
 Pro Leu Thr Ala Phe Leu Lys Leu Thr Ser Leu Gly Phe Ile Ile Gly

171/518

20	25	30
Val Ser Val Val Gly Asn Leu Leu Ile Ser Ile Leu Leu Val Lys Asp		
35	40	45
Lys Thr Leu His Arg Ala Pro Tyr Tyr Phe Leu Leu Asp Leu Cys Cys		
50	55	60
Ser Asp Ile Leu Arg Ser Ala Ile Cys Phe Pro Phe Val Phe Asn Ser		
65	70	75
Val Lys Asn Gly Ser Thr Trp Thr Tyr Gly Thr Leu Thr Cys Lys Val		
85	90	95
Ile Ala Phe Leu Gly Val Leu Ser Cys Phe His Thr Ala Phe Met Leu		
100	105	110
Phe Cys Ile Ser Val Thr Arg Tyr Leu Ala Ile Ala His His Arg Phe		
115	120	125
Tyr Thr Lys Arg Leu Thr Phe Trp Thr Cys Leu Ala Val Ile Cys Met		
130	135	140
Val Trp Thr Leu Ser Val Ala Met Ala Phe Pro Pro Val Leu Asp Val		
145	150	155
Gly Thr Tyr Ser Phe Ile Arg Glu Glu Asp Gln Cys Thr Phe Gln His		
165	170	175
Arg Ser Phe Arg Ala Asn Asp Ser Leu Gly Phe Met Leu Leu Leu Ala		
180	185	190
Leu Ile Leu Leu Ala Thr Gln Leu Val Tyr Leu Lys Leu Ile Phe Phe		
195	200	205
Val His Asp Arg Arg Lys Met Lys Pro Val Gln Phe Val Ala Ala Val		
210	215	220
Ser Gln Asn Trp Thr Phe His Gly Pro Gly Ala Ser Gly Gln Ala Ala		
225	230	235
Ala Asn Trp Leu Ala Gly Phe Gly Arg Gly Pro Thr Pro Pro Thr Leu		
245	250	255

172/518

Leu Gly Ile Arg Gln Asn Ala Asn Thr Thr Gly Arg Arg Arg Leu Leu
 260 265 270
 Val Leu Asp Glu Phe Lys Met Glu Lys Arg Ile Ser Arg Met Phe Tyr
 275 280 285
 Ile Met Thr Phe Leu Phe Leu Thr Leu Trp Gly Pro Tyr Leu Val Ala
 290 295 300
 Cys Tyr Trp Arg Val Phe Ala Arg Gly Pro Val Val Pro Gly Gly Phe
 305 310 315 320
 Leu Thr Ala Ala Val Trp Met Ser Phe Ala Gln Ala Gly Ile Asn Pro
 325 330 335
 Phe Val Cys Ile Phe Ser Asn Arg Glu Leu Arg Arg Cys Phe Ser Thr
 340 345 350
 Thr Leu Leu Tyr Cys Arg Lys Ser Arg Leu Pro Arg Glu Pro Tyr Cys
 355 360 365
 Val Ile Ser Arg Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile
 370 375 380
 Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser
 385 390 395 400
 Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe
 405 410 415
 Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr
 420 425 430
 Thr Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met
 435 440 445
 Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln
 450 455 460
 Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala
 465 470 475 480
 Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys

173/518

	485	490	495
Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu			
500	505	510	
Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys			
515	520	525	
Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly			
530	535	540	
Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp			
545	550	555	560
Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala			
565	570	575	
Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu			
580	585	590	
Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn			
595	600	605	

<210> 74

<211> 572

<212> PRT

<213> Human

<400> 74

Met Asn Glu Asp Leu Lys Val Asn Leu Ser Gly Leu Pro Arg Asp Tyr			
5	10	15	
Leu Asp Ala Ala Ala Ala Glu Asn Ile Ser Ala Ala Val Ser Ser Arg			
20	25	30	
Val Pro Ala Val Glu Pro Glu Pro Glu Leu Val Val Asn Pro Trp Asp			
35	40	45	
Ile Val Leu Cys Thr Ser Gly Thr Leu Ile Ser Cys Glu Asn Ala Ile			

174/518

50	55	60
Val Val Leu Ile Ile Phe His Asn Pro Ser Leu Arg Ala Pro Met Phe		
65	70	75
Leu Leu Ile Gly Ser Leu Ala Leu Ala Asp Leu Leu Ala Gly Ile Gly		
85	90	95
Leu Ile Thr Asn Phe Val Phe Ala Tyr Leu Leu Gln Ser Glu Ala Thr		
100	105	110
Lys Leu Val Thr Ile Gly Leu Ile Val Ala Ser Phe Ser Ala Ser Val		
115	120	125
Cys Ser Leu Leu Ala Ile Thr Val Asp Arg Tyr Leu Ser Leu Tyr Tyr		
130	135	140
Ala Leu Thr Tyr His Ser Glu Arg Thr Val Thr Phe Thr Tyr Val Met		
145	150	155
Leu Val Met Leu Trp Gly Thr Ser Ile Cys Leu Gly Leu Leu Pro Val		
165	170	175
Met Gly Trp Asn Cys Leu Arg Asp Glu Ser Thr Cys Ser Val Val Arg		
180	185	190
Pro Leu Thr Lys Asn Asn Ala Ala Ile Leu Ser Val Ser Phe Leu Phe		
195	200	205
Met Phe Ala Leu Met Leu Gln Leu Tyr Ile Gln Ile Cys Lys Ile Val		
210	215	220
Met Arg His Ala His Gln Ile Ala Leu Gln His His Phe Leu Ala Thr		
225	230	235
Ser His Tyr Val Thr Thr Arg Lys Gly Val Ser Thr Leu Ala Ile Ile		
245	250	255
Leu Gly Thr Phe Ala Ala Cys Trp Met Pro Phe Thr Leu Tyr Ser Leu		
260	265	270
Ile Ala Asp Tyr Thr Tyr Pro Ser Ile Tyr Thr Tyr Ala Thr Leu Leu		
275	280	285

175/518

Pro Ala Thr Tyr Asn Ser Ile Ile Asn Pro Val Ile Tyr Ala Phe Arg
 290 295 300
 Asn Gln Glu Ile Gln Lys Ala Leu Cys Leu Ile Cys Cys Gly Cys Ile
 305 310 315 320
 Pro Ser Ser Leu Ala Gln Arg Ala Arg Ser Pro Ser Asp Val Ala Ser
 325 330 335
 Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu
 340 345 350
 Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu
 355 360 365
 Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr
 370 375 380
 Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Cys Tyr
 385 390 395 400
 Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg His Asp
 405 410 415
 Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile
 420 425 430
 Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe
 435 440 445
 Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe
 450 455 460
 Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn
 465 470 475 480
 Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys
 485 490 495
 Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu
 500 505 510
 Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu

176/518

515 520 525
 Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp
 530 535 540
 Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala
 545 550 555 560
 Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn
 565 570

<210> 75

<211> 613

<212> PRT

<213> Human

<400> 75

Met Asp Val Thr Ser Gln Ala Arg Gly Val Gly Leu Glu Met Tyr Leu
 5 10 15
 Gly Thr Ala Gln Pro Ala Ala Pro Asn Thr Thr Ser Pro Glu Leu Asn
 20 25 30
 Leu Ser His Pro Leu Leu Gly Thr Ala Leu Ala Asn Gly Thr Gly Glu
 35 40 45
 Leu Ser Glu His Gln Gln Tyr Val Ile Gly Leu Phe Leu Ser Cys Leu
 50 55 60
 Tyr Thr Ile Phe Leu Phe Pro Ile Gly Phe Val Gly Asn Ile Leu Ile
 65 70 75 80
 Leu Val Val Asn Ile Ser Phe Arg Glu Lys Met Thr Ile Pro Asp Leu
 85 90 95
 Tyr Phe Ile Asn Leu Ala Val Ala Asp Leu Ile Leu Val Ala Asp Ser
 100 105 110
 Leu Ile Glu Val Phe Asn Leu His Glu Arg Tyr Tyr Asp Ile Ala Val

177/518

115	120	125
Leu Cys Thr Phe Met Ser Leu Phe Leu Gln Val Asn Met Tyr Ser Ser		
130	135	140
Val Phe Phe Leu Thr Trp Met Ser Phe Asp Arg Tyr Ile Ala Leu Ala		
145	150	155
Arg Ala Met Arg Cys Ser Leu Phe Arg Thr Lys His His Ala Arg Leu		
165	170	175
Ser Cys Gly Leu Ile Trp Met Ala Ser Val Ser Ala Thr Leu Val Pro		
180	185	190
Phe Thr Ala Val His Leu Gln His Thr Asp Glu Ala Cys Phe Cys Phe		
195	200	205
Ala Asp Val Arg Glu Val Gln Trp Leu Glu Val Thr Leu Gly Phe Ile		
210	215	220
Val Pro Phe Ala Ile Ile Gly Leu Cys Tyr Ser Leu Ile Val Arg Val		
225	230	235
Leu Val Arg Ala His Arg His Arg Gly Leu Arg Pro Arg Arg Gln Lys		
245	250	255
Ala Leu Arg Met Ile Leu Ala Val Val Leu Val Phe Phe Val Cys Trp		
260	265	270
Leu Pro Glu Asn Val Phe Ile Ser Val His Leu Leu Gln Arg Thr Gln		
275	280	285
Pro Gly Ala Ala Pro Cys Lys Gln Ser Phe Arg His Ala His Pro Leu		
290	295	300
Thr Gly His Ile Val Asn Leu Ala Ala Phe Ser Asn Ser Cys Leu Asn		
305	310	315
Pro Leu Ile Tyr Ser Phe Leu Gly Glu Thr Phe Arg Asp Lys Leu Arg		
325	330	335
Leu Tyr Ile Glu Gln Lys Thr Asn Leu Pro Ala Leu Asn Arg Phe Cys		
340	345	350

178/518

His Ala Ala Leu Lys Ala Val Ile Pro Asp Ser Thr Glu Gln Ser Asp
 355 360 365
 Val Arg Phe Ser Ser Ala Val Ala Ser Lys Gly Glu Glu Leu Phe Thr
 370 375 380
 Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His
 385 390 395 400
 Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys
 405 410 415
 Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp
 420 425 430
 Pro Thr Leu Val Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg
 435 440 445
 Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro
 450 455 460
 Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn
 465 470 475 480
 Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn
 485 490 495
 Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu
 500 505 510
 Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met
 515 520 525
 Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His
 530 535 540
 Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn
 545 550 555 560
 Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu
 565 570 575
 Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His

590

605

610

〈213〉 Human

15

30

45

60

80

95

110

125

Glu Thr Thr Ser Cys Tyr Glu Lys Ile Phe Tyr Gly His Leu Leu Lys

180/518

130	135	140	
Lys Phe Arg Gln Pro Asn Phe Ala Arg Lys Leu Cys Ile Tyr Ile Trp			
145	150	155	160
Gly Val Val Leu Gly Ile Ile Ile Pro Val Thr Val Tyr Tyr Ser Val			
165	170	175	
Ile Glu Ala Thr Glu Gly Glu Glu Ser Leu Cys Tyr Asn Arg Gln Met			
180	185	190	
Glu Leu Gly Ala Met Ile Ser Gln Ile Ala Gly Leu Ile Gly Thr Thr			
195	200	205	
Phe Ile Gly Phe Ser Phe Leu Val Val Leu Thr Ser Tyr Tyr Ser Phe			
210	215	220	
Val Ser His Leu Arg Lys Ile Arg Thr Cys Thr Ser Ile Met Glu Lys			
225	230	235	240
Asp Leu Thr Tyr Ser Ser Val Lys Arg His Leu Leu Val Ile Gln Ile			
245	250	255	
Leu Leu Ile Val Cys Phe Leu Pro Tyr Ser Ile Phe Lys Pro Ile Phe			
260	265	270	
Tyr Val Leu His Gln Arg Asp Asn Cys Gln Gln Leu Asn Tyr Leu Ile			
275	280	285	
Glu Thr Lys Asn Ile Leu Thr Cys Leu Ala Ser Ala Arg Ser Ser Thr			
290	295	300	
Asp Pro Ile Ile Phe Leu Leu Leu Asp Lys Thr Phe Lys Lys Thr Leu			
305	310	315	320
Tyr Asn Leu Phe Thr Lys Ser Asn Ser Ala His Met Gln Ser Tyr Gly			
325	330	335	
Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val			
340	345	350	
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu			
355	360	365	

181/518

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 370 375 380
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
 385 390 395 400
 Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg
 405 410 415
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 420 425 430
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 435 440 445
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 450 455 460
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 465 470 475 480
 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 485 490 495
 Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser Val
 500 505 510
 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
 515 520 525
 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
 530 535 540
 Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
 545 550 555 560
 Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn
 565 570

<210> 77

<211> 1061

182/518

<212> PRT

<213> Human

<400> 77

Met Gly Gly Arg Val Phe Leu Val Phe Leu Ala Phe Cys Val Trp Leu
 5 10 15
 Thr Leu Pro Gly Ala Glu Thr Gln Asp Ser Arg Gly Cys Ala Arg Trp
 20 25 30
 Cys Pro Gln Asp Ser Ser Cys Val Asn Ala Thr Ala Cys Arg Cys Asn
 35 40 45
 Pro Gly Phe Ser Ser Phe Ser Glu Ile Ile Thr Thr Pro Met Glu Thr
 50 55 60
 Cys Asp Asp Ile Asn Glu Cys Ala Thr Leu Ser Lys Val Ser Cys Gly
 65 70 75 80
 Lys Phe Ser Asp Cys Trp Asn Thr Glu Gly Ser Tyr Asp Cys Val Cys
 85 90 95
 Ser Pro Gly Tyr Glu Pro Val Ser Gly Ala Lys Thr Phe Lys Asn Glu
 100 105 110
 Ser Glu Asn Thr Cys Gln Asp Val Asp Glu Cys Gln Gln Asn Pro Arg
 115 120 125
 Leu Cys Lys Ser Tyr Gly Thr Cys Val Asn Thr Leu Gly Ser Tyr Thr
 130 135 140
 Cys Gln Cys Leu Pro Gly Phe Lys Phe Ile Pro Glu Asp Pro Lys Val
 145 150 155 160
 Cys Thr Asp Val Asn Glu Cys Thr Ser Gly Gln Asn Pro Cys His Ser
 165 170 175
 Ser Thr His Cys Leu Asn Asn Val Gly Ser Tyr Gln Cys Arg Cys Arg
 180 185 190
 Pro Gly Trp Gln Pro Ile Pro Gly Ser Pro Asn Gly Pro Asn Asn Thr

183/518

195	200	205
Val Cys Glu Asp Val Asp Glu Cys Ser Ser Gly Gln His Gln Cys Asp		
210	215	220
Ser Ser Thr Val Cys Phe Asn Thr Val Gly Ser Tyr Ser Cys Arg Cys		
225	230	235
Arg Pro Gly Trp Lys Pro Arg His Gly Ile Pro Asn Asn Gln Lys Asp		
245	250	255
Thr Val Cys Glu Asp Met Thr Phe Ser Thr Trp Thr Pro Pro Pro Gly		
260	265	270
Val His Ser Gln Thr Leu Ser Arg Phe Phe Asp Lys Val Gln Asp Leu		
275	280	285
Gly Arg Asp Tyr Lys Pro Gly Leu Ala Asn Asn Thr Ile Gln Ser Ile		
290	295	300
Leu Gln Ala Leu Asp Glu Leu Leu Glu Val Pro Gly Asp Leu Glu Thr		
305	310	315
Leu Pro Arg Leu Gln Gln His Cys Val Ala Ser His Leu Leu Asp Gly		
325	330	335
Leu Glu Asp Val Leu Arg Gly Leu Ser Lys Asn Leu Ser Asn Gly Leu		
340	345	350
Leu Asn Phe Ser Tyr Pro Ala Gly Thr Glu Leu Ser Leu Glu Val Gln		
355	360	365
Lys Gln Val Asp Arg Ser Val Thr Leu Arg Gln Asn Gln Ala Val Met		
370	375	380
Gln Leu Asp Trp Asn Gln Ala Gln Lys Ser Gly Asp Pro Gly Pro Ser		
385	390	395
Val Val Gly Leu Val Ser Ile Pro Gly Met Gly Lys Leu Leu Ala Glu		
405	410	415
Ala Pro Leu Val Leu Glu Pro Glu Lys Gln Met Leu Leu His Glu Thr		
420	425	430

184/518

His Gln Gly Leu Leu Gln Asp Gly Ser Pro Ile Leu Leu Ser Asp Val
 435 440 445
 Ile Ser Ala Phe Leu Ser Asn Asn Asp Thr Gln Asn Leu Ser Ser Pro
 450 455 460
 Val Thr Phe Thr Phe Ser His Arg Ser Val Ile Pro Arg Gln Lys Val
 465 470 475 480
 Leu Cys Val Phe Trp Glu His Gly Gln Asn Gly Cys Gly His Trp Ala
 485 490 495
 Thr Thr Gly Cys Ser Thr Ile Gly Thr Arg Asp Thr Ser Thr Ile Cys
 500 505 510
 Arg Cys Thr His Leu Ser Ser Phe Ala Val Leu Met Ala His Tyr Asp
 515 520 525
 Val Gln Glu Glu Asp Pro Val Leu Thr Val Ile Thr Tyr Met Gly Leu
 530 535 540
 Ser Val Ser Leu Leu Cys Leu Leu Leu Ala Ala Leu Thr Phe Leu Leu
 545 550 555 560
 Cys Lys Ala Ile Gln Asn Thr Ser Thr Ser Leu His Leu Gln Leu Ser
 565 570 575
 Leu Cys Leu Phe Leu Ala His Leu Leu Phe Leu Val Ala Ile Asp Gln
 580 585 590
 Thr Gly His Lys Val Leu Cys Ser Ile Ile Ala Gly Thr Leu His Tyr
 595 600 605
 Leu Tyr Leu Ala Thr Leu Thr Trp Met Leu Leu Glu Ala Leu Tyr Leu
 610 615 620
 Phe Leu Thr Ala Arg Asn Leu Thr Val Val Asn Tyr Ser Ser Ile Asn
 625 630 635 640
 Arg Phe Met Lys Lys Leu Met Phe Pro Val Gly Tyr Gly Val Pro Ala
 645 650 655
 Val Thr Val Ala Ile Ser Ala Ala Ser Arg Pro His Leu Tyr Gly Thr

185/518

660	665	670
Pro Ser Arg Cys Trp Leu Gln	Pro Glu Lys Gly Phe Ile Trp Gly Phe	
675	680	685
Leu Gly Pro Val Cys Ala Ile Phe Ser Val Asn Leu Val Leu Phe Leu		
690	695	700
Val Thr Leu Trp Ile Leu Lys Asn Arg Leu Ser Ser Leu Asn Ser Glu		
705	710	715
Val Ser Thr Leu Arg Asn Thr Arg Met Leu Ala Phe Lys Ala Thr Ala		
725	730	735
Gln Leu Phe Ile Leu Gly Cys Thr Trp Cys Leu Gly Ile Leu Gln Val		
740	745	750
Gly Pro Ala Ala Arg Val Met Ala Tyr Leu Phe Thr Ile Ile Asn Ser		
755	760	765
Leu Gln Gly Val Phe Ile Phe Leu Val Tyr Cys Leu Leu Ser Gln Gln		
770	775	780
Val Arg Glu Gln Tyr Gly Lys Trp Ser Lys Gly Ile Arg Lys Leu Lys		
785	790	795
Thr Glu Ser Glu Met His Thr Leu Ser Ser Ser Ala Lys Ala Asp Thr		
805	810	815
Ser Lys Pro Ser Thr Val Asn Ala Ser Lys Gly Glu Glu Leu Phe Thr		
820	825	830
Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His		
835	840	845
Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys		
850	855	860
Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp		
865	870	875
Pro Thr Leu Val Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg		
885	890	895

186/518

Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro
 900 905 910
 Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn
 915 920 925
 Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn
 930 935 940
 Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu
 945 950 955 960
 Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met
 965 970 975
 Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His
 980 985 990
 Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn
 995 1000 1005
 Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu
 1010 1015 1020
 Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His
 1025 1030 1035 1040
 Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met
 1045 1050 1055
 Asp Glu Leu Tyr Asn
 1060

<210> 78

<211> 753

<212> PRT

<213> Human

<400> 78

187/518

Met Gly His Asn Gly Ser Trp Ile Ser Pro Asn Ala Ser Glu Pro His
 5 10 15
 Asn Ala Ser Gly Ala Glu Ala Ala Gly Val Asn Arg Ser Ala Leu Gly
 20 25 30
 Glu Phe Gly Glu Ala Gln Leu Tyr Arg Gln Phe Thr Thr Thr Val Gln
 35 40 45
 Val Val Ile Phe Ile Gly Ser Leu Leu Gly Asn Phe Met Val Leu Trp
 50 55 60
 Ser Thr Cys Arg Thr Thr Val Phe Lys Ser Val Thr Asn Arg Phe Ile
 65 70 75 80
 Lys Asn Leu Ala Cys Ser Gly Ile Cys Ala Ser Leu Val Cys Val Pro
 85 90 95
 Phe Asp Ile Ile Leu Ser Thr Ser Pro His Cys Cys Trp Trp Ile Tyr
 100 105 110
 Thr Met Leu Phe Cys Lys Val Val Lys Phe Leu His Lys Val Phe Cys
 115 120 125
 Ser Val Thr Ile Leu Ser Phe Pro Ala Ile Ala Leu Asp Arg Tyr Tyr
 130 135 140
 Ser Val Leu Tyr Pro Leu Glu Arg Lys Ile Ser Asp Ala Lys Ser Arg
 145 150 155 160
 Glu Leu Val Met Tyr Ile Trp Ala His Ala Val Val Ala Ser Val Pro
 165 170 175
 Val Phe Ala Val Thr Asn Val Ala Asp Ile Tyr Ala Thr Ser Thr Cys
 180 185 190
 Thr Glu Val Trp Ser Asn Ser Leu Gly His Leu Val Tyr Val Leu Val
 195 200 205
 Tyr Asn Ile Thr Thr Val Ile Val Pro Val Val Val Val Phe Leu Phe
 210 215 220
 Leu Ile Leu Ile Arg Arg Ala Leu Ser Ala Ser Gln Lys Lys Lys Val

188/518

225 230 235 240
 Ile Ile Ala Ala Leu Arg Thr Pro Gln Asn Thr Ile Ser Ile Pro Tyr
 245 250 255
 Ala Ser Gln Arg Glu Ala Glu Leu His Ala Thr Leu Leu Ser Met Val
 260 265 270
 Met Val Phe Ile Leu Cys Ser Val Pro Tyr Ala Thr Leu Val Val Tyr
 275 280 285
 Gln Thr Val Leu Asn Val Pro Asp Thr Ser Val Phe Leu Leu Leu Thr
 290 295 300
 Ala Val Trp Leu Pro Lys Val Ser Leu Leu Ala Asn Pro Val Leu Phe
 305 310 315 320
 Leu Thr Val Asn Lys Ser Val Arg Lys Cys Leu Ile Gly Thr Leu Val
 325 330 335
 Gln Leu His His Arg Tyr Ser Arg Arg Asn Val Val Ser Thr Gly Ser
 340 345 350
 Gly Met Ala Glu Ala Ser Leu Glu Pro Ser Ile Arg Ser Gly Ser Gln
 355 360 365
 Leu Leu Glu Met Phe His Ile Gly Gln Gln Gln Ile Phe Lys Pro Thr
 370 375 380
 Glu Asp Glu Glu Glu Ser Glu Ala Lys Tyr Ile Gly Ser Ala Asp Phe
 385 390 395 400
 Gln Ala Lys Glu Ile Phe Ser Thr Cys Leu Glu Gly Glu Gln Gly Pro
 405 410 415
 Gln Phe Ala Pro Ser Ala Pro Pro Leu Ser Thr Val Asp Ser Val Ser
 420 425 430
 Gln Val Ala Pro Ala Ala Pro Val Glu Pro Glu Thr Phe Pro Asp Lys
 435 440 445
 Tyr Ser Leu Gln Phe Gly Phe Gly Pro Phe Glu Leu Pro Pro Gln Trp
 450 455 460

189/518

Leu Ser Glu Thr Arg Asn Ser Lys Lys Arg Leu Leu Pro Pro Leu Gly
 465 470 475 480
 Asn Thr Pro Glu Glu Leu Ile Gln Thr Lys Val Pro Lys Val Gly Arg
 485 490 495
 Val Glu Arg Lys Met Ser Arg Asn Asn Lys Val Ser Ile Phe Pro Lys
 500 505 510
 Val Asp Ser Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro
 515 520 525
 Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val
 530 535 540
 Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys
 545 550 555 560
 Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val
 565 570 575
 Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His
 580 585 590
 Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val
 595 600 605
 Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg
 610 615 620
 Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu
 625 630 635 640
 Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu
 645 650 655
 Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
 660 665 670
 Lys Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp
 675 680 685
 Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly

190/518

690	695	700
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser		
705	710	715
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu		
725	730	735
Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr		
740	745	750

Asn

<210> 79

<211> 600

<212> PRT

<213> Human

<400> 79

Met Asp Leu His Leu Phe Asp Tyr Ala Glu Pro Gly Asn Phe Ser Asp		
5	10	15
Ile Ser Trp Pro Cys Asn Ser Ser Asp Cys Ile Val Val Asp Thr Val		
20	25	30
Met Cys Pro Asn Met Pro Asn Lys Ser Val Leu Leu Tyr Thr Leu Ser		
35	40	45
Phe Ile Tyr Ile Phe Ile Phe Val Ile Gly Met Ile Ala Asn Ser Val		
50	55	60
Val Val Trp Val Asn Ile Gln Ala Lys Thr Thr Gly Tyr Asp Thr His		
65	70	75
Cys Tyr Ile Leu Asn Leu Ala Ile Ala Asp Leu Trp Val Val Leu Thr		
85	90	95
Ile Pro Val Trp Val Val Ser Leu Val Gln His Asn Gln Trp Pro Met		
100	105	110

191/518

Gly Glu Leu Thr Cys Lys Val Thr His Leu Ile Phe Ser Ile Asn Leu
 115 120 125
 Phe Gly Ser Ile Phe Phe Leu Thr Cys Met Ser Val Asp Arg Tyr Leu
 130 135 140
 Ser Ile Thr Tyr Phe Thr Asn Thr Pro Ser Ser Arg Lys Lys Met Val
 145 150 155 160
 Arg Arg Val Val Cys Ile Leu Val Trp Leu Leu Ala Phe Cys Val Ser
 165 170 175
 Leu Pro Asp Thr Tyr Tyr Leu Lys Thr Val Thr Ser Ala Ser Asn Asn
 180 185 190
 Glu Thr Tyr Cys Arg Ser Phe Tyr Pro Glu His Ser Ile Lys Glu Trp
 195 200 205
 Leu Ile Gly Met Glu Leu Val Ser Val Val Leu Gly Phe Ala Val Pro
 210 215 220
 Phe Ser Ile Ile Ala Val Phe Tyr Phe Leu Leu Ala Arg Ala Ile Ser
 225 230 235 240
 Ala Ser Ser Asp Gln Glu Lys His Ser Ser Arg Lys Ile Ile Phe Ser
 245 250 255
 Tyr Val Val Val Phe Leu Val Cys Trp Leu Pro Tyr His Val Ala Val
 260 265 270
 Leu Leu Asp Ile Phe Ser Ile Leu His Tyr Ile Pro Phe Thr Cys Arg
 275 280 285
 Leu Glu His Ala Leu Phe Thr Ala Leu His Val Thr Gln Cys Leu Ser
 290 295 300
 Leu Val His Cys Cys Val Asn Pro Val Leu Tyr Ser Phe Ile Asn Arg
 305 310 315 320
 Asn Tyr Arg Tyr Glu Leu Met Lys Ala Phe Ile Phe Lys Tyr Ser Ala
 325 330 335
 Lys Thr Gly Leu Thr Lys Leu Ile Asp Ala Ser Arg Val Ser Glu Thr

192/518

340	345	350	
Glu Tyr Ser Ala Leu Glu Gln Ser Thr Lys Ala Ser Lys Gly Glu Glu			
355	360	365	
Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val			
370	375	380	
Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr			
385	390	395	400
Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro			
405	410	415	
Val Pro Trp Pro Thr Leu Val Thr Thr Leu Cys Tyr Gly Val Gln Cys			
420	425	430	
Phe Ser Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser			
435	440	445	
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp			
450	455	460	
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr			
465	470	475	480
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly			
485	490	495	
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val			
500	505	510	
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys			
515	520	525	
Thr Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr			
530	535	540	
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn			
545	550	555	560
His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys			
565	570	575	

193/518

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr

580

585

590

His Gly Met Asp Glu Leu Tyr Asn

595

600

<210> 80

<211> 672

<212> PRT

<213> Human

<400> 80

Met Glu Asp Leu Phe Ser Pro Ser Ile Leu Pro Pro Ala Pro Asn Ile

5

10

15

Ser Val Pro Ile Leu Leu Gly Trp Gly Leu Asn Leu Thr Leu Gly Gln

20

25

30

Gly Ala Pro Ala Ser Gly Pro Pro Ser Arg Arg Val Arg Leu Val Phe

35

40

45

Leu Gly Val Ile Leu Val Val Ala Val Ala Gly Asn Thr Thr Val Leu

50

55

60

Cys Arg Leu Cys Gly Gly Gly Gly Pro Trp Ala Gly Pro Lys Arg Arg

65

70

75

80

Lys Met Asp Phe Leu Leu Val Gln Leu Ala Leu Ala Asp Leu Tyr Ala

85

90

95

Cys Gly Gly Thr Ala Leu Ser Gln Leu Ala Trp Glu Leu Leu Gly Glu

100

105

110

Pro Arg Ala Ala Thr Gly Asp Leu Ala Cys Arg Phe Leu Gln Leu Leu

115

120

125

Gln Ala Ser Gly Arg Gly Ala Ser Ala His Leu Val Val Leu Ile Ala

130

135

140

194/518

Leu Glu Arg Arg Arg Ala Val Arg Leu Pro His Gly Arg Pro Leu Pro
 145 150 155 160
 Ala Arg Ala Leu Ala Ala Leu Gly Trp Leu Leu Ala Leu Leu Ala
 165 170 175
 Leu Pro Pro Ala Phe Val Val Arg Gly Asp Ser Pro Ser Pro Leu Pro
 180 185 190
 Pro Pro Pro Pro Pro Thr Ser Leu Gln Pro Gly Ala Pro Pro Ala Ala
 195 200 205
 Arg Ala Trp Pro Gly Gln Arg Arg Cys His Gly Ile Phe Ala Pro Leu
 210 215 220
 Pro Arg Trp His Leu Gln Val Tyr Ala Phe Tyr Glu Ala Val Ala Gly
 225 230 235 240
 Phe Val Ala Pro Val Thr Val Leu Gly Val Ala Cys Gly His Leu Leu
 245 250 255
 Ser Val Trp Trp Arg His Arg Pro Gln Ala Pro Ala Ala Ala Ala Pro
 260 265 270
 Trp Ser Ala Ser Pro Gly Arg Ala Pro Ala Pro Ser Ala Leu Pro Arg
 275 280 285
 Ala Lys Val Gln Ser Leu Lys Met Ser Leu Leu Leu Ala Leu Leu Phe
 290 295 300
 Val Gly Cys Glu Leu Pro Tyr Phe Ala Ala Arg Leu Ala Ala Ala Trp
 305 310 315 320
 Ser Ser Gly Pro Ala Gly Asp Trp Glu Gly Glu Gly Leu Ser Ala Ala
 325 330 335
 Leu Arg Val Val Ala Met Ala Asn Ser Ala Leu Asn Pro Phe Val Tyr
 340 345 350
 Leu Phe Phe Gln Ala Gly Asp Cys Arg Leu Arg Arg Gln Leu Arg Lys
 355 360 365
 Arg Leu Gly Ser Leu Cys Cys Ala Pro Gln Gly Gly Ala Glu Asp Glu

195/518

370	375	380	
Glu Gly Pro Arg Gly His Gln Ala Leu Tyr Arg Gln Arg Trp Pro His			
385	390	395	400
Pro His Tyr His His Ala Arg Arg Glu Pro Leu Asp Glu Gly Gly Leu			
405	410	415	
Arg Pro Pro Pro Pro Arg Pro Arg Pro Leu Pro Cys Ser Cys Glu Ser			
420	425	430	
Ala Phe Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile			
435	440	445	
Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser			
450	455	460	
Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe			
465	470	475	480
Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr			
485	490	495	
Thr Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met			
500	505	510	
Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln			
515	520	525	
Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala			
530	535	540	
Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys			
545	550	555	560
Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu			
565	570	575	
Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys			
580	585	590	
Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly			
595	600	605	

196/518

Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
610 615 620
Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala
625 630 635 640
Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
645 650 655
Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn
660 665 670

<210> 81

<211> 542

<212> PRT

<213> Human

<400> 81

Met Leu Ser Thr Gly Val Val Ser Phe Phe Ser Leu Lys Ser Asp Ser
5 10 15
Ala Pro Pro Trp Met Val Leu Ala Val Leu Trp Cys Ser Met Ala Gln
20 25 30
Thr Leu Leu Leu Pro Ser Phe Ile Trp Ser Cys Glu Arg Tyr Arg Ala
35 40 45
Asp Val Arg Thr Val Trp Glu Gln Cys Val Ala Ile Met Ser Glu Glu
50 55 60
Asp Gly Asp Asp Asp Gly Gly Cys Asp Asp Tyr Ala Glu Gly Arg Val
65 70 75 80
Cys Lys Val Arg Phe Asp Ala Asn Gly Ala Thr Gly Pro Gly Ser Arg
85 90 95
Asp Pro Ala Gln Val Lys Leu Leu Pro Gly Arg His Met Leu Phe Pro
100 105 110

197/518

Pro Leu Glu Arg Val His Tyr Leu Gln Val Pro Leu Ser Arg Arg Leu
 115 120 125
 Ser His Asp Glu Thr Asn Ile Phe Ser Thr Pro Arg Glu Pro Gly Ser
 130 135 140
 Phe Leu His Lys Trp Ser Ser Ser Asp Asp Ile Arg Val Leu Pro Ala
 145 150 155 160
 Gln Ser Arg Ala Leu Gly Gly Pro Pro Glu Tyr Leu Gly Gln Arg His
 165 170 175
 Arg Leu Glu Asp Glu Glu Asp Glu Glu Glu Ala Glu Gly Gly Gly Leu
 180 185 190
 Ala Ser Leu Arg Gln Phe Leu Glu Ser Gly Val Leu Gly Ser Gly Gly
 195 200 205
 Gly Pro Pro Arg Gly Pro Gly Phe Phe Arg Glu Glu Ile Thr Thr Phe
 210 215 220
 Ile Asp Glu Thr Pro Leu Pro Ser Pro Thr Ala Ser Pro Gly His Ser
 225 230 235 240
 Pro Arg Arg Pro Arg Pro Leu Gly Leu Ser Pro Arg Arg Leu Ser Leu
 245 250 255
 Gly Ser Pro Glu Ser Arg Ala Val Gly Leu Pro Leu Gly Leu Ser Ala
 260 265 270
 Gly Arg Arg Cys Ser Leu Thr Gly Gly Glu Glu Ser Ala Arg Ala Trp
 275 280 285
 Gly Gly Ser Trp Gly Pro Gly Asn Pro Ile Phe Pro Gln Leu Thr Leu
 290 295 300
 Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 305 310 315 320
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 325 330 335
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys

198/518

340	345	350
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu		
355	360	365
Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg		
370	375	380
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg		
385	390	395
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val		
405	410	415
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile		
420	425	430
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn		
435	440	445
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly		
450	455	460
Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser Val		
465	470	475
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro		
485	490	495
Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser		
500	505	510
Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val		
515	520	525
Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn		
530	535	540

<210> 82

<211> 571

<212> PRT

199/518

<213> Human

<400> 82

```

Met Pro Ala Asn Tyr Thr Cys Thr Arg Pro Asp Gly Asp Asn Thr Asp
      5              10              15
Phe Arg Tyr Phe Ile Tyr Ala Val Thr Tyr Thr Val Ile Leu Val Pro
      20              25              30
Gly Leu Ile Gly Asn Ile Leu Ala Leu Trp Val Phe Tyr Gly Tyr Met
      35              40              45
Lys Glu Thr Lys Arg Ala Val Ile Phe Met Ile Asn Leu Ala Ile Ala
      50              55              60
Asp Leu Leu Gln Val Leu Ser Leu Pro Leu Arg Ile Phe Tyr Tyr Leu
      65              70              75              80
Asn His Asp Trp Pro Phe Gly Pro Gly Leu Cys Met Phe Cys Phe Tyr
      85              90              95
Leu Lys Tyr Val Asn Met Tyr Ala Ser Ile Tyr Phe Leu Val Cys Ile
      100             105             110
Ser Val Arg Arg Phe Trp Phe Leu Met Tyr Pro Phe Arg Phe His Asp
      115             120             125
Cys Lys Gln Lys Tyr Asp Leu Tyr Ile Ser Ile Ala Gly Trp Leu Ile
      130             135             140
Ile Cys Leu Ala Cys Val Leu Phe Pro Leu Leu Arg Thr Ser Asp Asp
      145             150             155             160
Thr Ser Gly Asn Arg Thr Lys Cys Phe Val Asp Leu Pro Thr Arg Asn
      165             170             175
Val Asn Leu Ala Gln Ser Val Val Met Met Thr Ile Gly Glu Leu Ile
      180             185             190
Gly Phe Val Thr Pro Leu Leu Ile Val Leu Tyr Cys Thr Trp Lys Thr
      195             200             205

```

200/518

Val Leu Ser Leu Gln Asp Lys Tyr Pro Met Ala Gln Asp Leu Gly Glu
 210 215 220
 Lys Gln Lys Ala Leu Lys Met Ile Leu Thr Cys Ala Gly Val Phe Leu
 225 230 235 240
 Ile Cys Phe Ala Pro Tyr His Phe Ser Phe Pro Leu Asp Phe Leu Val
 245 250 255
 Lys Ser Asn Glu Ile Lys Ser Cys Leu Ala Arg Arg Val Ile Leu Ile
 260 265 270
 Phe His Ser Val Ala Leu Cys Leu Ala Ser Leu Asn Ser Cys Leu Asp
 275 280 285
 Pro Val Ile Tyr Tyr Phe Ser Thr Asn Glu Phe Arg Arg Arg Leu Ser
 290 295 300
 Arg Gln Asp Leu His Asp Ser Ile Gln Leu His Ala Lys Ser Phe Val
 305 310 315 320
 Ser Asn His Thr Ala Ser Thr Met Thr Pro Glu Leu Cys Ala Ser Lys
 325 330 335
 Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp
 340 345 350
 Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly
 355 360 365
 Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly
 370 375 380
 Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Cys Tyr Gly
 385 390 395 400
 Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg His Asp Phe
 405 410 415
 Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe
 420 425 430
 Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu

201/518

435	440	445	
Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys			
450	455	460	
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser			
465	470	475	480
His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val			
485	490	495	
Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala			
500	505	510	
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu			
515	520	525	
Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro			
530	535	540	
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala			
545	550	555	560
Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn			
565	570		

<210> 83

<211> 577

<212> PRT

<213> Human

<400> 83

Met Asn Gly Leu Glu Val Ala Pro Pro Gly Leu Ile Thr Asn Phe Ser
5 10 15
Leu Ala Thr Ala Glu Gln Cys Gly Gln Glu Thr Pro Leu Glu Asn Met
20 25 30
Leu Phe Ala Ser Phe Tyr Leu Leu Asp Phe Ile Leu Ala Leu Val Gly

202/518

35	40	45
Asn Thr Leu Ala Leu Trp Leu Phe Ile Arg Asp His Lys Ser Gly Thr		
50	55	60
Pro Ala Asn Val Phe Leu Met His Leu Ala Val Ala Asp Leu Ser Cys		
65	70	75
Val Leu Val Leu Pro Thr Arg Leu Val Tyr His Phe Ser Gly Asn His		
85	90	95
Trp Pro Phe Gly Glu Ile Ala Cys Arg Leu Thr Gly Phe Leu Phe Tyr		
100	105	110
Leu Asn Met Tyr Ala Ser Ile Tyr Phe Leu Thr Cys Ile Ser Ala Asp		
115	120	125
Arg Phe Leu Ala Ile Val His Pro Val Lys Ser Leu Lys Leu Arg Arg		
130	135	140
Pro Leu Tyr Ala His Leu Ala Cys Ala Phe Leu Trp Val Val Val Ala		
145	150	155
Val Ala Met Ala Pro Leu Leu Val Ser Pro Gln Thr Val Gln Thr Asn		
165	170	175
His Thr Val Val Cys Leu Gln Leu Tyr Arg Glu Lys Ala Ser His His		
180	185	190
Ala Leu Val Ser Leu Ala Val Ala Phe Thr Phe Pro Phe Ile Thr Thr		
195	200	205
Val Thr Cys Tyr Leu Leu Ile Ile Arg Ser Leu Arg Gln Gly Leu Arg		
210	215	220
Val Glu Lys Arg Leu Lys Thr Lys Ala Val Arg Met Ile Ala Ile Val		
225	230	235
Leu Ala Ile Phe Leu Val Cys Phe Val Pro Tyr His Val Asn Arg Ser		
245	250	255
Val Tyr Val Leu His Tyr Arg Ser His Gly Ala Ser Cys Ala Thr Gln		
260	265	270

203/518

Arg Ile Leu Ala Leu Ala Asn Arg Ile Thr Ser Cys Leu Thr Ser Leu
 275 280 285
 Asn Gly Ala Leu Asp Pro Ile Met Tyr Phe Phe Val Ala Glu Lys Phe
 290 295 300
 Arg His Ala Leu Cys Asn Leu Leu Cys Gly Lys Arg Leu Lys Gly Pro
 305 310 315 320
 Pro Pro Ser Phe Glu Gly Lys Thr Asn Glu Ser Ser Leu Ser Ala Lys
 325 330 335
 Ser Glu Leu Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro
 340 345 350
 Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val
 355 360 365
 Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys
 370 375 380
 Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val
 385 390 395 400
 Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His
 405 410 415
 Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val
 420 425 430
 Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg
 435 440 445
 Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu
 450 455 460
 Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu
 465 470 475 480
 Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
 485 490 495
 Lys Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp

204/518

500	505	510
Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly		
515	520	525
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser		
530	535	540
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu		
545	550	555
Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr		
565	570	575

Asn

<210> 84

<211> 547

<212> PRT

<213> Human

<400> 84

Met Asn Gly Thr Tyr Asn Thr Cys Gly Ser Ser Asp Leu Thr Trp Pro		
5	10	15
Pro Ala Ile Lys Leu Gly Phe Tyr Ala Tyr Leu Gly Val Leu Leu Val		
20	25	30
Leu Gly Leu Leu Leu Asn Ser Leu Ala Leu Trp Val Phe Cys Cys Arg		
35	40	45
Met Gln Gln Trp Thr Glu Thr Arg Ile Tyr Met Thr Asn Leu Ala Val		
50	55	60
Ala Asp Leu Cys Leu Leu Cys Thr Leu Pro Phe Val Leu His Ser Leu		
65	70	75
Arg Asp Thr Ser Asp Thr Pro Leu Cys Gln Leu Ser Gln Gly Ile Tyr		
85	90	95

205/518

Leu Thr Asn Arg Tyr Met Ser Ile Ser Leu Val Thr Ala Ile Ala Val
100 105 110
Asp Arg Tyr Val Ala Val Arg His Pro Leu Arg Ala Arg Gly Leu Arg
115 120 125
Ser Pro Arg Gln Ala Ala Ala Val Cys Ala Val Leu Trp Val Leu Val
130 135 140
Ile Gly Ser Leu Val Ala Arg Trp Leu Leu Gly Ile Gln Glu Gly Gly
145 150 155 160
Phe Cys Phe Arg Ser Thr Arg His Asn Phe Asn Ser Met Ala Phe Pro
165 170 175
Leu Leu Gly Phe Tyr Leu Pro Leu Ala Val Val Val Phe Cys Ser Leu
180 185 190
Lys Val Val Thr Ala Leu Ala Gln Arg Pro Pro Thr Asp Val Gly Gln
195 200 205
Ala Glu Ala Thr Arg Lys Ala Ala Arg Met Val Trp Ala Asn Leu Leu
210 215 220
Val Phe Val Val Cys Phe Leu Pro Leu His Val Gly Leu Thr Val Arg
225 230 235 240
Leu Ala Val Gly Trp Asn Ala Cys Ala Leu Leu Glu Thr Ile Arg Arg
245 250 255
Ala Leu Tyr Ile Thr Ser Lys Leu Ser Asp Ala Asn Cys Cys Leu Asp
260 265 270
Ala Ile Cys Tyr Tyr Tyr Met Ala Lys Glu Phe Gln Glu Ala Ser Ala
275 280 285
Leu Ala Val Ala Pro Arg Ala Lys Ala His Lys Ser Gln Asp Ser Leu
290 295 300
Cys Val Thr Leu Ala Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
305 310 315 320
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe

206/518

	325		330		335
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr					
	340		345		350
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr					
	355		360		365
Leu Val Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro					
	370		375		380
Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly					
385		390		395	400
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys					
	405		410		415
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile					
	420		425		430
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His					
	435		440		445
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp					
	450		455		460
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile					
465		470		475	480
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro					
	485		490		495
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr					
	500		505		510
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val					
	515		520		525
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu					
	530		535		540
Leu Tyr Asn					
545					

207/518

<210> 85

<211> 679

<212> PRT

<213> Human

<400> 85

Met Ala Ile His Lys Ala Leu Val Met Cys Leu Gly Leu Pro Leu Phe
5 10 15
Leu Phe Pro Gly Ala Trp Ala Gln Gly His Val Pro Pro Gly Cys Ser
20 25 30
Gln Gly Leu Asn Pro Leu Tyr Tyr Asn Leu Cys Asp Arg Ser Gly Ala
35 40 45
Trp Gly Ile Val Leu Glu Ala Val Ala Gly Ala Gly Ile Val Thr Thr
50 55 60
Phe Val Leu Thr Ile Ile Leu Val Ala Ser Leu Pro Phe Val Gln Asp
65 70 75 80
Thr Lys Lys Arg Ser Leu Leu Gly Thr Gln Val Phe Phe Leu Leu Gly
85 90 95
Thr Leu Gly Leu Phe Cys Leu Val Phe Ala Cys Val Val Lys Pro Asp
100 105 110
Phe Ser Thr Cys Ala Ser Arg Arg Phe Leu Phe Gly Val Leu Phe Ala
115 120 125
Ile Cys Phe Ser Cys Leu Ala Ala His Val Phe Ala Leu Asn Phe Leu
130 135 140
Ala Arg Lys Asn His Gly Pro Arg Gly Trp Val Ile Phe Thr Val Ala
145 150 155 160
Leu Leu Leu Thr Leu Val Glu Val Ile Ile Asn Thr Glu Trp Leu Ile
165 170 175

208/518

Ile Thr Leu Val Arg Gly Ser Gly Glu Gly Gly Pro Gln Gly Asn Ser
 180 185 190
 Ser Ala Gly Trp Ala Val Ala Ser Pro Cys Ala Ile Ala Asn Met Asp
 195 200 205
 Phe Val Met Ala Leu Ile Tyr Val Met Leu Leu Leu Leu Gly Ala Phe
 210 215 220
 Leu Gly Ala Trp Pro Ala Leu Cys Gly Arg Tyr Lys Arg Trp Arg Lys
 225 230 235 240
 His Gly Val Phe Val Leu Leu Thr Thr Ala Thr Ser Val Ala Ile Trp
 245 250 255
 Val Val Trp Ile Val Met Tyr Thr Tyr Gly Asn Lys Gln His Asn Ser
 260 265 270
 Pro Thr Trp Asp Asp Pro Thr Leu Ala Ile Ala Leu Ala Ala Asn Ala
 275 280 285
 Trp Ala Phe Val Leu Phe Tyr Val Ile Pro Glu Val Ser Gln Val Thr
 290 295 300
 Lys Ser Ser Pro Glu Gln Ser Tyr Gln Gly Asp Met Tyr Pro Thr Arg
 305 310 315 320
 Gly Val Gly Tyr Glu Thr Ile Leu Lys Glu Gln Lys Gly Gln Ser Met
 325 330 335
 Phe Val Glu Asn Lys Ala Phe Ser Met Asp Glu Pro Val Ala Ala Lys
 340 345 350
 Arg Pro Val Ser Pro Tyr Ser Gly Tyr Asn Gly Gln Leu Leu Thr Ser
 355 360 365
 Val Tyr Gln Pro Thr Glu Met Ala Leu Met His Lys Val Pro Ser Glu
 370 375 380
 Gly Ala Tyr Asp Ile Ile Leu Pro Arg Ala Thr Ala Asn Ser Gln Val
 385 390 395 400
 Met Gly Ser Ala Asn Ser Thr Leu Arg Ala Glu Asp Met Tyr Ser Ala

209/518

405	410	415
Gln Ser His Gln Ala Ala Thr Pro Pro Lys Asp Gly Lys Asn Ser Gln		
420	425	430
Val Phe Arg Asn Pro Tyr Val Trp Asp Ala Ser Lys Gly Glu Glu Leu		
435	440	445
Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn		
450	455	460
Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr		
465	470	475
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val		
485	490	495
Pro Trp Pro Thr Leu Val Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe		
500	505	510
Ser Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala		
515	520	525
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp		
530	535	540
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu		
545	550	555
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn		
565	570	575
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr		
580	585	590
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr		
595	600	605
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln		
610	615	620
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His		
625	630	635
		640

210/518

Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
 645 650 655
 Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His
 660 665 670
 Gly Met Asp Glu Leu Tyr Asn
 675

<210> 86

<211> 625

<212> PRT

<213> Human

<400> 86

Met Asn Arg His His Leu Gln Asp His Phe Leu Glu Ile Asp Lys Lys
 5 10 15
 Asn Cys Cys Val Phe Arg Asp Asp Phe Ile Ala Lys Val Leu Pro Pro
 20 25 30
 Val Leu Gly Leu Glu Phe Ile Phe Gly Leu Leu Gly Asn Gly Leu Ala
 35 40 45
 Leu Trp Ile Phe Cys Phe His Leu Lys Ser Trp Lys Ser Ser Arg Ile
 50 55 60
 Phe Leu Phe Asn Leu Ala Val Ala Asp Phe Leu Leu Ile Ile Cys Leu
 65 70 75 80
 Pro Phe Val Met Asp Tyr Tyr Val Arg Arg Ser Asp Trp Lys Phe Gly
 85 90 95
 Asp Ile Pro Cys Arg Leu Val Leu Phe Met Phe Ala Met Asn Arg Gln
 100 105 110
 Gly Ser Ile Ile Phe Leu Thr Val Val Ala Val Asp Arg Tyr Phe Arg
 115 120 125

211/518

Val Val His Pro His His Ala Leu Asn Lys Ile Ser Asn Trp Thr Ala

130

135

140

Ala Ile Ile Ser Cys Leu Leu Trp Gly Ile Thr Val Gly Leu Thr Val

145

150

155

160

His Leu Leu Lys Lys Lys Leu Leu Ile Gln Asn Gly Pro Ala Asn Val

165

170

175

Cys Ile Ser Phe Ser Ile Cys His Thr Phe Arg Trp His Glu Ala Met

180

185

190

Phe Leu Leu Glu Phe Leu Leu Pro Leu Gly Ile Ile Leu Phe Cys Ser

195

200

205

Ala Arg Ile Ile Trp Ser Leu Arg Gln Arg Gln Met Asp Arg His Ala

210

215

220

Lys Ile Lys Arg Ala Ile Thr Phe Ile Met Val Val Ala Ile Val Phe

225

230

235

240

Val Ile Cys Phe Leu Pro Ser Val Val Val Arg Ile Arg Ile Phe Trp

245

250

255

Leu Leu His Thr Ser Gly Thr Gln Asn Cys Glu Val Tyr Arg Ser Val

260

265

270

Asp Leu Ala Phe Phe Ile Thr Leu Ser Phe Thr Tyr Met Asn Ser Met

275

280

285

Leu Asp Pro Val Val Tyr Tyr Phe Ser Ser Pro Ser Phe Pro Asn Phe

290

295

300

Phe Ser Thr Leu Ile Asn Arg Cys Leu Gln Arg Lys Met Thr Gly Glu

305

310

315

320

Pro Asp Asn Asn Arg Ser Thr Ser Val Glu Leu Thr Gly Asp Pro Asn

325

330

335

Lys Thr Arg Gly Ala Pro Glu Ala Leu Met Ala Asn Ser Gly Glu Pro

340

345

350

Trp Ser Pro Ser Tyr Leu Gly Pro Thr Ser Asn Asn His Ser Lys Lys

212/518

355	360	365
Gly His Cys His Gln Glu Pro Ala Ser Leu Glu Lys Gln Leu Gly Cys		
370	375	380
Cys Ile Glu Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro		
385	390	395
Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val		
405	410	415
Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys		
420	425	430
Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val		
435	440	445
Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His		
450	455	460
Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val		
465	470	475
Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg		
485	490	495
Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu		
500	505	510
Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu		
515	520	525
Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln		
530	535	540
Lys Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp		
545	550	555
Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly		
565	570	575
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser		
580	585	590

213/518

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu

595

600

605

Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr

610

615

620

Asn

625

<210> 87

<211> 778

<212> PRT

<213> Human

<400> 87

Met Asn Ser Thr Gly His Leu Gln Asp Ala Pro Asn Ala Thr Ser Leu

5

10

15

His Val Pro His Ser Gln Glu Gly Asn Ser Thr Ser Leu Gln Glu Gly

20

25

30

Leu Gln Asp Leu Ile His Thr Ala Thr Leu Val Thr Cys Thr Phe Leu

35

40

45

Leu Ala Val Ile Phe Cys Leu Gly Ser Tyr Gly Asn Phe Ile Val Phe

50

55

60

Leu Ser Phe Phe Asp Pro Ala Phe Arg Lys Phe Arg Thr Asn Phe Asp

65

70

75

80

Phe Met Ile Leu Asn Leu Ser Phe Cys Asp Leu Phe Ile Cys Gly Val

85

90

95

Thr Ala Pro Met Phe Thr Phe Val Leu Phe Phe Ser Ser Ala Ser Ser

100

105

110

Ile Pro Asp Ala Phe Cys Phe Thr Phe His Leu Thr Ser Ser Gly Phe

115

120

125

214/518

Ile Ile Met Ser Leu Lys Thr Val Ala Val Ile Ala Leu His Arg Leu
 130 135 140
 Arg Met Val Leu Gly Lys Gln Pro Asn Arg Thr Ala Ser Phe Pro Cys
 145 150 155 160
 Thr Val Leu Leu Thr Leu Leu Leu Trp Ala Thr Ser Phe Thr Leu Ala
 165 170 175
 Thr Leu Ala Thr Leu Lys Thr Ser Lys Ser His Leu Cys Leu Pro Met
 180 185 190
 Ser Ser Leu Ile Ala Gly Lys Gly Lys Ala Ile Leu Ser Leu Tyr Val
 195 200 205
 Val Asp Phe Thr Phe Cys Val Ala Val Val Ser Val Ser Tyr Ile Met
 210 215 220
 Ile Ala Gln Thr Leu Arg Lys Asn Ala Gln Val Arg Lys Cys Pro Pro
 225 230 235 240
 Val Ile Thr Val Asp Ala Ser Arg Pro Gln Pro Phe Met Gly Val Pro
 245 250 255
 Val Gln Gly Gly Gly Asp Pro Ile Gln Cys Ala Met Pro Ala Leu Tyr
 260 265 270
 Arg Asn Gln Asn Tyr Asn Lys Leu Gln His Val Gln Thr Arg Gly Tyr
 275 280 285
 Thr Lys Ser Pro Asn Gln Leu Val Thr Pro Ala Ala Ser Arg Leu Gln
 290 295 300
 Leu Val Ser Ala Ile Asn Leu Ser Thr Ala Lys Asp Ser Lys Ala Val
 305 310 315 320
 Val Thr Cys Val Ile Ile Val Leu Ser Val Leu Val Cys Cys Leu Pro
 325 330 335
 Leu Gly Ile Ser Leu Val Gln Val Val Leu Ser Ser Asn Gly Ser Phe
 340 345 350
 Ile Leu Tyr Gln Phe Glu Leu Phe Gly Phe Thr Leu Ile Phe Phe Lys

215/518

355	360	365
Ser Gly Leu Asn Pro Phe Ile Tyr Ser Arg Asn Ser Ala Gly Leu Arg		
370	375	380
Arg Lys Val Leu Trp Cys Leu Gln Tyr Ile Gly Leu Gly Phe Phe Cys		
385	390	395
Cys Lys Gln Lys Thr Arg Leu Arg Ala Met Gly Lys Gly Asn Leu Glu		
405	410	415
Val Asn Arg Asn Lys Ser Ser His His Glu Thr Asn Ser Ala Tyr Met		
420	425	430
Leu Ser Pro Lys Pro Gln Lys Lys Phe Val Asp Gln Ala Cys Gly Pro		
435	440	445
Ser His Ser Lys Glu Ser Met Val Ser Pro Lys Ile Ser Ala Gly His		
450	455	460
Gln His Cys Gly Gln Ser Ser Ser Thr Pro Ile Asn Thr Arg Ile Glu		
465	470	475
Pro Tyr Tyr Ser Ile Tyr Asn Ser Ser Pro Ser Gln Glu Glu Ser Ser		
485	490	495
Pro Cys Asn Leu Gln Pro Val Asn Ser Phe Gly Phe Ala Asn Ser Tyr		
500	505	510
Ile Ala Met His Tyr His Thr Thr Asn Asp Leu Val Gln Glu Tyr Asp		
515	520	525
Ser Thr Ser Ala Lys Gln Ile Pro Val Pro Ser Val Ala Ser Lys Gly		
530	535	540
Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly		
545	550	555
Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp		
565	570	575
Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys		
580	585	590

216/518

Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Cys Tyr Gly Val
 595 600 605
 Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe
 610 615 620
 Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe
 625 630 635 640
 Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly
 645 650 655
 Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
 660 665 670
 Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His
 675 680 685
 Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn
 690 695 700
 Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp
 705 710 715 720
 His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro
 725 730 735
 Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn
 740 745 750
 Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly
 755 760 765
 Ile Thr His Gly Met Asp Glu Leu Tyr Asn
 770 775

<210> 88

<211> 584

<212> PRT

<213> Human

217/518

<400> 88

Met Tyr Asn Gly Ser Cys Cys Arg Ile Glu Gly Asp Thr Ile Ser Gln
 5 10 15
 Val Met Pro Pro Leu Leu Ile Val Ala Phe Val Leu Gly Ala Leu Gly
 20 25 30
 Asn Gly Val Ala Leu Cys Gly Phe Cys Phe His Met Lys Thr Trp Lys
 35 40 45
 Pro Ser Thr Val Tyr Leu Phe Asn Leu Ala Val Ala Asp Phe Leu Leu
 50 55 60
 Met Ile Cys Leu Pro Phe Arg Thr Asp Tyr Tyr Leu Arg Arg Arg His
 65 70 75 80
 Trp Ala Phe Gly Asp Ile Pro Cys Arg Val Gly Leu Phe Thr Leu Ala
 85 90 95
 Met Asn Arg Ala Gly Ser Ile Val Phe Leu Thr Val Val Ala Ala Asp
 100 105 110
 Arg Tyr Phe Lys Val Val His Pro His His Ala Val Asn Thr Ile Ser
 115 120 125
 Thr Arg Val Ala Ala Gly Ile Val Cys Thr Leu Trp Ala Leu Val Ile
 130 135 140
 Leu Gly Thr Val Tyr Leu Leu Leu Glu Asn His Leu Cys Val Gln Glu
 145 150 155 160
 Thr Ala Val Ser Cys Glu Ser Phe Ile Met Glu Ser Ala Asn Gly Trp
 165 170 175
 His Asp Ile Met Phe Gln Leu Glu Phe Phe Met Pro Leu Gly Ile Ile
 180 185 190
 Leu Phe Cys Ser Phe Lys Ile Val Trp Ser Leu Arg Arg Arg Gln Gln
 195 200 205
 Leu Ala Arg Gln Ala Arg Met Lys Lys Ala Thr Arg Phe Ile Met Val

218/518

210	215	220
Val Ala Ile Val Phe Ile Thr Cys Tyr Leu Pro Ser Val Ser Ala Arg		
225	230	235
Leu Tyr Phe Leu Trp Thr Val Pro Ser Ser Ala Cys Asp Pro Ser Val		
245	250	255
His Gly Ala Leu His Ile Thr Leu Ser Phe Thr Tyr Met Asn Ser Met		
260	265	270
Leu Asp Pro Leu Val Tyr Tyr Phe Ser Ser Pro Ser Phe Pro Lys Phe		
275	280	285
Tyr Asn Lys Leu Lys Ile Cys Ser Leu Lys Pro Lys Gln Pro Gly His		
290	295	300
Ser Lys Thr Gln Arg Pro Glu Glu Met Pro Ile Ser Asn Leu Gly Arg		
305	310	315
Arg Ser Cys Ile Ser Val Ala Asn Ser Phe Gln Ser Gln Ser Asp Gly		
325	330	335
Gln Trp Asp Pro His Ile Val Glu Trp His Ala Ser Lys Gly Glu Glu		
340	345	350
Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val		
355	360	365
Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr		
370	375	380
Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro		
385	390	395
Val Pro Trp Pro Thr Leu Val Thr Thr Leu Cys Tyr Gly Val Gln Cys		
405	410	415
Phe Ser Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser		
420	425	430
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp		
435	440	445

219/518

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
 450 455 460
 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
 465 470 475 480
 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
 485 490 495
 Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
 500 505 510
 Thr Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
 515 520 525
 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
 530 535 540
 His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
 545 550 555 560
 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
 565 570 575
 His Gly Met Asp Glu Leu Tyr Asn
 580

<210> 89

<211> 585

<212> PRT

<213> Human

<400> 89

Met Gly Asp Glu Leu Ala Pro Cys Pro Val Gly Thr Thr Ala Trp Pro
 5 10 15
 Ala Leu Ile Gln Leu Ile Ser Lys Thr Pro Cys Met Pro Gln Ala Ala
 20 25 30

220/518

Ser Asn Thr Ser Leu Gly Leu Gly Asp Leu Arg Val Pro Ser Ser Met
 35 40 45
 Leu Tyr Trp Leu Phe Leu Pro Ser Ser Leu Leu Ala Ala Ala Thr Leu
 50 55 60
 Ala Val Ser Pro Leu Leu Leu Val Thr Ile Leu Arg Asn Gln Arg Leu
 65 70 75 80
 Arg Gln Glu Pro His Tyr Leu Leu Pro Ala Asn Ile Leu Leu Ser Asp
 85 90 95
 Leu Ala Tyr Ile Leu Leu His Met Leu Ile Ser Ser Ser Ser Leu Gly
 100 105 110
 Gly Trp Glu Leu Gly Arg Met Ala Cys Gly Ile Leu Thr Asp Ala Val
 115 120 125
 Phe Ala Ala Cys Thr Ser Thr Ile Leu Ser Phe Thr Ala Ile Val Leu
 130 135 140
 His Thr Tyr Leu Ala Val Ile His Pro Leu Arg Tyr Leu Ser Phe Met
 145 150 155 160
 Ser His Gly Ala Ala Trp Lys Ala Val Ala Leu Ile Trp Leu Val Ala
 165 170 175
 Cys Cys Phe Pro Thr Phe Leu Ile Trp Leu Ser Lys Trp Gln Asp Ala
 180 185 190
 Gln Leu Glu Glu Gln Gly Ala Ser Tyr Ile Leu Pro Pro Ser Met Gly
 195 200 205
 Thr Gln Pro Gly Cys Gly Leu Leu Val Ile Val Thr Tyr Thr Ser Ile
 210 215 220
 Leu Cys Val Leu Phe Leu Cys Thr Ala Leu Ile Ala Asn Cys Phe Trp
 225 230 235 240
 Arg Ile Tyr Ala Glu Ala Lys Thr Ser Gly Ile Trp Gly Gln Gly Tyr
 245 250 255
 Ser Arg Ala Arg Gly Thr Leu Leu Ile His Ser Val Leu Ile Thr Leu

221/518

260	265	270
Tyr Val Ser Thr Gly Val Val Phe Ser Leu Asp Met Val Leu Thr Arg		
275	280	285
Tyr His His Ile Asp Ser Gly Thr His Thr Trp Leu Leu Ala Ala Asn		
290	295	300
Ser Glu Val Leu Met Met Leu Pro Arg Ala Met Leu Pro Tyr Leu Tyr		
305	310	315
Leu Leu Arg Tyr Arg Gln Leu Leu Gly Met Val Arg Gly His Leu Pro		
325	330	335
Ser Arg Arg His Gln Ala Ile Phe Thr Ile Ser Ala Ser Lys Gly Glu		
340	345	350
Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp		
355	360	365
Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala		
370	375	380
Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu		
385	390	395
Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Cys Tyr Gly Val Gln		
405	410	415
Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys		
420	425	430
Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys		
435	440	445
Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp		
450	455	460
Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp		
465	470	475
Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn		
485	490	495

222/518

Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe

500

505

510

Lys Thr Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His

515

520

525

Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp

530

535

540

Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu

545

550

555

560

Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile

565

570

575

Thr His Gly Met Asp Glu Leu Tyr Asn

580

585

<210> 90

<211> 611

<212> PRT

<213> Human

<400> 90

Met Arg Met Glu Asp Glu Asp Tyr Asn Thr Ser Ile Ser Tyr Gly Asp

5

10

15

Glu Tyr Pro Asp Tyr Leu Asp Ser Ile Val Val Leu Glu Asp Leu Ser

20

25

30

Pro Leu Glu Ala Arg Val Thr Arg Ile Phe Leu Val Val Val Tyr Ser

35

40

45

Ile Val Cys Phe Leu Gly Ile Leu Gly Asn Gly Leu Val Ile Ile Ile

50

55

60

Ala Thr Phe Lys Met Lys Lys Thr Val Asn Met Val Trp Phe Leu Asn

65

70

75

80

223/518

Leu Ala Val Ala Asp Phe Leu Phe Asn Val Phe Leu Pro Ile His Ile
 85 90 95
 Thr Tyr Ala Ala Met Asp Tyr His Trp Val Phe Gly Thr Ala Met Cys
 100 105 110
 Lys Ile Ser Asn Phe Leu Leu Ile His Asn Met Phe Thr Ser Val Phe
 115 120 125
 Leu Leu Thr Ile Ile Ser Ser Asp Arg Cys Ile Ser Val Leu Leu Pro
 130 135 140
 Val Trp Ser Gln Asn His Arg Ser Val Arg Leu Ala Tyr Met Ala Cys
 145 150 155 160
 Met Val Ile Trp Val Leu Ala Phe Phe Leu Ser Ser Pro Ser Leu Val
 165 170 175
 Phe Arg Asp Thr Ala Asn Leu His Gly Lys Ile Ser Cys Phe Asn Asn
 180 185 190
 Phe Ser Leu Ser Thr Pro Gly Ser Ser Ser Trp Pro Thr His Ser Gln
 195 200 205
 Met Asp Pro Val Gly Tyr Ser Arg His Met Val Val Thr Val Thr Arg
 210 215 220
 Phe Leu Cys Gly Phe Leu Val Pro Val Leu Ile Ile Thr Ala Cys Tyr
 225 230 235 240
 Leu Thr Ile Val Cys Lys Leu Gln Arg Asn Arg Leu Ala Lys Thr Lys
 245 250 255
 Lys Pro Phe Lys Ile Ile Val Thr Ile Ile Ile Thr Phe Phe Leu Cys
 260 265 270
 Trp Cys Pro Tyr His Thr Leu Asn Leu Leu Glu Leu His His Thr Ala
 275 280 285
 Met Pro Gly Ser Val Phe Ser Leu Gly Leu Pro Leu Ala Thr Ala Leu
 290 295 300
 Ala Ile Ala Asn Ser Cys Met Asn Pro Ile Leu Tyr Val Phe Met Gly

224/518

305	310	315	320
Gln Asp Phe Lys Lys Phe Lys Val Ala Leu Phe Ser Arg Leu Val Asn			
325	330	335	
Ala Leu Ser Glu Asp Thr Gly His Ser Ser Tyr Pro Ser His Arg Ser			
340	345	350	
Phe Thr Lys Met Ser Ser Met Asn Glu Arg Thr Ser Met Asn Glu Arg			
355	360	365	
Glu Thr Gly Met Leu Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val			
370	375	380	
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe			
385	390	395	400
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr			
405	410	415	
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr			
420	425	430	
Leu Val Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro			
435	440	445	
Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly			
450	455	460	
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys			
465	470	475	480
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile			
485	490	495	
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His			
500	505	510	
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp			
515	520	525	
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile			
530	535	540	

225/518

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 545 550 555 560
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 565 570 575
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 580 585 590
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 595 600 605
 Leu Tyr Asn
 610

<210> 91

<211> 591

<212> PRT

<213> Rat

<400> 91

Met Glu Val Ser Arg Glu Met Leu Phe Glu Glu Leu Asp Asn Tyr Ser
 5 10 15
 Tyr Ala Leu Glu Tyr Tyr Ser Gln Glu Pro Asp Ala Glu Glu Asn Val
 20 25 30
 Tyr Pro Gly Ile Val His Trp Ile Ser Leu Leu Leu Tyr Ala Leu Ala
 35 40 45
 Phe Val Leu Gly Ile Pro Gly Asn Ala Ile Val Ile Trp Phe Met Gly
 50 55 60
 Phe Lys Trp Lys Lys Thr Val Thr Thr Leu Trp Phe Leu Asn Leu Ala
 65 70 75 80
 Ile Ala Asp Phe Val Phe Val Leu Phe Leu Pro Leu Tyr Ile Ser Tyr
 85 90 95

226/518

Val	Ala	Leu	Ser	Phe	His	Trp	Pro	Phe	Gly	Arg	Trp	Leu	Cys	Lys	Leu
		100						105					110		
Asn	Ser	Phe	Ile	Ala	Gln	Leu	Asn	Met	Phe	Ser	Ser	Val	Phe	Phe	Leu
		115					120					125			
Thr	Val	Ile	Ser	Leu	Asp	Arg	Tyr	Ile	His	Leu	Ile	His	Pro	Gly	Leu
	130					135					140				
Ser	His	Pro	His	Arg	Thr	Leu	Lys	Asn	Ser	Leu	Leu	Val	Val	Leu	Phe
145				150					155					160	
Val	Trp	Leu	Leu	Ala	Ser	Leu	Leu	Gly	Gly	Pro	Thr	Leu	Tyr	Phe	Arg
			165					170					175		
Asp	Thr	Val	Glu	Val	Asn	Asn	Arg	Ile	Ile	Cys	Tyr	Asn	Asn	Phe	Gln
		180					185					190			
Glu	Tyr	Glu	Leu	Thr	Leu	Met	Arg	His	His	Val	Leu	Thr	Trp	Val	Lys
	195					200						205			
Phe	Leu	Phe	Gly	Tyr	Leu	Leu	Pro	Leu	Leu	Thr	Met	Ser	Ser	Cys	Tyr
	210					215					220				
Leu	Cys	Leu	Ile	Phe	Lys	Thr	Lys	Lys	Gln	Asn	Ile	Leu	Ile	Ser	Ser
225				230					235					240	
Lys	His	Leu	Trp	Met	Ile	Leu	Ser	Val	Val	Ile	Ala	Phe	Met	Val	Cys
			245					250				255			
Trp	Thr	Pro	Phe	His	Leu	Phe	Ser	Ile	Trp	Glu	Leu	Ser	Ile	His	His
		260					265					270			
Asn	Ser	Ser	Phe	Gln	Asn	Val	Leu	Gln	Gly	Gly	Ile	Pro	Leu	Ser	Thr
		275					280				285				
Gly	Leu	Ala	Phe	Leu	Asn	Ser	Cys	Leu	Asn	Pro	Ile	Leu	Tyr	Val	Leu
	290					295				300					
Ile	Ser	Lys	Lys	Phe	Gln	Ala	Arg	Phe	Arg	Ala	Ser	Val	Ala	Glu	Val
305				310					315					320	
Leu	Lys	Arg	Ser	Leu	Trp	Glu	Ala	Ser	Cys	Ser	Gly	Thr	Val	Ser	Glu

227/518

325	330	335
Gln Leu Arg Ser Ala Glu Thr Lys Ser Leu Ser Leu Leu Glu Thr Ala		
340	345	350
Gln Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu		
355	360	365
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly		
370	375	380
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile		
385	390	395
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr		
405	410	415
Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys		
420	425	430
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu		
435	440	445
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu		
450	455	460
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly		
465	470	475
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr		
485	490	495
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn		
500	505	510
Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser		
515	520	525
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly		
530	535	540
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu		
545	550	555
		560

228/518

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe

565

570

575

Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn

580

585

590

<210> 92

<211> 568

<212> PRT

<213> Human

<400> 92

Met Met Trp Gly Ala Gly Ser Pro Leu Ala Trp Leu Ser Ala Gly Ser

5

10

15

Gly Asn Val Asn Val Ser Ser Val Gly Pro Ala Glu Gly Pro Thr Gly

20

25

30

Pro Ala Ala Pro Leu Pro Ser Pro Lys Ala Trp Asp Val Val Leu Cys

35

40

45

Ile Ser Gly Thr Leu Val Ser Cys Glu Asn Ala Leu Val Val Ala Ile

50

55

60

Ile Val Gly Thr Pro Ala Phe Arg Ala Pro Met Phe Leu Leu Val Gly

65

70

75

80

Ser Leu Ala Val Ala Asp Leu Leu Ala Gly Leu Gly Leu Val Leu His

85

90

95

Phe Ala Ala Val Phe Cys Ile Gly Ser Ala Glu Met Ser Leu Val Leu

100

105

110

Val Gly Val Leu Ala Met Ala Phe Thr Ala Ser Ile Gly Ser Leu Leu

115

120

125

Ala Ile Thr Val Asp Arg Tyr Leu Ser Leu Tyr Asn Ala Leu Thr Tyr

130

135

140

229/518

Tyr Ser Glu Thr Thr Val Thr Arg Thr Tyr Val Met Leu Ala Leu Val
 145 150 155 160
 Trp Gly Gly Ala Leu Gly Leu Gly Leu Leu Pro Val Leu Ala Trp Asn
 165 170 175
 Cys Leu Asp Gly Leu Thr Thr Cys Gly Val Val Tyr Pro Leu Ser Lys
 180 185 190
 Asn His Leu Val Val Leu Ala Ile Ala Phe Phe Met Val Phe Gly Ile
 195 200 205
 Met Leu Gln Leu Tyr Ala Gln Ile Cys Arg Ile Val Cys Arg His Ala
 210 215 220
 Gln Gln Ile Ala Leu Gln Arg His Leu Leu Pro Ala Ser His Tyr Val
 225 230 235 240
 Ala Thr Arg Lys Gly Ile Ala Thr Leu Ala Val Val Leu Gly Ala Phe
 245 250 255
 Ala Ala Cys Trp Leu Pro Phe Thr Val Tyr Cys Leu Leu Gly Asp Ala
 260 265 270
 His Ser Pro Pro Leu Tyr Thr Tyr Leu Thr Leu Leu Pro Ala Thr Tyr
 275 280 285
 Asn Ser Met Ile Asn Pro Ile Ile Tyr Ala Phe Arg Asn Gln Asp Val
 290 295 300
 Gln Lys Val Leu Trp Ala Val Cys Cys Cys Cys Ser Ser Ser Lys Ile
 305 310 315 320
 Pro Phe Arg Ser Arg Ser Pro Ser Asp Val Ala Ser Lys Gly Glu Glu
 325 330 335
 Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val
 340 345 350
 Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr
 355 360 365
 Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro

230/518

370 375 380
 Val Pro Trp Pro Thr Leu Val Thr Thr Leu Cys Tyr Gly Val Gln Cys
 385 390 395 400
 Phe Ser Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
 405 410 415
 Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
 420 425 430
 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
 435 440 445
 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
 450 455 460
 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
 465 470 475 480
 Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
 485 490 495
 Thr Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
 500 505 510
 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
 515 520 525
 His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
 530 535 540
 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
 545 550 555 560
 His Gly Met Asp Glu Leu Tyr Asn
 565

<210> 93

<211> 600

<212> PRT

231/518

<213> Human

<400> 93

Met Asn Ala Ser Ala Ala Ser Leu Asn Asp Ser Gln Val Val Val Val
5 10 15
Ala Ala Glu Gly Ala Ala Ala Ala Thr Ala Ala Gly Gly Pro Asp
20 25 30
Thr Gly Glu Trp Gly Pro Pro Ala Ala Ala Leu Gly Ala Gly Gly
35 40 45
Gly Ala Asn Gly Ser Leu Glu Leu Ser Ser Gln Leu Ser Ala Gly Pro
50 55 60
Pro Gly Leu Leu Leu Pro Ala Val Asn Pro Trp Asp Val Leu Leu Cys
65 70 75 80
Val Ser Gly Thr Val Ile Ala Gly Glu Asn Ala Leu Val Val Ala Leu
85 90 95
Ile Ala Ser Thr Pro Ala Leu Arg Thr Pro Met Phe Val Leu Val Gly
100 105 110
Ser Leu Ala Thr Ala Asp Leu Leu Ala Gly Cys Gly Leu Ile Leu His
115 120 125
Phe Val Phe Gln Tyr Leu Val Pro Ser Glu Thr Val Ser Leu Leu Thr
130 135 140
Val Gly Phe Leu Val Ala Ser Phe Ala Ala Ser Val Ser Ser Leu Leu
145 150 155 160
Ala Ile Thr Val Asp Arg Tyr Leu Ser Leu Tyr Asn Ala Leu Thr Tyr
165 170 175
Tyr Ser Arg Arg Thr Leu Leu Gly Val His Leu Leu Leu Ala Ala Thr
180 185 190
Trp Thr Val Ser Leu Gly Leu Gly Leu Leu Pro Val Leu Gly Trp Asn
195 200 205

232/518

Cys Leu Ala Glu Arg Ala Ala Cys Ser Val Val Arg Pro Leu Ala Arg
 210 215 220
 Ser His Val Ala Leu Leu Ser Ala Ala Phe Phe Met Val Phe Gly Ile
 225 230 235 240
 Met Leu His Leu Tyr Val Arg Ile Cys Gln Val Val Trp Arg His Ala
 245 250 255
 His Gln Ile Ala Leu Gln Gln His Cys Leu Ala Pro Pro His Leu Ala
 260 265 270
 Ala Thr Arg Lys Gly Val Gly Thr Leu Ala Val Val Leu Gly Thr Phe
 275 280 285
 Gly Ala Ser Trp Leu Pro Phe Ala Ile Tyr Cys Val Val Gly Ser His
 290 295 300
 Glu Asp Pro Ala Val Tyr Thr Tyr Ala Thr Leu Leu Pro Ala Thr Tyr
 305 310 315 320
 Asn Ser Met Ile Asn Pro Ile Ile Tyr Ala Phe Arg Asn Gln Glu Ile
 325 330 335
 Gln Arg Ala Leu Trp Leu Leu Leu Cys Gly Cys Phe Gln Ser Lys Val
 340 345 350
 Pro Phe Arg Ser Arg Ser Pro Ser Glu Val Ala Ser Lys Gly Glu Glu
 355 360 365
 Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val
 370 375 380
 Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr
 385 390 395 400
 Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
 405 410 415
 Val Pro Trp Pro Thr Leu Val Thr Thr Leu Cys Tyr Gly Val Gln Cys
 420 425 430
 Phe Ser Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser

233/518

435	440	445
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp		
450	455	460
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr		
465	470	475
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly		
485	490	495
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val		
500	505	510
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys		
515	520	525
Thr Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr		
530	535	540
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn		
545	550	555
His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys		
565	570	575
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr		
580	585	590
His Gly Met Asp Glu Leu Tyr Asn		
595	600	

<210> 94

<211> 595

<212> PRT

<213> Human

<400> 94

Met Ala Thr Thr Val Pro Asp Gly Cys Arg Asn Gly Leu Lys Ser Lys

234/518

	5		10		15
Tyr Tyr Arg Leu Cys Asp Lys Ala Glu Ala Trp Gly Ile Val Leu Glu					
	20		25		30
Thr Val Ala Thr Ala Gly Val Val Thr Ser Val Ala Phe Met Leu Thr					
	35		40		45
Leu Pro Ile Leu Val Cys Lys Val Gln Asp Ser Asn Arg Arg Lys Met					
	50		55		60
Leu Pro Thr Gln Phe Leu Phe Leu Leu Gly Val Leu Gly Ile Phe Gly					
65		70		75	80
Leu Thr Phe Ala Phe Ile Ile Gly Leu Asp Gly Ser Thr Gly Pro Thr					
	85		90		95
Arg Phe Phe Leu Phe Gly Ile Leu Phe Ser Ile Cys Phe Ser Cys Leu					
	100		105		110
Leu Ala His Ala Val Ser Leu Thr Lys Leu Val Arg Gly Arg Lys Pro					
	115		120		125
Leu Ser Leu Leu Val Ile Leu Gly Leu Ala Val Gly Phe Ser Leu Val					
	130		135		140
Gln Asp Val Ile Ala Ile Glu Tyr Ile Val Leu Thr Met Asn Arg Thr					
145		150		155	160
Asn Val Asn Val Phe Ser Glu Leu Ser Ala Pro Arg Arg Asn Glu Asp					
	165		170		175
Phe Val Leu Leu Leu Thr Tyr Val Leu Phe Leu Met Ala Leu Thr Phe					
	180		185		190
Leu Met Ser Ser Phe Thr Phe Cys Gly Ser Phe Thr Gly Trp Lys Arg					
	195		200		205
His Gly Ala His Ile Tyr Leu Thr Met Leu Leu Ser Ile Ala Ile Trp					
	210		215		220
Val Ala Trp Ile Thr Leu Leu Met Leu Pro Asp Phe Asp Arg Arg Trp					
225		230		235	240

235/518

Asp Asp Thr Ile Leu Ser Ser Ala Leu Ala Ala Asn Gly Trp Val Phe			
245	250	255	
Leu Leu Ala Tyr Val Ser Pro Glu Phe Trp Leu Leu Thr Lys Gln Arg			
260	265	270	
Asn Pro Met Asp Tyr Pro Val Glu Asp Ala Phe Cys Lys Pro Gln Leu			
275	280	285	
Val Lys Lys Ser Tyr Gly Val Glu Asn Arg Ala Tyr Ser Gln Glu Glu			
290	295	300	
Ile Thr Gln Gly Phe Glu Glu Thr Gly Asp Thr Leu Tyr Ala Pro Tyr			
305	310	315	320
Ser Thr His Phe Gln Leu Gln Asn Gln Pro Pro Gln Lys Glu Phe Ser			
325	330	335	
Ile Pro Arg Ala His Ala Trp Pro Ser Pro Tyr Lys Asp Tyr Glu Val			
340	345	350	
Lys Lys Glu Gly Ser Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val			
355	360	365	
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe			
370	375	380	
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr			
385	390	395	400
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr			
405	410	415	
Leu Val Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro			
420	425	430	
Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly			
435	440	445	
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys			
450	455	460	
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile			

236/518

465 470 475 480
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 485 490 495
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 500 505 510
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile
 515 520 525
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 530 535 540
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 545 550 555 560
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 565 570 575
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 580 585 590
 Leu Tyr Asn
 595

<210> 95

<211> 657

<212> PRT

<213> Human

<400> 95

Met Leu Ala Ala Ala Phe Ala Asp Ser Asn Ser Ser Ser Met Asn Val
 5 10 15
 Ser Phe Ala His Leu His Phe Ala Gly Gly Tyr Leu Pro Ser Asp Ser
 20 25 30
 Gln Asp Trp Arg Thr Ile Ile Pro Ala Leu Leu Val Ala Val Cys Leu

237/518

35	40	45
Val Gly Phe Val Gly Asn Leu Cys Val Ile Gly Ile Leu Leu His Asn		
50	55	60
Ala Trp Lys Gly Lys Pro Ser Met Ile His Ser Leu Ile Leu Asn Leu		
65	70	75
Ser Leu Ala Asp Leu Ser Leu Leu Leu Phe Ser Ala Pro Ile Arg Ala		
85	90	95
Thr Ala Tyr Ser Lys Ser Val Trp Asp Leu Gly Trp Phe Val Cys Lys		
100	105	110
Ser Ser Asp Trp Phe Ile His Thr Cys Met Ala Ala Lys Ser Leu Thr		
115	120	125
Ile Val Val Val Ala Lys Val Cys Phe Met Tyr Ala Ser Asp Pro Ala		
130	135	140
Lys Gln Val Ser Ile His Asn Tyr Thr Ile Trp Ser Val Leu Val Ala		
145	150	155
Ile Trp Thr Val Ala Ser Leu Leu Pro Leu Pro Glu Trp Phe Phe Ser		
165	170	175
Thr Ile Arg His His Glu Gly Val Glu Met Cys Leu Val Asp Val Pro		
180	185	190
Ala Val Ala Glu Glu Phe Met Ser Met Phe Gly Lys Leu Tyr Pro Leu		
195	200	205
Leu Ala Phe Gly Leu Pro Leu Phe Phe Ala Ser Phe Tyr Phe Trp Arg		
210	215	220
Ala Tyr Asp Gln Cys Lys Lys Arg Gly Thr Lys Thr Gln Asn Leu Arg		
225	230	235
Asn Gln Ile Arg Ser Lys Gln Val Thr Val Met Leu Leu Ser Ile Ala		
245	250	255
Ile Ile Ser Ala Leu Leu Trp Leu Pro Glu Trp Val Ala Trp Leu Trp		
260	265	270

238/518

Val Trp His Leu Lys Ala Ala Gly Pro Ala Pro Pro Gln Gly Phe Ile
 275 280 285
 Ala Leu Ser Gln Val Leu Met Phe Ser Ile Ser Ser Ala Asn Pro Leu
 290 295 300
 Ile Phe Leu Val Met Ser Glu Glu Phe Arg Glu Gly Leu Lys Gly Val
 305 310 315 320
 Trp Lys Trp Met Ile Thr Lys Lys Pro Pro Thr Val Ser Glu Ser Gln
 325 330 335
 Glu Thr Pro Ala Gly Asn Ser Glu Gly Leu Pro Asp Lys Val Pro Ser
 340 345 350
 Pro Glu Ser Pro Ala Ser Ile Pro Glu Lys Glu Lys Pro Ser Ser Pro
 355 360 365
 Ser Ser Gly Lys Gly Lys Thr Glu Lys Ala Glu Ile Pro Ile Leu Pro
 370 375 380
 Asp Val Glu Gln Phe Trp His Glu Arg Asp Thr Val Pro Ser Val Gln
 385 390 395 400
 Asp Asn Asp Pro Ile Pro Trp Glu His Glu Asp Gln Glu Thr Gly Glu
 405 410 415
 Gly Val Lys Thr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro
 420 425 430
 Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val
 435 440 445
 Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys
 450 455 460
 Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val
 465 470 475 480
 Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His
 485 490 495
 Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val

239/518

500	505	510
Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg		
515	520	525
Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu		
530	535	540
Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu		
545	550	555
Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln		
565	570	575
Lys Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp		
580	585	590
Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly		
595	600	605
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser		
610	615	620
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu		
625	630	635
Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr		
645	650	655
Asn		

<210> 96

<211> 657

<212> PRT

<213> Human

<400> 96

Met Leu Ala Ala Ala Phe Ala Asp Ser Asn Ser Ser Ser Met Asn Val

5

10

15

240/518

Ser Phe Ala His Leu His Phe Ala Gly Gly Tyr Leu Pro Ser Asp Ser
 20 25 30
 Gln Asp Trp Arg Thr Ile Ile Pro Ala Leu Leu Val Ala Val Cys Leu
 35 40 45
 Val Gly Phe Val Gly Asn Leu Cys Val Ile Gly Ile Leu Leu His Asn
 50 55 60
 Ala Trp Lys Gly Lys Pro Ser Met Ile His Ser Leu Ile Leu Asn Leu
 65 70 75 80
 Ser Leu Ala Asp Leu Ser Leu Leu Leu Phe Ser Ala Pro Ile Arg Ala
 85 90 95
 Thr Ala Tyr Ser Lys Ser Val Trp Asp Leu Gly Trp Phe Val Cys Lys
 100 105 110
 Ser Ser Asp Trp Phe Ile His Thr Cys Met Ala Ala Lys Ser Leu Thr
 115 120 125
 Ile Val Val Val Ala Lys Val Cys Phe Met Tyr Ala Ser Asp Pro Ala
 130 135 140
 Lys Gln Val Ser Ile His Asn Tyr Thr Ile Trp Ser Val Leu Val Ala
 145 150 155 160
 Ile Trp Thr Val Ala Ser Leu Leu Pro Leu Pro Glu Trp Phe Phe Ser
 165 170 175
 Thr Ile Arg His His Glu Gly Val Glu Met Cys Leu Val Asp Val Pro
 180 185 190
 Ala Val Ala Glu Glu Phe Met Ser Met Phe Gly Lys Leu Tyr Pro Leu
 195 200 205
 Leu Ala Phe Gly Leu Pro Leu Phe Phe Ala Ser Phe Tyr Phe Trp Arg
 210 215 220
 Ala Tyr Asp Gln Cys Lys Lys Arg Gly Thr Lys Thr Gln Asn Leu Arg
 225 230 235 240
 Asn Gln Ile Arg Ser Lys Gln Val Thr Val Met Leu Leu Ser Ile Ala

241/518

	245		250		255
Ile Ile Ser Ala Val Leu Trp Leu Pro Glu Trp Val Ala Trp Leu Trp					
	260		265		270
Val Trp His Leu Lys Ala Ala Gly Pro Ala Pro Pro Gln Gly Phe Ile					
	275		280		285
Ala Leu Ser Gln Val Leu Met Phe Ser Ile Ser Ser Ala Asn Pro Leu					
	290		295		300
Ile Phe Leu Val Met Ser Glu Glu Phe Arg Glu Gly Leu Lys Gly Val					
305		310		315	320
Trp Lys Trp Met Ile Thr Lys Lys Pro Pro Thr Val Ser Glu Ser Gln					
	325		330		335
Glu Thr Pro Ala Gly Asn Ser Glu Gly Leu Pro Asp Lys Val Pro Ser					
	340		345		350
Pro Glu Ser Pro Ala Ser Ile Pro Glu Lys Glu Lys Pro Ser Ser Pro					
	355		360		365
Ser Ser Gly Lys Gly Lys Thr Glu Lys Ala Glu Ile Pro Ile Leu Pro					
	370		375		380
Asp Val Glu Gln Phe Trp His Glu Arg Asp Thr Val Pro Ser Val Gln					
385		390		395	400
Asp Asn Asp Pro Ile Pro Trp Glu His Glu Asp Gln Glu Thr Gly Glu					
	405		410		415
Gly Val Lys Thr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro					
	420		425		430
Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val					
	435		440		445
Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys					
	450		455		460
Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val					
465		470		475	480

242/518

Thr	Thr	Leu	Cys	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His
				485					490					495	
Met	Lys	Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val
				500				505					510		
Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg
		515					520					525			
Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu
	530					535				540					
Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu
545					550					555					560
Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln
			565					570					575		
Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Thr	Arg	His	Asn	Ile	Glu	Asp
		580						585					590		
Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly
	595					600						605			
Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser
610						615					620				
Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu
625					630					635					640
Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	Leu	Tyr
				645					650						655

<210> 97

<211> 1232

<212> PRT

<213> Human

<400> 97

Met	Val	Cys	Ser	Ala	Ala	Pro	Leu	Leu	Leu	Leu	Ala	Thr	Thr	Leu	Pro
				5				10						15	
Leu	Leu	Gly	Ser	Pro	Val	Ala	Gln	Ala	Ser	Gln	Pro	Gly	Gln	Ser	Gln
				20				25						30	
Ala	Gly	Gly	Glu	Ser	Gly	Ser	Gly	Gln	Leu	Leu	Asp	Gln	Glu	Asn	Gly
				35				40						45	
Ala	Gly	Glu	Ser	Ala	Leu	Val	Ser	Val	Tyr	Val	His	Leu	Asp	Phe	Pro
				50				55						60	
Asp	Lys	Thr	Trp	Pro	Pro	Glu	Leu	Ser	Arg	Thr	Leu	Thr	Leu	Pro	Ala
65						70					75				80
Ala	Ser	Ala	Ser	Ser	Ser	Pro	Arg	Pro	Leu	Leu	Thr	Gly	Leu	Arg	Leu
						85					90				95
Thr	Thr	Glu	Cys	Asn	Val	Asn	His	Lys	Gly	Asn	Phe	Tyr	Cys	Ala	Cys
						100					105				110
Leu	Ser	Gly	Tyr	Gln	Trp	Asn	Thr	Ser	Ile	Cys	Leu	His	Tyr	Pro	Pro
						115					120				125
Cys	Gln	Ser	Leu	His	Asn	His	Gln	Pro	Cys	Gly	Cys	Leu	Val	Phe	Ser
						130					135				140
His	Pro	Glu	Pro	Gly	Tyr	Cys	Gln	Leu	Leu	Pro	Pro	Val	Pro	Gly	Ile
145						150					155				160
Leu	Asn	Leu	Asn	Ser	Gln	Leu	Gln	Met	Pro	Gly	Asp	Thr	Leu	Ser	Leu
						165					170				175
Thr	Leu	His	Leu	Ser	Gln	Glu	Ala	Thr	Asn	Leu	Ser	Trp	Phe	Leu	Arg
						180					185				190
His	Pro	Gly	Ser	Pro	Ser	Pro	Ile	Leu	Leu	Gln	Pro	Gly	Thr	Gln	Val
						195					200				205
Ser	Val	Thr	Ser	Ser	His	Gly	Gln	Ala	Ala	Leu	Ser	Val	Ser	Asn	Met
						210					215				220

244/518

Ser His His Trp Ala Gly Glu Tyr Met Ser Cys Phe Glu Ala Gln Gly
 225 230 235 240
 Phe Lys Trp Asn Leu Tyr Glu Val Val Arg Val Pro Leu Lys Ala Thr
 245 250 255
 Asp Val Ala Arg Leu Pro Tyr Gln Leu Ser Ile Ser Cys Ala Thr Ser
 260 265 270
 Pro Gly Phe Gln Leu Ser Cys Cys Ile Pro Ser Thr Asn Leu Ala Tyr
 275 280 285
 Thr Ala Ala Trp Ser Pro Gly Glu Gly Ser Lys Ala Ser Ser Phe Asn
 290 295 300
 Glu Ser Gly Ser Gln Cys Phe Val Leu Ala Val Gln Arg Cys Pro Met
 305 310 315 320
 Ala Asp Thr Thr Tyr Thr Cys Asp Leu Gln Ser Leu Gly Leu Ala Pro
 325 330 335
 Leu Arg Val Pro Ile Ser Ile Thr Ile Ile Gln Asp Gly Asp Ile Thr
 340 345 350
 Cys Pro Glu Asp Ala Ser Val Leu Thr Trp Asn Val Thr Lys Ala Gly
 355 360 365
 His Val Ala Gln Ala Pro Cys Pro Glu Ser Lys Arg Gly Ile Val Arg
 370 375 380
 Arg Leu Cys Gly Ala Asp Gly Val Trp Gly Pro Val His Ser Ser Cys
 385 390 395 400
 Thr Asp Ala Arg Leu Leu Ala Leu Phe Thr Arg Thr Lys Leu Leu Gln
 405 410 415
 Ala Gly Gln Gly Ser Pro Ala Glu Glu Val Pro Gln Ile Leu Ala Gln
 420 425 430
 Leu Pro Gly Gln Ala Ala Glu Ala Ser Ser Pro Ser Asp Leu Leu Thr
 435 440 445
 Leu Leu Ser Thr Met Lys Tyr Val Ala Lys Val Val Ala Glu Ala Arg

245/518

450	455	460	
Ile Gln Leu Asp Arg Arg Ala Leu Lys Asn Leu Leu Ile Ala Thr Asp			
465	470	475	480
Lys Val Leu Asp Met Asp Thr Arg Ser Leu Trp Thr Leu Ala Gln Ala			
485	490	495	
Arg Lys Pro Trp Ala Gly Ser Thr Leu Leu Leu Ala Val Glu Thr Leu			
500	505	510	
Ala Cys Ser Leu Cys Pro Gln Asp Tyr Pro Phe Ala Phe Ser Leu Pro			
515	520	525	
Asn Val Leu Leu Gln Ser Gln Leu Phe Gly Pro Thr Phe Pro Ala Asp			
530	535	540	
Tyr Ser Ile Ser Phe Pro Thr Arg Pro Pro Leu Gln Ala Gln Ile Pro			
545	550	555	560
Arg His Ser Leu Ala Pro Leu Val Arg Asn Gly Thr Glu Ile Ser Ile			
565	570	575	
Thr Ser Leu Val Leu Arg Lys Leu Asp His Leu Leu Pro Ser Asn Tyr			
580	585	590	
Gly Gln Gly Leu Gly Asp Ser Leu Tyr Ala Thr Pro Gly Leu Val Leu			
595	600	605	
Val Ile Ser Ile Met Ala Gly Asp Arg Ala Phe Ser Gln Gly Glu Val			
610	615	620	
Ile Met Asp Phe Gly Asn Thr Asp Gly Ser Pro His Cys Val Phe Trp			
625	630	635	640
Asp His Ser Leu Phe Gln Gly Arg Gly Gly Trp Ser Lys Glu Gly Cys			
645	650	655	
Gln Ala Gln Val Ala Ser Ala Ser Pro Thr Ala Gln Cys Leu Cys Gln			
660	665	670	
His Leu Thr Ala Phe Ser Val Leu Met Ser Pro His Thr Val Pro Glu			
675	680	685	

246/518

Glu Pro Ala Leu Ala Leu Leu Thr Gln Val Gly Leu Gly Ala Ser Ile
 690 695 700
 Leu Ala Leu Leu Val Cys Leu Gly Val Tyr Trp Leu Val Trp Arg Val
 705 710 715 720
 Val Val Arg Asn Lys Ile Ser Tyr Phe Arg His Ala Ala Leu Leu Asn
 725 730 735
 Met Val Phe Cys Leu Leu Ala Ala Asp Thr Cys Phe Leu Gly Ala Pro
 740 745 750
 Phe Leu Ser Pro Gly Pro Arg Ser Pro Leu Cys Leu Ala Ala Ala Phe
 755 760 765
 Leu Cys His Phe Leu Tyr Leu Ala Thr Phe Phe Trp Met Leu Ala Gln
 770 775 780
 Ala Leu Val Leu Ala His Gln Leu Leu Phe Val Phe His Gln Leu Ala
 785 790 795 800
 Lys His Arg Val Leu Pro Leu Met Val Leu Leu Gly Tyr Leu Cys Pro
 805 810 815
 Leu Gly Leu Ala Gly Val Thr Leu Gly Leu Tyr Leu Pro Gln Gly Gln
 820 825 830
 Tyr Leu Arg Glu Gly Glu Cys Trp Leu Asp Gly Lys Gly Gly Ala Leu
 835 840 845
 Tyr Thr Phe Val Gly Pro Val Leu Ala Ile Ile Gly Val Asn Gly Leu
 850 855 860
 Val Leu Ala Met Ala Met Leu Lys Leu Leu Arg Pro Ser Leu Ser Glu
 865 870 875 880
 Gly Pro Pro Ala Glu Lys Arg Gln Ala Leu Leu Gly Val Ile Lys Ala
 885 890 895
 Leu Leu Ile Leu Thr Pro Ile Phe Gly Leu Thr Trp Gly Leu Gly Leu
 900 905 910
 Ala Thr Leu Leu Glu Glu Val Ser Thr Val Pro His Tyr Ile Phe Thr

247/518

915	920	925
Ile Leu Asn Thr Leu Gln Gly Val Phe Ile Leu Leu Phe Gly Cys Leu		
930	935	940
Met Asp Arg Lys Ile Gln Glu Ala Leu Arg Lys Arg Phe Cys Arg Ala		
945	950	955
Gln Ala Pro Ser Ser Thr Ile Ser Leu Ala Thr Asn Glu Gly Cys Ile		
965	970	975
Leu Glu His Ser Lys Gly Gly Ser Asp Thr Ala Arg Lys Thr Asp Ala		
980	985	990
Ser Glu Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile		
995	1000	1005
Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser		
1010	1015	1020
Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe		
1025	1030	1035
Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr		
1045	1050	1055
Thr Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met		
1060	1065	1070
Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln		
1075	1080	1085
Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala		
1090	1095	1100
Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys		
1105	1110	1115
Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu		
1125	1130	1135
Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys		
1140	1145	1150

248/518

Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly

1155

1160

1165

Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp

1170

1175

1180

Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala

1185

1190

1195

1200

Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu

1205

1210

1215

Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn

1220

1225

1230

<210> 98

<211> 931

<212> PRT

<213> Human

<400> 98

Met Thr Pro Gln Ser Leu Leu Gln Thr Thr Leu Phe Leu Leu Ser Leu

5

10

15

Leu Phe Leu Val Gln Gly Ala His Gly Arg Gly His Arg Glu Asp Phe

20

25

30

Arg Phe Cys Ser Gln Arg Asn Gln Thr His Arg Ser Ser Leu His Tyr

35

40

45

Lys Pro Thr Pro Asp Leu Arg Ile Ser Ile Glu Asn Ser Glu Glu Ala

50

55

60

Leu Thr Val His Ala Pro Phe Pro Ala Ala His Pro Ala Ser Arg Ser

65

70

75

80

Phe Pro Asp Pro Arg Gly Leu Tyr His Phe Cys Leu Tyr Trp Asn Arg

85

90

95

249/518

His Ala Gly Arg Leu His Leu Leu Tyr Gly Lys Arg Asp Phe Leu Leu
 100 105 110
 Ser Asp Lys Ala Ser Ser Leu Leu Cys Phe Gln His Gln Glu Glu Ser
 115 120 125
 Leu Ala Gln Gly Pro Pro Leu Leu Ala Thr Ser Val Thr Ser Trp Trp
 130 135 140
 Ser Pro Gln Asn Ile Ser Leu Pro Ser Ala Ala Ser Phe Thr Phe Ser
 145 150 155 160
 Phe His Ser Pro Pro His Thr Ala Ala His Asn Ala Ser Val Asp Met
 165 170 175
 Cys Glu Leu Lys Arg Asp Leu Gln Leu Leu Ser Gln Phe Leu Lys His
 180 185 190
 Pro Gln Lys Ala Ser Arg Arg Pro Ser Ala Ala Pro Ala Ser Gln Gln
 195 200 205
 Leu Gln Ser Leu Glu Ser Lys Leu Thr Ser Val Arg Phe Met Gly Asp
 210 215 220
 Met Val Ser Phe Glu Glu Asp Arg Ile Asn Ala Thr Val Trp Lys Leu
 225 230 235 240
 Gln Pro Thr Ala Gly Leu Gln Asp Leu His Ile His Ser Arg Gln Glu
 245 250 255
 Glu Glu Gln Ser Glu Ile Met Glu Tyr Ser Val Leu Leu Pro Arg Thr
 260 265 270
 Leu Phe Gln Arg Thr Lys Gly Arg Ser Gly Glu Ala Glu Lys Arg Leu
 275 280 285
 Leu Leu Val Asp Phe Ser Ser Gln Ala Leu Phe Gln Asp Lys Asn Ser
 290 295 300
 Ser Gln Val Leu Gly Glu Lys Val Leu Gly Ile Val Val Gln Asn Thr
 305 310 315 320
 Lys Val Ala Asn Leu Thr Glu Pro Val Val Leu Thr Phe Gln His Gln

250/518

325	330	335
Leu Gln Pro Lys Asn Val Thr Leu Gln Cys Val Phe Trp Val Glu Asp		
340	345	350
Pro Thr Leu Ser Ser Pro Gly His Trp Ser Ser Ala Gly Cys Glu Thr		
355	360	365
Val Arg Arg Glu Thr Gln Thr Ser Cys Phe Cys Asn His Leu Thr Tyr		
370	375	380
Phe Ala Val Leu Met Val Ser Ser Val Glu Val Asp Ala Val His Lys		
385	390	395
His Tyr Leu Ser Leu Leu Ser Tyr Val Gly Cys Val Val Ser Ala Leu		
405	410	415
Ala Cys Leu Val Thr Ile Ala Ala Tyr Leu Cys Ser Arg Val Pro Leu		
420	425	430
Pro Cys Arg Arg Lys Pro Arg Asp Tyr Thr Ile Lys Val His Met Asn		
435	440	445
Leu Leu Leu Ala Val Phe Leu Leu Asp Thr Ser Phe Leu Leu Ser Glu		
450	455	460
Pro Val Ala Leu Thr Gly Ser Glu Ala Gly Cys Arg Ala Ser Ala Ile		
465	470	475
Phe Leu His Phe Ser Leu Leu Thr Cys Leu Ser Trp Met Gly Leu Glu		
485	490	495
Gly Tyr Asn Leu Tyr Arg Leu Val Val Glu Val Phe Gly Thr Tyr Val		
500	505	510
Pro Gly Tyr Leu Leu Lys Leu Ser Ala Met Gly Trp Gly Phe Pro Ile		
515	520	525
Phe Leu Val Thr Leu Val Ala Leu Val Asp Val Asp Asn Tyr Gly Pro		
530	535	540
Ile Ile Leu Ala Val His Arg Thr Pro Glu Gly Val Ile Tyr Pro Ser		
545	550	555
		560

251/518

Met Cys Trp Ile Arg Asp Ser Leu Val Ser Tyr Ile Thr Asn Leu Gly
 565 570 575
 Leu Phe Ser Leu Val Phe Leu Phe Asn Met Ala Met Leu Ala Thr Met
 580 585 590
 Val Val Gln Ile Leu Arg Leu Arg Pro His Thr Gln Lys Trp Ser His
 595 600 605
 Val Leu Thr Leu Leu Gly Leu Ser Leu Val Leu Gly Leu Pro Trp Ala
 610 615 620
 Leu Ile Phe Phe Ser Phe Ala Ser Gly Thr Phe Gln Leu Val Val Leu
 625 630 635 640
 Tyr Leu Phe Ser Ile Ile Thr Ser Phe Gln Gly Phe Leu Ile Phe Ile
 645 650 655
 Trp Tyr Trp Ser Met Arg Leu Gln Ala Arg Gly Gly Pro Ser Pro Leu
 660 665 670
 Lys Ser Asn Ser Asp Ser Ala Arg Leu Pro Ile Ser Ser Gly Ser Thr
 675 680 685
 Ser Ser Ser Arg Ile Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 690 695 700
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 705 710 715 720
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 725 730 735
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 740 745 750
 Leu Val Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 755 760 765
 Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 770 775 780
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys

252/518

785	790	795	800
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile			
805	810	815	
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His			
820	825	830	
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp			
835	840	845	
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile			
850	855	860	
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro			
865	870	875	880
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr			
885	890	895	
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val			
900	905	910	
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu			
915	920	925	
Leu Tyr Asn			
930			

<210> 99

<211> 1584

<212> PRT

<213> Human

<400> 99

Met Lys Ser Pro Arg Arg Thr Thr Leu Cys Leu Met Phe Ile Val Ile		
5	10	15
Tyr Ser Ser Lys Ala Ala Leu Asn Trp Asn Tyr Glu Ser Thr Ile His		

20					25					30						
Pro	Leu	Ser	Leu	His	Glu	His	Glu	Pro	Ala	Gly	Glu	Glu	Ala	Leu	Arg	
35					40					45						
Gln	Lys	Arg	Ala	Val	Ala	Thr	Lys	Ser	Pro	Thr	Ala	Glu	Glu	Tyr	Thr	
50					55					60						
Val	Asn	Ile	Glu	Ile	Ser	Phe	Glu	Asn	Ala	Ser	Phe	Leu	Asp	Pro	Ile	
65					70					75					80	
Lys	Ala	Tyr	Leu	Asn	Ser	Leu	Ser	Phe	Pro	Ile	His	Gly	Asn	Asn	Thr	
85					90					95						
Asp	Gln	Ile	Thr	Asp	Ile	Leu	Ser	Ile	Asn	Val	Thr	Thr	Val	Cys	Arg	
100					105					110						
Pro	Ala	Gly	Asn	Glu	Ile	Trp	Cys	Ser	Cys	Glu	Thr	Gly	Tyr	Gly	Trp	
115					120					125						
Pro	Arg	Glu	Arg	Cys	Leu	His	Asn	Leu	Ile	Cys	Gln	Glu	Arg	Asp	Val	
130					135					140						
Phe	Leu	Pro	Gly	His	His	Cys	Ser	Cys	Leu	Lys	Glu	Leu	Pro	Pro	Asn	
145					150					155					160	
Gly	Pro	Phe	Cys	Leu	Leu	Gln	Glu	Asp	Val	Thr	Leu	Asn	Met	Arg	Val	
165					170					175						
Arg	Leu	Asn	Val	Gly	Phe	Gln	Glu	Asp	Leu	Met	Asn	Thr	Ser	Ser	Ala	
180					185					190						
Leu	Tyr	Arg	Ser	Tyr	Lys	Thr	Asp	Leu	Glu	Thr	Ala	Phe	Arg	Lys	Gly	
195					200					205						
Tyr	Gly	Ile	Leu	Pro	Gly	Phe	Lys	Gly	Val	Thr	Val	Thr	Gly	Phe	Lys	
210					215					220						
Ser	Gly	Ser	Val	Val	Val	Thr	Tyr	Glu	Val	Lys	Thr	Thr	Pro	Pro	Ser	
225					230					235					240	
Leu	Glu	Leu	Ile	His	Lys	Ala	Asn	Glu	Gln	Val	Val	Gln	Ser	Leu	Asn	
245					250					255						

254/518

Gln Thr Tyr Lys Met Asp Tyr Asn Ser Phe Gln Ala Val Thr Ile Asn
 260 265 270
 Glu Ser Asn Phe Phe Val Thr Pro Glu Ile Ile Phe Glu Gly Asp Thr
 275 280 285
 Val Ser Leu Val Cys Glu Lys Glu Val Leu Ser Ser Asn Val Ser Trp
 290 295 300
 Arg Tyr Glu Glu Gln Gln Leu Glu Ile Gln Asn Ser Ser Arg Phe Ser
 305 310 315 320
 Ile Tyr Thr Ala Leu Phe Asn Asn Met Thr Ser Val Ser Lys Leu Thr
 325 330 335
 Ile His Asn Ile Thr Pro Gly Asp Ala Gly Glu Tyr Val Cys Lys Leu
 340 345 350
 Ile Leu Asp Ile Phe Glu Tyr Glu Cys Lys Lys Lys Ile Asp Val Met
 355 360 365
 Pro Ile Gln Ile Leu Ala Asn Glu Glu Met Lys Val Met Cys Asp Asn
 370 375 380
 Asn Pro Val Ser Leu Asn Cys Cys Ser Gln Gly Asn Val Asn Trp Ser
 385 390 395 400
 Lys Val Glu Trp Lys Gln Glu Gly Lys Ile Asn Ile Pro Gly Thr Pro
 405 410 415
 Glu Thr Asp Ile Asp Ser Ser Cys Ser Arg Tyr Thr Leu Lys Ala Asp
 420 425 430
 Gly Thr Gln Cys Pro Ser Gly Ser Ser Gly Thr Thr Val Ile Tyr Thr
 435 440 445
 Cys Glu Phe Ile Ser Ala Tyr Gly Ala Arg Gly Ser Ala Asn Ile Lys
 450 455 460
 Val Thr Phe Ile Ser Val Ala Asn Leu Thr Ile Thr Pro Asp Pro Ile
 465 470 475 480
 Ser Val Ser Glu Gly Gln Asn Phe Ser Ile Lys Cys Ile Ser Asp Val

255/518

485	490	495
Ser Asn Tyr Asp Glu Val Tyr Trp Asn Thr Ser Ala Gly Ile Lys Ile		
500	505	510
Tyr Gln Arg Phe Tyr Thr Thr Arg Arg Tyr Leu Asp Gly Ala Glu Ser		
515	520	525
Val Leu Thr Val Lys Thr Ser Thr Arg Glu Trp Asn Gly Thr Tyr His		
530	535	540
Cys Ile Phe Arg Tyr Lys Asn Ser Tyr Ser Ile Ala Thr Lys Asp Val		
545	550	555
Ile Val His Pro Leu Pro Leu Lys Leu Asn Ile Met Val Asp Pro Leu		
565	570	575
Glu Ala Thr Val Ser Cys Ser Gly Ser His His Ile Lys Cys Cys Ile		
580	585	590
Glu Glu Asp Gly Asp Tyr Lys Val Thr Phe His Met Gly Ser Ser Ser		
595	600	605
Leu Pro Ala Ala Lys Glu Val Asn Lys Lys Gln Val Cys Tyr Lys His		
610	615	620
Asn Phe Asn Ala Ser Ser Val Ser Trp Cys Ser Lys Thr Val Asp Val		
625	630	635
Cys Cys His Phe Thr Asn Ala Ala Asn Asn Ser Val Trp Ser Pro Ser		
645	650	655
Met Lys Leu Asn Leu Val Pro Gly Glu Asn Ile Thr Cys Gln Asp Pro		
660	665	670
Val Ile Gly Val Gly Glu Pro Gly Lys Val Ile Gln Lys Leu Cys Arg		
675	680	685
Phe Ser Asn Val Pro Ser Ser Pro Glu Ser Pro Ile Gly Gly Thr Ile		
690	695	700
Thr Tyr Lys Cys Val Gly Ser Gln Trp Glu Glu Lys Arg Asn Asp Cys		
705	710	715
		720

256/518

Ile Ser Ala Pro Ile Asn Ser Leu Leu Gln Met Ala Lys Ala Leu Ile
 725 730 735
 Lys Ser Pro Ser Gln Asp Glu Met Leu Pro Thr Tyr Leu Lys Asp Leu
 740 745 750
 Ser Ile Ser Ile Asp Lys Ala Glu His Glu Ile Ser Ser Ser Pro Gly
 755 760 765
 Ser Leu Gly Ala Ile Ile Asn Ile Leu Asp Leu Leu Ser Thr Val Pro
 770 775 780
 Thr Gln Val Asn Ser Glu Met Met Thr His Val Leu Ser Thr Val Asn
 785 790 795 800
 Val Ile Leu Gly Lys Pro Val Leu Asn Thr Trp Lys Val Leu Gln Gln
 805 810 815
 Gln Trp Thr Asn Gln Ser Ser Gln Leu Leu His Ser Val Glu Arg Phe
 820 825 830
 Ser Gln Ala Leu Gln Ser Gly Asp Ser Pro Pro Leu Ser Phe Ser Gln
 835 840 845
 Thr Asn Val Gln Met Ser Ser Thr Val Ile Lys Ser Ser His Pro Glu
 850 855 860
 Thr Tyr Gln Gln Arg Phe Val Phe Pro Tyr Phe Asp Leu Trp Gly Asn
 865 870 875 880
 Val Val Ile Asp Lys Ser Tyr Leu Glu Asn Leu Gln Ser Asp Ser Ser
 885 890 895
 Ile Val Thr Met Ala Phe Pro Thr Leu Gln Ala Ile Leu Ala Gln Asp
 900 905 910
 Ile Gln Glu Asn Asn Phe Ala Glu Ser Leu Val Met Thr Thr Thr Val
 915 920 925
 Ser His Asn Thr Thr Met Pro Phe Arg Ile Ser Met Thr Phe Lys Asn
 930 935 940
 Asn Ser Pro Ser Gly Gly Glu Thr Lys Cys Val Phe Trp Asn Phe Arg

257/518

945	950	955	960
Leu Ala Asn Asn Thr Gly Gly Trp Asp Ser Ser Gly Cys Tyr Val Glu			
	965	970	975
Glu Gly Asp Gly Asp Asn Val Thr Cys Ile Cys Asp His Leu Thr Ser			
	980	985	990
Phe Ser Ile Leu Met Ser Pro Asp Ser Pro Asp Pro Ser Ser Leu Leu			
	995	1000	1005
Gly Ile Leu Leu Asp Ile Ile Ser Tyr Val Gly Val Gly Phe Ser Ile			
	1010	1015	1020
Leu Ser Leu Ala Ala Cys Leu Val Val Glu Ala Val Val Trp Lys Ser			
	1025	1030	1035
Val Thr Lys Asn Arg Thr Ser Tyr Met Arg His Thr Cys Ile Val Asn			
	1045	1050	1055
Ile Ala Ala Ser Leu Leu Val Ala Asn Thr Trp Phe Ile Val Val Ala			
	1060	1065	1070
Ala Ile Gln Asp Asn Arg Tyr Ile Leu Cys Lys Thr Ala Cys Val Ala			
	1075	1080	1085
Ala Thr Phe Phe Ile His Phe Phe Tyr Leu Ser Val Phe Phe Trp Met			
	1090	1095	1100
Leu Thr Leu Gly Leu Met Leu Phe Tyr Arg Leu Val Phe Ile Leu His			
	1105	1110	1115
Glu Thr Ser Arg Ser Thr Gln Lys Ala Ile Ala Phe Cys Leu Gly Tyr			
	1125	1130	1135
Gly Cys Pro Leu Ala Ile Ser Val Ile Thr Leu Gly Ala Thr Gln Pro			
	1140	1145	1150
Arg Glu Val Tyr Thr Arg Lys Asn Val Cys Trp Leu Asn Trp Glu Asp			
	1155	1160	1165
Thr Lys Ala Leu Leu Ala Phe Ala Ile Pro Ala Leu Ile Ile Val Val			
	1170	1175	1180

258/518

Val Asn Ile Thr Ile Thr Ile Val Val Ile Thr Lys Ile Leu Arg Pro			
1185	1190	1195	1200
Ser Ile Gly Asp Lys Pro Cys Lys Gln Glu Lys Ser Ser Leu Phe Gln			
	1205	1210	1215
Ile Ser Lys Ser Ile Gly Val Leu Thr Pro Leu Leu Gly Leu Thr Trp			
	1220	1225	1230
Gly Phe Gly Leu Thr Thr Val Phe Pro Gly Thr Asn Leu Val Phe His			
	1235	1240	1245
Ile Ile Phe Ala Ile Leu Asn Val Phe Gln Gly Leu Phe Ile Leu Leu			
	1250	1255	1260
Phe Gly Cys Leu Trp Asp Leu Lys Val Gln Glu Ala Leu Leu Asn Lys			
1265	1270	1275	1280
Phe Ser Leu Ser Arg Trp Ser Ser Gln His Ser Lys Ser Thr Ser Leu			
	1285	1290	1295
Gly Ser Ser Thr Pro Val Phe Ser Met Ser Ser Pro Ile Ser Arg Arg			
	1300	1305	1310
Phe Asn Asn Leu Phe Gly Lys Thr Gly Thr Tyr Asn Val Ser Thr Pro			
	1315	1320	1325
Glu Ala Thr Ser Ser Ser Leu Glu Asn Ser Ser Ser Ala Ser Ser Leu			
	1330	1335	1340
Leu Asn Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile			
1345	1350	1355	1360
Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser			
	1365	1370	1375
Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe			
	1380	1385	1390
Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr			
	1395	1400	1405
Thr Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met			

259/518

1410 1415 1420
 Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln
 1425 1430 1435 1440
 Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala
 1445 1450 1455
 Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys
 1460 1465 1470
 Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu
 1475 1480 1485
 Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
 1490 1495 1500
 Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly
 1505 1510 1515 1520
 Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 1525 1530 1535
 Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala
 1540 1545 1550
 Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
 1555 1560 1565
 Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn
 1570 1575 1580

<210> 100

<211> 645

<212> PRT

<213> Human

<400> 100

Met Ser Leu Asn Ser Ser Leu Ser Cys Arg Lys Glu Leu Ser Asn Leu

5

15

20

25

30

35

40

45

50

55

60

65

70

75

80

85

90

95

100

105.

110

115

120

125

130

135

140

145

150

155

160

165

170

175

180

185

190

195

200

205

210

215

220

225

230

235

240

261/518

Asn Ser Ser Thr Ser Thr Ser Ser Ser Gly Ser Arg Arg Asn Ala Phe
 245 250 255
 Gln Gly Val Val Tyr Ser Ala Asn Gln Cys Lys Ala Leu Ile Thr Ile
 260 265 270
 Leu Val Val Leu Gly Ala Phe Met Val Thr Trp Gly Pro Tyr Met Val
 275 280 285
 Val Ile Ala Ser Glu Ala Leu Trp Gly Lys Ser Ser Val Ser Pro Ser
 290 295 300
 Leu Glu Thr Trp Ala Thr Trp Leu Ser Phe Ala Ser Ala Val Cys His
 305 310 315 320
 Pro Leu Ile Tyr Gly Leu Trp Asn Lys Thr Val Arg Lys Glu Leu Leu
 325 330 335
 Gly Met Cys Phe Gly Asp Arg Tyr Tyr Arg Glu Pro Phe Val Gln Arg
 340 345 350
 Gln Arg Thr Ser Arg Leu Phe Ser Ile Ser Asn Arg Ile Thr Asp Leu
 355 360 365
 Gly Leu Ser Pro His Leu Thr Ala Leu Met Ala Gly Gly Gln Pro Leu
 370 375 380
 Gly His Ser Ser Ser Thr Gly Asp Thr Gly Phe Ser Cys Ser Gln Asp
 385 390 395 400
 Ser Gly Asn Leu Arg Ala Leu Ala Ser Lys Gly Glu Glu Leu Phe Thr
 405 410 415
 Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His
 420 425 430
 Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys
 435 440 445
 Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp
 450 455 460
 Pro Thr Leu Val Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg

262/518

465 470 475 480
 Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro
 485 490 495
 Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn
 500 505 510
 Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn
 515 520 525
 Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu
 530 535 540
 Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met
 545 550 555 560
 Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His
 565 570 575
 Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn
 580 585 590
 Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu
 595 600 605
 Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His
 610 615 620
 Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met
 625 630 635 640
 Asp Glu Leu Tyr Asn
 645

<210> 101

<211> 637

<212> PRT

<213> Human

263/518

<400> 101

Met	Ala	Gln	Arg	Ala	Phe	Pro	Asn	Pro	Tyr	Ala	Asp	Tyr	Asn	Lys	Ser
				5					10					15	
Leu	Ala	Glu	Gly	Tyr	Phe	Asp	Ala	Ala	Gly	Arg	Leu	Thr	Pro	Glu	Phe
				20					25					30	
Ser	Gln	Arg	Leu	Thr	Asn	Lys	Ile	Arg	Glu	Leu	Leu	Gln	Gln	Met	Glu
				35				40						45	
Arg	Gly	Leu	Lys	Ser	Ala	Asp	Pro	Arg	Asp	Gly	Thr	Gly	Tyr	Thr	Gly
				50				55						60	
Trp	Ala	Gly	Ile	Ala	Val	Leu	Tyr	Leu	His	Leu	Tyr	Asp	Val	Phe	Gly
				65				70						75	
Asp	Pro	Ala	Tyr	Leu	Gln	Leu	Ala	His	Gly	Tyr	Val	Lys	Gln	Ser	Leu
								85						90	
Asn	Cys	Leu	Thr	Lys	Arg	Ser	Ile	Thr	Phe	Leu	Cys	Gly	Asp	Ala	Gly
								100						105	
Pro	Leu	Ala	Val	Ala	Ala	Val	Leu	Tyr	His	Lys	Met	Asn	Asn	Glu	Lys
								115						120	
Gln	Ala	Glu	Asp	Cys	Ile	Thr	Arg	Leu	Ile	His	Leu	Asn	Lys	Ile	Asp
								130						135	
Pro	His	Ala	Pro	Asn	Glu	Met	Leu	Tyr	Gly	Arg	Ile	Gly	Tyr	Ile	Tyr
								145						150	
Ala	Leu	Leu	Phe	Val	Asn	Lys	Asn	Phe	Gly	Val	Glu	Lys	Ile	Pro	Gln
								165						170	
Ser	His	Ile	Gln	Gln	Ile	Cys	Glu	Thr	Ile	Leu	Thr	Ser	Gly	Glu	Asn
								180						185	
Leu	Ala	Arg	Lys	Arg	Asn	Phe	Thr	Ala	Lys	Ser	Pro	Leu	Met	Tyr	Glu
								195						200	
Trp	Tyr	Gln	Glu	Tyr	Tyr	Val	Gly	Ala	Ala	His	Gly	Leu	Ala	Gly	Ile
								210						215	

264/518

Tyr Tyr Tyr Leu Met Gln Pro Ser Leu Gln Val Ser Gln Gly Lys Leu			
225	230	235	240
His Ser Leu Val Lys Pro Ser Val Asp Tyr Val Cys Gln Leu Lys Phe			
	245	250	255
Pro Ser Gly Asn Tyr Pro Pro Cys Ile Gly Asp Asn Arg Asp Leu Leu			
	260	265	270
Val His Trp Cys His Gly Ala Pro Gly Val Ile Tyr Met Leu Ile Gln			
	275	280	285
Ala Tyr Lys Val Phe Arg Glu Glu Lys Tyr Leu Cys Asp Ala Tyr Gln			
	290	295	300
Cys Ala Asp Val Ile Trp Gln Tyr Gly Leu Leu Lys Lys Gly Tyr Gly			
305	310	315	320
Leu Cys His Gly Ser Ala Gly Asn Ala Tyr Ala Phe Leu Thr Leu Tyr			
	325	330	335
Asn Leu Thr Gln Asp Met Lys Tyr Leu Tyr Arg Ala Cys Lys Phe Ala			
	340	345	350
Glu Trp Cys Leu Glu Tyr Gly Glu His Gly Cys Arg Thr Pro Asp Thr			
	355	360	365
Pro Phe Ser Leu Phe Glu Gly Met Ala Gly Thr Ile Tyr Phe Leu Ala			
	370	375	380
Asp Leu Leu Val Pro Thr Lys Ala Arg Phe Pro Ala Phe Glu Leu Ala			
385	390	395	400
Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu			
	405	410	415
Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly			
	420	425	430
Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr			
	435	440	445
Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Cys			

265/518

450	455	460	
Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg His			
465	470	475	480
Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr			
	485	490	495
Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys			
	500	505	510
Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp			
	515	520	525
Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr			
	530	535	540
Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile			
545	550	555	560
Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser Val Gln			
	565	570	575
Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val			
	580	585	590
Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys			
	595	600	605
Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr			
	610	615	620
Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn			
625	630	635	

<210> 102

<211> 613

<212> PRT

<213> Human

266/518

<400> 102

Met Ala Asn Ala Ser Glu Pro Gly Gly Ser Gly Gly Gly Glu Ala Ala
 5 10 15
 Ala Leu Gly Leu Lys Leu Ala Thr Leu Ser Leu Leu Leu Cys Val Ser
 20 25 30
 Leu Ala Gly Asn Val Leu Phe Ala Leu Leu Ile Val Arg Glu Arg Ser
 35 40 45
 Leu His Arg Ala Pro Tyr Tyr Leu Leu Leu Asp Leu Cys Leu Ala Asp
 50 55 60
 Gly Leu Arg Ala Leu Ala Cys Leu Pro Ala Val Met Leu Ala Ala Arg
 65 70 75 80
 Arg Ala Ala Ala Ala Ala Gly Ala Pro Pro Gly Ala Leu Gly Cys Lys
 85 90 95
 Leu Leu Ala Phe Leu Ala Ala Leu Phe Cys Phe His Ala Ala Phe Leu
 100 105 110
 Leu Leu Gly Val Gly Val Thr Arg Tyr Leu Ala Ile Ala His His Arg
 115 120 125
 Phe Tyr Ala Glu Arg Leu Ala Gly Trp Pro Cys Ala Ala Met Leu Val
 130 135 140
 Cys Ala Ala Trp Ala Leu Ala Leu Ala Ala Ala Phe Pro Pro Val Leu
 145 150 155 160
 Asp Gly Gly Gly Asp Asp Glu Asp Ala Pro Cys Ala Leu Glu Gln Arg
 165 170 175
 Pro Asp Gly Ala Pro Gly Ala Leu Gly Phe Leu Leu Leu Leu Ala Val
 180 185 190
 Val Val Gly Ala Thr His Leu Val Tyr Leu Arg Leu Leu Phe Phe Ile
 195 200 205
 His Asp Arg Arg Lys Met Arg Pro Ala Arg Leu Val Pro Ala Val Ser
 210 215 220

267/518

His Asp Trp Thr Phe His Gly Pro Gly Ala Thr Gly Gln Ala Ala Ala
 225 230 235 240
 Asn Trp Thr Ala Gly Phe Gly Arg Gly Pro Thr Pro Pro Ala Leu Val
 245 250 255
 Gly Ile Arg Pro Ala Gly Pro Gly Arg Gly Ala Arg Arg Leu Leu Val
 260 265 270
 Leu Glu Glu Phe Lys Thr Glu Lys Arg Leu Cys Lys Met Phe Tyr Ala
 275 280 285
 Val Thr Leu Leu Phe Leu Leu Leu Trp Gly Pro Tyr Val Val Ala Ser
 290 295 300
 Tyr Leu Arg Val Leu Val Arg Pro Gly Ala Val Pro Gln Ala Tyr Leu
 305 310 315 320
 Thr Ala Ser Val Trp Leu Thr Phe Ala Gln Ala Gly Ile Asn Pro Val
 325 330 335
 Val Cys Phe Leu Phe Asn Arg Glu Leu Arg Asp Cys Phe Arg Ala Gln
 340 345 350
 Phe Pro Cys Cys Gln Ser Pro Arg Thr Thr Gln Ala Thr His Pro Cys
 355 360 365
 Asp Leu Lys Gly Ile Gly Leu Ala Ser Lys Gly Glu Glu Leu Phe Thr
 370 375 380
 Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His
 385 390 395 400
 Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys
 405 410 415
 Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp
 420 425 430
 Pro Thr Leu Val Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg
 435 440 445
 Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro

268/518

450 455 460
 Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn
 465 470 475 480
 Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn
 485 490 495
 Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu
 500 505 510
 Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met
 515 520 525
 Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His
 530 535 540
 Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn
 545 550 555 560
 Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu
 565 570 575
 Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His
 580 585 590
 Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met
 595 600 605
 Asp Glu Leu Tyr Asn
 610

<210> 103

<211> 1145

<212> PRT

<213> Human

<400> 103

Met Asp Thr Ser Arg Leu Gly Val Leu Leu Ser Leu Pro Val Leu Leu

269/518

	5	10	15
Gln Leu Ala Thr Gly Gly Ser Ser Pro Arg Ser Gly Val Leu Leu Arg			
20	25	30	
Gly Cys Pro Thr His Cys His Cys Glu Pro Asp Gly Arg Met Leu Leu			
35	40	45	
Arg Val Asp Cys Ser Asp Leu Gly Leu Ser Glu Leu Pro Ser Asn Leu			
50	55	60	
Ser Val Phe Thr Ser Tyr Leu Asp Leu Ser Met Asn Asn Ile Ser Gln			
65	70	75	80
Leu Leu Pro Asn Pro Leu Pro Ser Leu Arg Phe Leu Glu Glu Leu Arg			
85	90	95	
Leu Ala Gly Asn Ala Leu Thr Tyr Val Pro Lys Gly Ala Phe Thr Gly			
100	105	110	
Leu Tyr Ser Leu Lys Val Leu Met Leu Gln Asn Asn Gln Leu Arg His			
115	120	125	
Val Pro Thr Glu Ala Leu Gln Asn Leu Arg Ser Leu Gln Ser Leu Arg			
130	135	140	
Leu Asp Ala Asn His Ile Ser Tyr Val Pro Pro Ser Cys Phe Ser Gly			
145	150	155	160
Leu His Ser Leu Arg His Leu Trp Leu Asp Asp Asn Ala Leu Thr Glu			
165	170	175	
Ile Pro Val Gln Ala Phe Arg Ser Leu Ser Ala Leu Gln Ala Met Thr			
180	185	190	
Leu Ala Leu Asn Lys Ile His His Ile Pro Asp Tyr Ala Phe Gly Asn			
195	200	205	
Leu Ser Ser Leu Val Val Leu His Leu His Asn Asn Arg Ile His Ser			
210	215	220	
Leu Gly Lys Lys Cys Phe Asp Gly Leu His Ser Leu Glu Thr Leu Asp			
225	230	235	240

270/518

Leu Asn Tyr Asn Asn Leu Asp Glu Phe Pro Thr Ala Ile Arg Thr Leu
 245 250 255
 Ser Asn Leu Lys Glu Leu Gly Phe His Ser Asn Asn Ile Arg Ser Ile
 260 265 270
 Pro Glu Lys Ala Phe Val Gly Asn Pro Ser Leu Ile Thr Ile His Phe
 275 280 285
 Tyr Asp Asn Pro Ile Gln Phe Val Gly Arg Ser Ala Phe Gln His Leu
 290 295 300
 Pro Glu Leu Arg Thr Leu Thr Leu Asn Gly Ala Ser Gln Ile Thr Glu
 305 310 315 320
 Phe Pro Asp Leu Thr Gly Thr Ala Asn Leu Glu Ser Leu Thr Leu Thr
 325 330 335
 Gly Ala Gln Ile Ser Ser Leu Pro Gln Thr Val Cys Asn Gln Leu Pro
 340 345 350
 Asn Leu Gln Val Leu Asp Leu Ser Tyr Asn Leu Leu Glu Asp Leu Pro
 355 360 365
 Ser Phe Ser Val Cys Gln Lys Leu Gln Lys Ile Asp Leu Arg His Asn
 370 375 380
 Glu Ile Tyr Glu Ile Lys Val Asp Thr Phe Gln Gln Leu Leu Ser Leu
 385 390 395 400
 Arg Ser Leu Asn Leu Ala Trp Asn Lys Ile Ala Ile Ile His Pro Asn
 405 410 415
 Ala Phe Ser Thr Leu Pro Ser Leu Ile Lys Leu Asp Leu Ser Ser Asn
 420 425 430
 Leu Leu Ser Ser Phe Pro Ile Thr Gly Leu His Gly Leu Thr His Leu
 435 440 445
 Lys Leu Thr Gly Asn His Ala Leu Gln Ser Leu Ile Ser Ser Glu Asn
 450 455 460
 Phe Pro Glu Leu Lys Val Ile Glu Met Pro Tyr Ala Tyr Gln Cys Cys

271/518

465	470	475	480
Ala Phe Gly Val Cys Glu Asn Ala Tyr Lys Ile Ser Asn Gln Trp Asn			
	485	490	495
Lys Gly Asp Asn Ser Ser Met Asp Asp Leu His Lys Lys Asp Ala Gly			
	500	505	510
Met Phe Gln Ala Gln Asp Glu Arg Asp Leu Glu Asp Phe Leu Leu Asp			
	515	520	525
Phe Glu Glu Asp Leu Lys Ala Leu His Ser Val Gln Cys Ser Pro Ser			
	530	535	540
Pro Gly Pro Phe Lys Pro Cys Glu His Leu Leu Asp Gly Trp Leu Ile			
	545	550	555
Arg Ile Gly Val Trp Thr Ile Ala Val Leu Ala Leu Thr Cys Asn Ala			
	565	570	575
Leu Val Thr Ser Thr Val Phe Arg Ser Pro Leu Tyr Ile Ser Pro Ile			
	580	585	590
Lys Leu Leu Ile Gly Val Ile Ala Ala Val Asn Met Leu Thr Gly Val			
	595	600	605
Ser Ser Ala Val Leu Ala Gly Val Asp Ala Phe Thr Phe Gly Ser Phe			
	610	615	620
Ala Arg His Gly Ala Trp Trp Glu Asn Gly Val Gly Cys His Val Ile			
	625	630	635
Gly Phe Leu Ser Ile Phe Ala Ser Glu Ser Ser Val Phe Leu Leu Thr			
	645	650	655
Leu Ala Ala Leu Glu Arg Gly Phe Ser Val Lys Tyr Ser Ala Lys Phe			
	660	665	670
Glu Thr Lys Ala Pro Phe Ser Ser Leu Lys Val Ile Ile Leu Leu Cys			
	675	680	685
Ala Leu Leu Ala Leu Thr Met Ala Ala Val Pro Leu Leu Gly Gly Ser			
	690	695	700

272/518

Lys Tyr Gly Ala Ser Pro Leu Cys Leu Pro Leu Pro Phe Gly Glu Pro
 705 710 715 720
 Ser Thr Met Gly Tyr Met Val Ala Leu Ile Leu Leu Asn Ser Leu Cys
 725 730 735
 Phe Leu Met Met Thr Ile Ala Tyr Thr Lys Leu Tyr Cys Asn Leu Asp
 740 745 750
 Lys Gly Asp Leu Glu Asn Ile Trp Asp Cys Ser Met Val Lys His Ile
 755 760 765
 Ala Leu Leu Leu Phe Thr Asn Cys Ile Leu Asn Cys Pro Val Ala Phe
 770 775 780
 Leu Ser Phe Ser Ser Leu Ile Asn Leu Thr Phe Ile Ser Pro Glu Val
 785 790 795 800
 Ile Lys Phe Ile Leu Leu Val Val Val Pro Leu Pro Ala Cys Leu Asn
 805 810 815
 Pro Leu Leu Tyr Ile Leu Phe Asn Pro His Phe Lys Glu Asp Leu Val
 820 825 830
 Ser Leu Arg Lys Gln Thr Tyr Val Trp Thr Arg Ser Lys His Pro Ser
 835 840 845
 Leu Met Ser Ile Asn Ser Asp Asp Val Glu Lys Gln Ser Cys Asp Ser
 850 855 860
 Thr Gln Ala Leu Val Thr Phe Thr Ser Ser Ser Ile Thr Tyr Asp Leu
 865 870 875 880
 Pro Pro Ser Ser Val Pro Ser Pro Ala Tyr Pro Val Thr Glu Ser Cys
 885 890 895
 His Leu Ser Ser Val Ala Phe Val Pro Cys Leu Ala Ser Lys Gly Glu
 900 905 910
 Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp
 915 920 925
 Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala

273/518

930	935	940
Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu		
945	950	955
Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Cys Tyr Gly Val Gln		
965	970	975
Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys		
980	985	990
Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys		
995	1000	1005
Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp		
1010	1015	1020
Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp		
1025	1030	1035
Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn		
1045	1050	1055
Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe		
1060	1065	1070
Lys Thr Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His		
1075	1080	1085
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp		
1090	1095	1100
Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu		
1105	1110	1115
Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile		
1125	1130	1135
Thr His Gly Met Asp Glu Leu Tyr Asn		
1140	1145	

<210> 104

274/518

<211> 560

<212> PRT

<213> Human

<400> 104

```

Met Asp Ser Thr Ile Pro Val Leu Gly Thr Glu Leu Thr Pro Ile Asn
      5              10              15
Gly Arg Glu Glu Thr Pro Cys Tyr Lys Gln Thr Leu Ser Phe Thr Gly
      20              25              30
Leu Thr Cys Ile Val Ser Leu Val Ala Leu Thr Gly Asn Ala Val Val
      35              40              45
Leu Trp Leu Leu Gly Cys Arg Met Arg Arg Asn Ala Val Ser Ile Tyr
      50              55              60
Ile Leu Asn Leu Val Ala Ala Asp Phe Leu Phe Leu Ser Gly His Ile
      65              70              75              80
Ile Cys Ser Pro Leu Arg Leu Ile Asn Ile Arg His Pro Ile Ser Lys
      85              90              95
Ile Leu Ser Pro Val Met Thr Phe Pro Tyr Phe Ile Gly Leu Ser Met
      100             105             110
Leu Ser Ala Ile Ser Thr Glu Arg Cys Leu Ser Ile Leu Trp Pro Ile
      115             120             125
Trp Tyr His Cys Arg Arg Pro Arg Tyr Leu Ser Ser Val Met Cys Val
      130             135             140
Leu Leu Trp Ala Leu Ser Leu Leu Arg Ser Ile Leu Glu Trp Met Phe
      145             150             155             160
Cys Asp Phe Leu Phe Ser Gly Ala Asp Ser Val Trp Cys Glu Thr Ser
      165             170             175
Asp Phe Ile Thr Ile Ala Trp Leu Val Phe Leu Cys Val Val Leu Cys
      180             185             190

```

275/518

Gly Ser Ser Leu Val Leu Leu Val Arg Ile Leu Cys Gly Ser Arg Lys
 195 200 205
 Met Pro Leu Thr Arg Leu Tyr Val Thr Ile Leu Leu Thr Val Leu Val
 210 215 220
 Phe Leu Leu Cys Gly Leu Pro Phe Gly Ile Gln Trp Ala Leu Phe Ser
 225 230 235 240
 Arg Ile His Leu Asp Trp Lys Val Leu Phe Cys His Val His Leu Val
 245 250 255
 Ser Ile Phe Leu Ser Ala Leu Asn Ser Ser Ala Asn Pro Ile Ile Tyr
 260 265 270
 Phe Phe Val Gly Ser Phe Arg Gln Arg Gln Asn Arg Gln Asn Leu Lys
 275 280 285
 Leu Val Leu Gln Arg Ala Leu Gln Asp Thr Pro Glu Val Asp Glu Gly
 290 295 300
 Gly Gly Trp Leu Pro Gln Glu Thr Leu Glu Leu Ser Gly Ser Arg Leu
 305 310 315 320
 Glu Gln Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile
 325 330 335
 Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser
 340 345 350
 Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe
 355 360 365
 Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr
 370 375 380
 Thr Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met
 385 390 395 400
 Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln
 405 410 415
 Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala

276/518

420	425	430	
Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys			
435	440	445	
Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu			
450	455	460	
Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys			
465	470	475	480
Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly			
485	490	495	
Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp			
500	505	510	
Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala			
515	520	525	
Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu			
530	535	540	
Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn			
545	550	555	560

<210> 105

<211> 568

<212> PRT

<213> Human

<400> 105

Met Asp Pro Thr Thr Pro Ala Trp Gly Thr Glu Ser Thr Thr Val Asn		
5	10	15
Gly Asn Asp Gln Ala Leu Leu Leu Leu Cys Gly Lys Glu Thr Leu Ile		
20	25	30
Pro Val Phe Leu Ile Leu Phe Ile Ala Leu Val Gly Leu Val Gly Asn		

277/518

35	40	45
Gly Phe Val Leu Trp Leu Leu Gly Phe Arg Met Arg Arg Asn Ala Phe		
50	55	60
Ser Val Tyr Val Leu Ser Leu Ala Gly Ala Asp Phe Leu Phe Leu Cys		
65	70	75
Phe Gln Ile Ile Asn Cys Leu Val Tyr Leu Ser Asn Phe Phe Cys Ser		
85	90	95
Ile Ser Ile Asn Phe Pro Ser Phe Phe Thr Thr Val Met Thr Cys Ala		
100	105	110
Tyr Leu Ala Gly Leu Ser Met Leu Ser Thr Val Ser Thr Glu Arg Cys		
115	120	125
Leu Ser Val Leu Trp Pro Ile Trp Tyr Arg Cys Arg Arg Pro Arg His		
130	135	140
Leu Ser Ala Val Val Cys Val Leu Leu Trp Ala Leu Ser Leu Leu Leu		
145	150	155
Ser Ile Leu Glu Gly Lys Phe Cys Gly Phe Leu Phe Ser Asp Gly Asp		
165	170	175
Ser Gly Trp Cys Gln Thr Phe Asp Phe Ile Thr Ala Ala Trp Leu Ile		
180	185	190
Phe Leu Phe Met Val Leu Cys Gly Ser Ser Leu Ala Leu Leu Val Arg		
195	200	205
Ile Leu Cys Gly Ser Arg Gly Leu Pro Leu Thr Arg Leu Tyr Leu Thr		
210	215	220
Ile Leu Leu Thr Val Leu Val Phe Leu Leu Cys Gly Leu Pro Phe Gly		
225	230	235
Ile Gln Trp Phe Leu Ile Leu Trp Ile Trp Lys Asp Ser Asp Val Leu		
245	250	255
Phe Cys His Ile His Pro Val Ser Val Val Leu Ser Ser Leu Asn Ser		
260	265	270

278/518

Ser Ala Asn Pro Ile Ile Tyr Phe Phe Val Gly Ser Phe Arg Lys Gln
 275 280 285
 Trp Arg Leu Gln Gln Pro Ile Leu Lys Leu Ala Leu Gln Arg Ala Leu
 290 295 300
 Gln Asp Ile Ala Glu Val Asp His Ser Glu Gly Cys Phe Arg Gln Gly
 305 310 315 320
 Thr Pro Glu Met Ser Arg Ser Ser Leu Val Ala Ser Lys Gly Glu Glu
 325 330 335
 Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val
 340 345 350
 Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr
 355 360 365
 Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
 370 375 380
 Val Pro Trp Pro Thr Leu Val Thr Thr Leu Cys Tyr Gly Val Gln Cys
 385 390 395 400
 Phe Ser Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
 405 410 415
 Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
 420 425 430
 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
 435 440 445
 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
 450 455 460
 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
 465 470 475 480
 Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
 485 490 495
 Thr Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr

279/518

500	505	510
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn		
515	520	525
His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys		
530	535	540
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr		
545	550	555
His Gly Met Asp Glu Leu Tyr Asn		560
565		

<210> 106

<211> 550

<212> PRT

<213> Human

<400> 106

Met Met Glu Pro Arg Glu Ala Gly Gln His Val Gly Ala Ala Asn Ser		
5	10	15
Ala Gln Glu Asp Val Ala Phe Asn Leu Ile Ile Leu Ser Leu Thr Glu		
20	25	30
Gly Leu Gly Leu Gly Gly Leu Leu Gly Asn Gly Ala Val Leu Trp Leu		
35	40	45
Leu Ser Ser Asn Val Tyr Arg Asn Pro Phe Ala Ile Tyr Leu Leu Asp		
50	55	60
Val Ala Cys Ala Asp Leu Ile Phe Leu Gly Cys His Met Val Ala Ile		
65	70	75
Val Pro Asp Leu Leu Gln Gly Arg Leu Asp Phe Pro Gly Phe Val Gln		
85	90	95
Thr Ser Leu Ala Thr Leu Arg Phe Phe Cys Tyr Ile Val Gly Leu Ser		

280/518

100	105	110
Leu Leu Ala Ala Val Ser Val Glu Gln Cys Leu Ala Ala Leu Phe Pro		
115	120	125
Ala Trp Tyr Ser Cys Arg Arg Pro Arg His Leu Thr Thr Cys Val Cys		
130	135	140
Ala Leu Thr Trp Ala Leu Cys Leu Leu Leu His Leu Leu Leu Ser Ser		
145	150	155
Ala Cys Thr Gln Phe Phe Gly Glu Pro Ser Arg His Leu Cys Arg Thr		
165	170	175
Leu Trp Leu Val Ala Ala Val Leu Leu Ala Leu Leu Cys Cys Thr Met		
180	185	190
Cys Gly Ala Ser Leu Met Leu Leu Leu Arg Val Glu Arg Gly Pro Gln		
195	200	205
Arg Pro Pro Pro Arg Gly Phe Pro Gly Leu Ile Leu Leu Thr Val Leu		
210	215	220
Leu Phe Leu Phe Cys Gly Leu Pro Phe Gly Ile Tyr Trp Leu Ser Arg		
225	230	235
Asn Leu Leu Trp Tyr Ile Pro His Tyr Phe Tyr His Phe Ser Phe Leu		
245	250	255
Met Ala Ala Val His Cys Ala Ala Lys Pro Val Val Tyr Phe Cys Leu		
260	265	270
Gly Ser Ala Gln Gly Arg Arg Leu Pro Leu Arg Leu Val Leu Gln Arg		
275	280	285
Ala Leu Gly Asp Glu Ala Glu Leu Gly Ala Val Arg Glu Thr Ser Arg		
290	295	300
Arg Gly Leu Val Asp Ile Ala Ala Ala Ser Lys Gly Glu Glu Leu Phe		
305	310	315
Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly		
325	330	335

281/518

His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly
 340 345 350
 Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro
 355 360 365
 Trp Pro Thr Leu Val Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe Ser
 370 375 380
 Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met
 385 390 395 400
 Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly
 405 410 415
 Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val
 420 425 430
 Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile
 435 440 445
 Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile
 450 455 460
 Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr Arg
 465 470 475 480
 His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln
 485 490 495
 Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr
 500 505 510
 Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp
 515 520 525
 His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly
 530 535 540
 Met Asp Glu Leu Tyr Asn
 545 550

282/518

<210> 107

<211> 561

<212> PRT

<213> Human

<400> 107

Met Pro Leu Pro Val Pro Pro Ala Gly Ala Gln Lys Thr Pro Glu Asp
 5 10 15
 His Val Cys Leu His Leu Ala Gly Pro Ser Pro Ala Pro Ser Glu Pro
 20 25 30
 Ala Arg Met Phe Gly Leu Phe Gly Leu Trp Arg Thr Phe Asp Ser Val
 35 40 45
 Val Phe Tyr Leu Thr Leu Ile Val Gly Leu Gly Gly Pro Val Gly Asn
 50 55 60
 Gly Leu Val Leu Trp Asn Leu Gly Phe Arg Ile Lys Lys Gly Pro Phe
 65 70 75 80
 Ser Ile Tyr Leu Leu His Leu Ala Ala Ala Asp Phe Leu Phe Leu Ser
 85 90 95
 Cys Arg Val Gly Phe Ser Val Ala Gln Ala Ala Leu Gly Ala Gln Asp
 100 105 110
 Thr Leu Tyr Phe Val Leu Thr Phe Leu Trp Phe Ala Val Gly Leu Trp
 115 120 125
 Leu Leu Ala Ala Phe Ser Val Glu Arg Cys Leu Ser Asp Leu Phe Pro
 130 135 140
 Ala Cys Tyr Gln Gly Cys Arg Pro Arg His Ala Ser Ala Val Leu Cys
 145 150 155 160
 Ala Leu Val Trp Thr Pro Thr Leu Pro Ala Val Pro Leu Pro Ala Asn
 165 170 175
 Ala Cys Gly Leu Leu Arg Asn Ser Ala Cys Pro Leu Val Cys Pro Arg

283/518

180	185	190
Tyr His Val Ala Ser Val Thr Trp Phe Leu Val Leu Ala Arg Val Ala		
195	200	205
Trp Thr Ala Gly Val Val Leu Phe Val Trp Val Thr Cys Cys Ser Thr		
210	215	220
Arg Pro Arg Pro Arg Leu Tyr Gly Ile Val Leu Gly Ala Leu Leu Leu		
225	230	235
Leu Phe Phe Cys Gly Leu Pro Ser Val Phe Tyr Trp Ser Leu Gln Pro		
245	250	255
Leu Leu Asn Phe Leu Leu Pro Val Phe Ser Pro Leu Ala Thr Leu Leu		
260	265	270
Ala Cys Val Asn Ser Ser Ser Lys Pro Leu Ile Tyr Ser Gly Leu Gly		
275	280	285
Arg Gln Pro Gly Lys Arg Glu Pro Leu Arg Ser Val Leu Arg Arg Ala		
290	295	300
Leu Gly Glu Gly Ala Glu Leu Gly Ala Arg Gly Gln Ser Leu Pro Met		
305	310	315
Gly Leu Leu Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro		
325	330	335
Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val		
340	345	350
Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys		
355	360	365
Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val		
370	375	380
Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His		
385	390	395
Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val		
405	410	415

284/518

Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg

420

425

430

Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu

435

440

445

Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu

450

455

460

Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln

465

470

475

480

Lys Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp

485

490

495

Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly

500

505

510

Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser

515

520

525

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu

530

535

540

Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr

545

550

555

560

Asn

<210> 108

<211> 591

<212> PRT

<213> Human

<400> 108

Met Glu His Thr His Ala His Leu Ala Ala Asn Ser Ser Leu Ser Trp

5

10

15

Trp Ser Pro Gly Ser Ala Cys Gly Leu Gly Phe Val Pro Val Val Tyr

285/518

20	25	30
Tyr Ser. Leu Leu Leu Cys Leu Gly Leu Pro Ala Asn Ile Leu Thr Val		
35	40	45
Ile Ile Leu Ser Gln Leu Val Ala Arg Arg Gln Lys Ser Ser Tyr Asn		
50	55	60
Tyr Leu Leu Ala Leu Ala Ala Ala Asp Ile Leu Val Leu Phe Phe Ile		
65	70	75
Val Phe Val Asp Phe Leu Leu Glu Asp Phe Ile Leu Asn Met Gln Met		
85	90	95
Pro Gln Val Pro Asp Lys Ile Ile Glu Val Leu Glu Phe Ser Ser Ile		
100	105	110
His Thr Ser Ile Trp Ile Thr Val Pro Leu Thr Ile Asp Arg Tyr Ile		
115	120	125
Ala Val Cys His Pro Leu Lys Tyr His Thr Val Ser Tyr Pro Ala Arg		
130	135	140
Thr Arg Lys Val Ile Val Ser Val Tyr Ile Thr Cys Phe Leu Thr Ser		
145	150	155
Ile Pro Tyr Tyr Trp Trp Pro Asn Ile Trp Thr Glu Asp Tyr Ile Ser		
165	170	175
Thr Ser Val His His Val Leu Ile Trp Ile His Cys Phe Thr Val Tyr		
180	185	190
Leu Val Pro Cys Ser Ile Phe Phe Ile Leu Asn Ser Ile Ile Val Tyr		
195	200	205
Lys Leu Arg Arg Lys Ser Asn Phe Arg Leu Arg Gly Tyr Ser Thr Gly		
210	215	220
Lys Thr Thr Ala Ile Leu Phe Thr Ile Thr Ser Ile Phe Ala Thr Leu		
225	230	235
Trp Ala Pro Arg Ile Ile Met Ile Leu Tyr His Leu Tyr Gly Ala Pro		
245	250	255

286/518

Ile Gln Asn Arg Trp Leu Val His Ile Met Ser Asp Ile Ala Asn Met
 260 265 270
 Leu Ala Leu Leu Asn Thr Ala Ile Asn Phe Phe Leu Tyr Cys Phe Ile
 275 280 285
 Ser Lys Arg Phe Arg Thr Met Ala Ala Ala Thr Leu Lys Ala Phe Phe
 290 295 300
 Lys Cys Gln Lys Gln Pro Val Gln Phe Tyr Thr Asn His Asn Phe Ser
 305 310 315 320
 Ile Thr Ser Ser Pro Trp Ile Ser Pro Ala Asn Ser His Cys Ile Lys
 325 330 335
 Met Leu Val Tyr Gln Tyr Asp Lys Asn Gly Lys Pro Ile Lys Val Ser
 340 345 350
 Pro Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 355 360 365
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 370 375 380
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 385 390 395 400
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 405 410 415
 Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 420 425 430
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 435 440 445
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 450 455 460
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 465 470 475 480
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr

287/518

	485		490		495
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn					
	500		505		510
Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser					
	515		520		525
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly					
	530		535		540
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu					
	545		550		555
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe					
	565		570		575
Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn					
	580		585		590

<210> 109

<211> 596

<212> PRT

<213> Human

<400> 109

Met Pro Ser Val Ser Pro Ala Gly Pro Ser Ala Gly Ala Val Pro Asn			
	5	10	15
Ala Thr Ala Val Thr Thr Val Arg Thr Asn Ala Ser Gly Leu Glu Val			
	20	25	30
Pro Leu Phe His Leu Phe Ala Arg Leu Asp Glu Glu Leu His Gly Thr			
	35	40	45
Phe Pro Gly Leu Trp Leu Ala Leu Met Ala Val His Gly Ala Ile Phe			
	50	55	60
Leu Ala Gly Leu Val Leu Asn Gly Leu Ala Leu Tyr Val Phe Cys Cys			

288/518

65	70	75	80
Arg Thr Arg Ala Lys Thr Pro Ser Val Ile Tyr Thr Ile Asn Leu Val			
85	90	95	
Val Thr Asp Leu Leu Val Gly Leu Ser Leu Pro Thr Arg Phe Ala Val			
100	105	110	
Tyr Tyr Gly Ala Arg Gly Cys Leu Arg Cys Ala Phe Pro His Val Leu			
115	120	125	
Gly Tyr Phe Leu Asn Met His Cys Ser Ile Leu Phe Leu Thr Cys Ile			
130	135	140	
Cys Val Asp Arg Tyr Leu Ala Ile Val Arg Pro Glu Gly Ser Arg Arg			
145	150	155	160
Cys Arg Gln Pro Ala Cys Ala Arg Ala Val Cys Ala Phe Val Trp Leu			
165	170	175	
Ala Ala Gly Ala Val Thr Leu Ser Val Leu Gly Val Thr Gly Ser Arg			
180	185	190	
Pro Cys Cys Arg Val Phe Ala Leu Thr Val Leu Glu Phe Leu Leu Pro			
195	200	205	
Leu Leu Val Ile Ser Val Phe Thr Gly Arg Ile Met Cys Ala Leu Ser			
210	215	220	
Arg Pro Gly Leu Leu Arg Gln Gly Arg Gln Arg Arg Val Arg Ala Met			
225	230	235	240
Gln Leu Leu Leu Thr Val Leu Ile Ile Phe Leu Val Cys Phe Thr Pro			
245	250	255	
Phe His Ala Arg Gln Val Ala Val Ala Leu Trp Pro Asp Met Pro His			
260	265	270	
His Thr Ser Leu Val Val Tyr His Val Ala Val Thr Leu Ser Ser Leu			
275	280	285	
Asn Ser Cys Met Asp Pro Ile Val Tyr Cys Phe Val Thr Ser Gly Phe			
290	295	300	

289/518

Gln Ala Thr Val Arg Gly Leu Phe Gly Gln His Gly Glu Arg Glu Pro
 305 310 315 320
 Ser Ser Gly Asp Val Val Ser Met His Arg Ser Ser Lys Gly Ser Gly
 325 330 335
 Arg His His Ile Leu Ser Ala Gly Pro His Ala Leu Thr Gln Ala Leu
 340 345 350
 Ala Asn Gly Pro Glu Ala Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly
 355 360 365
 Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys
 370 375 380
 Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu
 385 390 395 400
 Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro
 405 410 415
 Thr Leu Val Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr
 420 425 430
 Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu
 435 440 445
 Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr
 450 455 460
 Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg
 465 470 475 480
 Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly
 485 490 495
 His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala
 500 505 510
 Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn
 515 520 525
 Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr

290/518

530 535 540
 Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser
 545 550 555 560
 Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met
 565 570 575
 Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp
 580 585 590
 Glu Leu Tyr Asn
 595

<210> 110
 <211> 543
 <212> PRT
 <213> Human

<400> 110
 Met Pro Gly His Asn Thr Ser Arg Asn Ser Ser Cys Asp Pro Ile Val
 5 10 15
 Thr Pro His Leu Ile Ser Leu Tyr Phe Ile Val Leu Ile Gly Gly Leu
 20 25 30
 Val Gly Val Ile Ser Ile Leu Phe Leu Leu Val Lys Met Asn Thr Arg
 35 40 45
 Ser Val Thr Thr Met Ala Val Ile Asn Leu Val Val Val His Ser Val
 50 55 60
 Phe Leu Leu Thr Val Pro Phe Arg Leu Thr Tyr Leu Ile Lys Lys Thr
 65 70 75 80
 Trp Met Phe Gly Leu Pro Phe Cys Lys Phe Val Ser Ala Met Leu His
 85 90 95
 Ile His Met Tyr Leu Thr Phe Leu Phe Tyr Val Val Ile Leu Val Thr

291/518

100	105	110	
Arg Tyr Leu Ile Phe Phe Lys Cys Lys Asp Lys Val Glu Phe Tyr Arg			
115	120	125	
Lys Leu His Ala Val Ala Ala Ser Ala Gly Met Trp Thr Leu Val Ile			
130	135	140	
Val Ile Val Val Pro Leu Val Val Ser Arg Tyr Gly Ile His Glu Glu			
145	150	155	160
Tyr Asn Glu Glu His Cys Phe Lys Phe His Lys Glu Leu Ala Tyr Thr			
165	170	175	
Tyr Val Lys Ile Ile Asn Tyr Met Ile Val Ile Phe Val Ile Ala Val			
180	185	190	
Ala Val Ile Leu Leu Val Phe Gln Val Phe Ile Ile Met Leu Met Val			
195	200	205	
Gln Lys Leu Arg His Ser Leu Leu Ser His Gln Glu Phe Trp Ala Gln			
210	215	220	
Leu Lys Asn Leu Phe Phe Ile Gly Val Ile Leu Val Cys Phe Leu Pro			
225	230	235	240
Tyr Gln Phe Phe Arg Ile Tyr Tyr Leu Asn Val Val Thr His Ser Asn			
245	250	255	
Ala Cys Asn Ser Lys Val Ala Phe Tyr Asn Glu Ile Phe Leu Ser Val			
260	265	270	
Thr Ala Ile Ser Cys Tyr Asp Leu Leu Leu Phe Val Phe Gly Gly Ser			
275	280	285	
His Trp Phe Lys Gln Lys Ile Ile Gly Leu Trp Asn Cys Val Leu Cys			
290	295	300	
Arg Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu			
305	310	315	320
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly			
325	330	335	

292/518

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
340 345 350
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
355 360 365
Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
370 375 380
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
385 390 395 400
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
405 410 415
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
420 425 430
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
435 440 445
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
450 455 460
Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser
465 470 475 480
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
485 490 495
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
500 505 510
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
515 520 525
Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn
530 535 540

<210> 111

<211> 577

293/518

<212> PRT

<213> Human

<400> 111

Met	Asn	Glu	Pro	Leu	Asp	Tyr	Leu	Ala	Asn	Ala	Ser	Asp	Phe	Pro	Asp
			5						10					15	
Tyr	Ala	Ala	Ala	Phe	Gly	Asn	Cys	Thr	Asp	Glu	Asn	Ile	Pro	Leu	Lys
			20					25					30		
Met	His	Tyr	Leu	Pro	Val	Ile	Tyr	Gly	Ile	Ile	Phe	Leu	Val	Gly	Phe
			35					40				45			
Pro	Gly	Asn	Ala	Val	Val	Ile	Ser	Thr	Tyr	Ile	Phe	Lys	Met	Arg	Pro
			50				55					60			
Trp	Lys	Ser	Ser	Thr	Ile	Ile	Met	Leu	Asn	Leu	Ala	Cys	Thr	Asp	Leu
			65			70				75				80	
Leu	Tyr	Leu	Thr	Ser	Leu	Pro	Phe	Leu	Ile	His	Tyr	Tyr	Ala	Ser	Gly
				85					90					95	
Glu	Asn	Trp	Ile	Phe	Gly	Asp	Phe	Met	Cys	Lys	Phe	Ile	Arg	Phe	Ser
				100				105					110		
Phe	His	Phe	Asn	Leu	Tyr	Ser	Ser	Ile	Leu	Phe	Leu	Thr	Cys	Phe	Ser
				115				120					125		
Ile	Phe	Arg	Tyr	Cys	Val	Ile	Ile	His	Pro	Met	Ser	Cys	Phe	Ser	Ile
				130				135					140		
His	Lys	Thr	Arg	Cys	Ala	Val	Val	Ala	Cys	Ala	Val	Val	Trp	Ile	Ile
				145			150			155				160	
Ser	Leu	Val	Ala	Val	Ile	Pro	Met	Thr	Phe	Leu	Ile	Thr	Ser	Thr	Asn
					165				170					175	
Arg	Thr	Asn	Arg	Ser	Ala	Cys	Leu	Asp	Leu	Thr	Ser	Ser	Asp	Glu	Leu
				180					185					190	
Asn	Thr	Ile	Lys	Trp	Tyr	Asn	Leu	Ile	Leu	Thr	Ala	Thr	Thr	Phe	Cys

294/518

195	200	205
Leu Pro Leu Val Ile Val Thr Leu Cys Tyr Thr Thr Ile Ile His Thr		
210	215	220
Leu Thr His Gly Leu Gln Thr Asp Ser Cys Leu Lys Gln Lys Ala Arg		
225	230	235
Arg Leu Thr Ile Leu Leu Leu Leu Ala Phe Tyr Val Cys Phe Leu Pro		
245	250	255
Phe His Ile Leu Arg Val Ile Arg Ile Glu Ser Arg Leu Leu Ser Ile		
260	265	270
Ser Cys Ser Ile Glu Asn Gln Ile His Glu Ala Tyr Ile Val Ser Arg		
275	280	285
Pro Leu Ala Ala Leu Asn Thr Phe Gly Asn Leu Leu Leu Tyr Val Val		
290	295	300
Val Ser Asp Asn Phe Gln Gln Ala Val Cys Ser Thr Val Arg Cys Lys		
305	310	315
Val Ser Gly Asn Leu Glu Gln Ala Lys Lys Ile Ser Tyr Ser Asn Asn		
325	330	335
Pro Ala Ser Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro		
340	345	350
Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val		
355	360	365
Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys		
370	375	380
Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val		
385	390	395
Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe*Ser Arg Tyr Pro Asp His		
405	410	415
Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val		
420	425	430

295/518

Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg
 435 440 445
 Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu
 450 455 460
 Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu
 465 470 475 480
 Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
 485 490 495
 Lys Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp
 500 505 510
 Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
 515 520 525
 Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser
 530 535 540
 Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
 545 550 555 560
 Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr
 565 570 575

Asn

<210> 112

<211> 569

<212> PRT

<213> Human

<400> 112

Met Ile Thr Leu Asn Asn Gln Asp Gln Pro Val Pro Phe Asn Ser Ser
 5 10 15
 His Pro Asp Glu Tyr Lys Ile Ala Ala Leu Val Phe Tyr Ser Cys Ile

	20		25		30
Phe Ile Ile Gly Leu Phe Val Asn Ile Thr Ala Leu Trp Val Phe Ser					
35		40		45	
Cys Thr Thr Lys Lys Arg Thr Thr Val Thr Ile Tyr Met Met Asn Val					
50		55		60	
Ala Leu Val Asp Leu Ile Phe Ile Met Thr Leu Pro Phe Arg Met Phe					
65		70		75	80
Tyr Tyr Ala Lys Asp Glu Trp Pro Phe Gly Glu Tyr Phe Cys Gln Ile					
	85		90		95
Leu Gly Ala Leu Thr Val Phe Tyr Pro Ser Ile Ala Leu Trp Leu Leu					
100		105		110	
Ala Phe Ile Ser Ala Asp Arg Tyr Met Ala Ile Val Gln Pro Lys Tyr					
115		120		125	
Ala Lys Glu Leu Lys Asn Thr Cys Lys Ala Val Leu Ala Cys Val Gly					
130		135		140	
Val Trp Ile Met Thr Leu Thr Thr Thr Thr Pro Leu Leu Leu Tyr					
145		150		155	160
Lys Asp Pro Asp Lys Asp Ser Thr Pro Ala Thr Cys Leu Lys Ile Ser					
	165		170		175
Asp Ile Ile Tyr Leu Lys Ala Val Asn Val Leu Asn Leu Thr Arg Leu					
180		185		190	
Thr Phe Phe Phe Leu Ile Pro Leu Phe Ile Met Ile Gly Cys Tyr Leu					
195		200		205	
Val Ile Ile His Asn Leu Leu His Gly Arg Thr Ser Lys Leu Lys Pro					
210		215		220	
Lys Val Lys Glu Lys Ser Ile Arg Ile Ile Ile Thr Leu Leu Val Gln					
225		230		235	240
Val Leu Val Cys Phe Met Pro Phe His Ile Cys Phe Ala Phe Leu Met					
	245		250		255

297/518

Leu Gly Thr Gly Glu Asn Ser Tyr Asn Pro Trp Gly Ala Phe Thr Thr
 260 265 270
 Phe Leu Met Asn Leu Ser Thr Cys Leu Asp Val Ile Leu Tyr Tyr Ile
 275 280 285
 Val Ser Lys Gln Phe Gln Ala Arg Val Ile Ser Val Met Leu Tyr Arg
 290 295 300
 Asn Tyr Leu Arg Ser Met Arg Arg Lys Ser Phe Arg Ser Gly Ser Leu
 305 310 315 320
 Arg Ser Leu Ser Asn Ile Asn Ser Glu Met Leu Ala Ser Lys Gly Glu
 325 330 335
 Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp
 340 345 350
 Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala
 355 360 365
 Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu
 370 375 380
 Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Cys Tyr Gly Val Gln
 385 390 395 400
 Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys
 405 410 415
 Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys
 420 425 430
 Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
 435 440 445
 Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
 450 455 460
 Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn
 465 470 475 480
 Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe

298/518

	485		490		495
Lys Thr Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His					
	500		505		510
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp					
	515		520		525
Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu					
	530		535		540
Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile					
	545		550		555
Thr His Gly Met Asp Glu Leu Tyr Asn					560
	565				

<210> 113

<211> 787

<212> PRT

<213> Human

<400> 113

Met Ala Thr Pro Arg Gly Leu Gly Ala Leu Leu Leu Leu Leu Leu			
	5	10	15
Pro Thr Ser Gly Gln Glu Lys Pro Thr Glu Gly Pro Arg Asn Thr Cys			
	20	25	30
Leu Gly Ser Asn Asn Met Tyr Asp Ile Phe Asn Leu Asn Asp Lys Ala			
	35	40	45
Leu Cys Phe Thr Lys Cys Arg Gln Ser Gly Ser Asp Ser Cys Asn Val			
	50	55	60
Glu Asn Leu Gln Arg Tyr Trp Leu Asn Tyr Glu Ala His Leu Met Lys			
	65	70	75
Glu Gly Leu Thr Gln Lys Val Asn Thr Pro Phe Leu Lys Ala Leu Val			80

299/518

	85	90	95
Gln Asn Leu Ser Thr Asn Thr Ala Glu Asp Phe Tyr Phe Ser Leu Glu			
100	105	110	
Pro Ser Gln Val Pro Arg Gln Val Met Lys Asp Glu Asp Lys Pro Pro			
115	120	125	
Asp Arg Val Arg Leu Pro Lys Ser Leu Phe Arg Ser Leu Pro Gly Asn			
130	135	140	
Arg Ser Val Val Arg Leu Ala Val Thr Ile Leu Asp Ile Gly Pro Gly			
145	150	155	160
Thr Leu Phe Lys Gly Pro Arg Leu Gly Leu Gly Asp Gly Ser Gly Val			
165	170	175	
Leu Asn Asn Arg Leu Val Gly Leu Ser Val Gly Gln Met His Val Thr			
180	185	190	
Lys Leu Ala Glu Pro Leu Glu Ile Val Phe Ser His Gln Arg Pro Pro			
195	200	205	
Pro Asn Met Thr Leu Thr Cys Val Phe Trp Asp Val Thr Lys Gly Thr			
210	215	220	
Thr Gly Asp Trp Ser Ser Glu Gly Cys Ser Thr Glu Val Arg Pro Glu			
225	230	235	240
Gly Thr Val Cys Cys Cys Asp His Leu Thr Phe Phe Ala Leu Leu Leu			
245	250	255	
Arg Pro Thr Leu Asp Gln Ser Thr Val His Ile Leu Thr Arg Ile Ser			
260	265	270	
Gln Ala Gly Cys Gly Val Ser Met Ile Phe Leu Ala Phe Thr Ile Ile			
275	280	285	
Leu Tyr Ala Phe Leu Arg Leu Ser Arg Glu Arg Phe Lys Ser Glu Asp			
290	295	300	
Ala Pro Lys Ile His Val Ala Leu Gly Gly Ser Leu Phe Leu Leu Asn			
305	310	315	320

300/518

Leu Ala Phe Leu Val Asn Val Gly Ser Gly Ser Lys Gly Ser Asp Ala
 325 330 335
 Ala Cys Trp Ala Arg Gly Ala Val Phe His Tyr Phe Leu Leu Cys Ala
 340 345 350
 Phe Thr Trp Met Gly Leu Glu Ala Phe His Leu Tyr Leu Leu Ala Val
 355 360 365
 Arg Val Phe Asn Thr Tyr Phe Gly His Tyr Phe Leu Lys Leu Ser Leu
 370 375 380
 Val Gly Trp Gly Leu Pro Ala Leu Met Val Ile Gly Thr Gly Ser Ala
 385 390 395 400
 Asn Ser Tyr Gly Leu Tyr Thr Ile Arg Asp Arg Glu Asn Arg Thr Ser
 405 410 415
 Leu Glu Leu Cys Trp Phe Arg Glu Gly Thr Thr Met Tyr Ala Leu Tyr
 420 425 430
 Ile Thr Val His Gly Tyr Phe Leu Ile Thr Phe Leu Phe Gly Met Val
 435 440 445
 Val Leu Ala Leu Val Val Trp Lys Ile Phe Thr Leu Ser Arg Ala Thr
 450 455 460
 Ala Val Lys Glu Arg Gly Lys Asn Arg Lys Lys Val Leu Thr Leu Leu
 465 470 475 480
 Gly Leu Ser Ser Leu Val Gly Val Thr Trp Gly Leu Ala Ile Phe Thr
 485 490 495
 Pro Leu Gly Leu Ser Thr Val Tyr Ile Phe Ala Leu Phe Asn Ser Leu
 500 505 510
 Gln Gly Val Phe Ile Cys Cys Trp Phe Thr Ile Leu Tyr Leu Pro Ser
 515 520 525
 Gln Ser Thr Thr Val Ser Ser Ser Thr Ala Arg Leu Asp Gln Ala His
 530 535 540
 Ser Ala Ser Gln Glu Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val

301/518

545	550	555	560
Val Pro Ile Leu Val	Glu Leu Asp Gly Asp Val	Asn Gly His Lys Phe	
	565	570	575
Ser Val Ser Gly Glu Gly Glu Gly	Asp Ala Thr Tyr Gly Lys Leu Thr		
	580	585	590
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr			
	595	600	605
Leu Val Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro			
	610	615	620
Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly			
625	630	635	640
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys			
	645	650	655
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile			
	660	665	670
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His			
	675	680	685
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp			
	690	695	700
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile			
705	710	715	720
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro			
	725	730	735
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr			
	740	745	750
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val			
	755	760	765
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu			
	770	775	780

302/518

Leu Tyr Asn

785

<210> 114

<211> 608

<212> PRT

<213> Human

<400> 114

Met Gly Asp Arg Arg Phe Ile Asp Phe Gln Phe Gln Asp Ser Asn Ser

5

10

15

Ser Leu Arg Pro Arg Leu Gly Asn Ala Thr Ala Asn Asn Thr Cys Ile

20

25

30

Val Asp Asp Ser Phe Lys Tyr Asn Leu Asn Gly Ala Val Tyr Ser Val

35

40

45

Val Phe Ile Leu Gly Leu Ile Thr Asn Ser Val Ser Leu Phe Val Phe

50

55

60

Cys Phe Arg Met Lys Met Arg Ser Glu Thr Ala Ile Phe Ile Thr Asn

65

70

75

80

Leu Ala Val Ser Asp Leu Leu Phe Val Cys Thr Leu Pro Phe Lys Ile

85

90

95

Phe Tyr Asn Phe Asn Arg His Trp Pro Phe Gly Asp Thr Leu Cys Lys

100

105

110

Ile Ser Gly Thr Ala Phe Leu Thr Asn Ile Tyr Gly Ser Met Leu Phe

115

120

125

Leu Thr Cys Ile Ser Val Asp Arg Phe Leu Ala Ile Val Tyr Pro Phe

130

135

140

Arg Ser Arg Thr Ile Arg Thr Arg Arg Asn Ser Ala Ile Val Cys Ala

145

150

155

160

303/518

Gly Val Trp Ile Leu Val Leu Ser Gly Gly Ile Ser Ala Ser Leu Phe
 165 170 175
 Ser Thr Thr Asn Val Asn Asn Ala Thr Thr Thr Cys Phe Glu Gly Phe
 180 185 190
 Ser Lys Arg Val Trp Lys Thr Tyr Leu Ser Lys Ile Thr Ile Phe Ile
 195 200 205
 Glu Val Val Gly Phe Ile Ile Pro Leu Ile Leu Asn Val Ser Cys Ser
 210 215 220
 Ser Val Val Leu Arg Thr Leu Arg Lys Pro Ala Thr Leu Ser Gln Ile
 225 230 235 240
 Gly Thr Asn Lys Lys Lys Val Leu Lys Met Ile Thr Val His Met Ala
 245 250 255
 Val Phe Val Val Cys Phe Val Pro Tyr Asn Ser Val Leu Phe Leu Tyr
 260 265 270
 Ala Leu Val Arg Ser Gln Ala Ile Thr Asn Cys Phe Leu Glu Arg Phe
 275 280 285
 Ala Lys Ile Met Tyr Pro Ile Thr Leu Cys Leu Ala Thr Leu Asn Cys
 290 295 300
 Cys Phe Asp Pro Phe Ile Tyr Tyr Phe Thr Leu Glu Ser Phe Gln Lys
 305 310 315 320
 Ser Phe Tyr Ile Asn Ala His Ile Arg Met Glu Ser Leu Phe Lys Thr
 325 330 335
 Glu Thr Pro Leu Thr Thr Lys Pro Ser Leu Pro Ala Ile Gln Glu Glu
 340 345 350
 Val Ser Asp Gln Thr Thr Asn Asn Gly Gly Glu Leu Met Leu Glu Ser
 355 360 365
 Thr Phe Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile
 370 375 380
 Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser

304/518

385	390	395	400
Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe			
405	410	415	
Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr			
420	425	430	
Thr Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met			
435	440	445	
Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln			
450	455	460	
Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala			
465	470	475	480
Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys			
485	490	495	
Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu			
500	505	510	
Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys			
515	520	525	
Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly			
530	535	540	
Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp			
545	550	555	560
Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala			
565	570	575	
Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu			
580	585	590	
Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn			
595	600	605	

<210> 115

305/518

<211> 577

<212> PRT

<213> Human

<400> 115

Met	Ala	Asn	Leu	Asp	Lys	Tyr	Thr	Glu	Thr	Phe	Lys	Met	Gly	Ser	Asn
			5						10					15	
Ser	Thr	Ser	Thr	Ala	Glu	Ile	Tyr	Cys	Asn	Val	Thr	Asn	Val	Lys	Phe
			20					25					30		
Gln	Tyr	Ser	Leu	Tyr	Ala	Thr	Thr	Tyr	Ile	Leu	Ile	Phe	Ile	Pro	Gly
			35					40					45		
Leu	Leu	Ala	Asn	Ser	Ala	Ala	Leu	Trp	Val	Leu	Cys	Arg	Phe	Ile	Ser
			50				55					60			
Lys	Lys	Asn	Lys	Ala	Ile	Ile	Phe	Met	Ile	Asn	Leu	Ser	Val	Ala	Asp
			65			70				75				80	
Leu	Ala	His	Val	Leu	Ser	Leu	Pro	Leu	Arg	Ile	Tyr	Tyr	Tyr	Ile	Ser
				85					90					95	
His	His	Trp	Pro	Phe	Gln	Arg	Ala	Leu	Cys	Leu	Leu	Cys	Phe	Tyr	Leu
			100					105					110		
Lys	Tyr	Leu	Asn	Met	Tyr	Ala	Ser	Ile	Cys	Phe	Leu	Thr	Cys	Ile	Ser
			115					120					125		
Leu	Gln	Arg	Cys	Phe	Phe	Leu	Leu	Lys	Pro	Phe	Arg	Ala	Arg	Asp	Trp
			130				135					140			
Lys	Arg	Arg	Tyr	Asp	Val	Gly	Ile	Ser	Ala	Ala	Ile	Trp	Ile	Val	Val
			145				150				155			160	
Gly	Thr	Ala	Cys	Leu	Pro	Phe	Pro	Ile	Leu	Arg	Ser	Thr	Asp	Leu	Asn
				165					170					175	
Asn	Asn	Lys	Ser	Cys	Phe	Ala	Asp	Leu	Gly	Tyr	Lys	Gln	Met	Asn	Ala
			180						185					190	

306/518

Val Ala Leu Val Gly Met Ile Thr Val Ala Glu Leu Ala Gly Phe Val
 195 200 205
 Ile Pro Val Ile Ile Ile Ala Trp Cys Thr Trp Lys Thr Thr Ile Ser
 210 215 220
 Leu Arg Gln Pro Pro Met Ala Phe Gln Gly Ile Ser Glu Arg Gln Lys
 225 230 235 240
 Ala Leu Arg Met Val Phe Met Cys Ala Ala Val Phe Phe Ile Cys Phe
 245 250 255
 Thr Pro Tyr His Ile Asn Phe Ile Phe Tyr Thr Met Val Lys Glu Thr
 260 265 270
 Ile Ile Ser Ser Cys Pro Val Val Arg Ile Ala Leu Tyr Phe His Pro
 275 280 285
 Phe Cys Leu Cys Leu Ala Ser Leu Cys Cys Leu Leu Asp Pro Ile Leu
 290 295 300
 Tyr Tyr Phe Met Ala Ser Glu Phe Arg Asp Gln Leu Ser Arg His Gly
 305 310 315 320
 Ser Ser Val Thr Arg Ser Arg Leu Met Ser Lys Glu Ser Gly Ser Ser
 325 330 335
 Met Ile Gly Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro
 340 345 350
 Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val
 355 360 365
 Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys
 370 375 380
 Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val
 385 390 395 400
 Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His
 405 410 415
 Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val

307/518

420	425	430	
Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg			
435	440	445	
Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu			
450	455	460	
Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu			
465	470	475	480
Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln			
485	490	495	
Lys Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp			
500	505	510	
Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly			
515	520	525	
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser			
530	535	540	
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu			
545	550	555	560
Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr			
565	570	575	
Asn			

<210> 116

<211> 851

<212> PRT

<213> Human

<400> 116

Met Arg Ala Pro Gly Ala Leu Leu Ala Arg Met Ser Arg Leu Leu Leu

5

10

15

308/518

Leu Leu Leu Leu Lys Val Ser Ala Ser Ser Ala Leu Gly Val Ala Pro
 20 25 30
 Ala Ser Arg Asn Glu Thr Cys Leu Gly Glu Ser Cys Ala Pro Thr Val
 35 40 45
 Ile Gln Arg Arg Gly Arg Asp Ala Trp Gly Pro Gly Asn Ser Ala Arg
 50 55 60
 Asp Val Leu Arg Ala Arg Ala Pro Arg Glu Glu Gln Gly Ala Ala Phe
 65 70 75 80
 Leu Ala Gly Pro Ser Trp Asp Leu Pro Ala Ala Pro Gly Arg Asp Pro
 85 90 95
 Ala Ala Gly Arg Gly Ala Glu Ala Ser Ala Ala Gly Pro Pro Gly Pro
 100 105 110
 Pro Thr Arg Pro Pro Gly Pro Trp Arg Trp Lys Gly Ala Arg Gly Gln
 115 120 125
 Glu Pro Ser Glu Thr Leu Gly Arg Gly Asn Pro Thr Ala Leu Gln Leu
 130 135 140
 Phe Leu Gln Ile Ser Glu Glu Glu Glu Lys Gly Pro Arg Gly Ala Gly
 145 150 155 160
 Ile Ser Gly Arg Ser Gln Glu Gln Ser Val Lys Thr Val Pro Gly Ala
 165 170 175
 Ser Asp Leu Phe Tyr Trp Pro Arg Arg Ala Gly Lys Leu Gln Gly Ser
 180 185 190
 His His Lys Pro Leu Ser Lys Thr Ala Asn Gly Leu Ala Gly His Glu
 195 200 205
 Gly Trp Thr Ile Ala Leu Pro Gly Arg Ala Leu Ala Gln Asn Gly Ser
 210 215 220
 Leu Gly Glu Gly Ile His Glu Pro Gly Gly Pro Arg Arg Gly Asn Ser
 225 230 235 240
 Thr Asn Arg Arg Val Arg Leu Lys Asn Pro Phe Tyr Pro Leu Thr Gln

309/518

	245	250	255
Glu Ser Tyr Gly Ala Tyr Ala Val Met Cys Leu Ser Val Val Ile Phe			
	260	265	270
Gly Thr Gly Ile Ile Gly Asn Leu Ala Val Met Cys Ile Val Cys His			
	275	280	285
Asn Tyr Tyr Met Arg Ser Ile Ser Asn Ser Leu Leu Ala Asn Leu Ala			
	290	295	300
Phe Trp Asp Phe Leu Ile Ile Phe Phe Cys Leu Pro Leu Val Ile Phe			
	305	310	315
His Glu Leu Thr Lys Lys Trp Leu Leu Glu Asp Phe Ser Cys Lys Ile			
	325	330	335
Val Pro Tyr Ile Glu Val Ala Ser Leu Gly Val Thr Thr Phe Thr Leu			
	340	345	350
Cys Ala Leu Cys Ile Asp Arg Phe Arg Ala Ala Thr Asn Val Gln Met			
	355	360	365
Tyr Tyr Glu Met Ile Glu Asn Cys Ser Ser Thr Thr Ala Lys Leu Ala			
	370	375	380
Val Ile Trp Val Gly Ala Leu Leu Leu Ala Leu Pro Glu Val Val Leu			
	385	390	395
Arg Gln Leu Ser Lys Glu Asp Leu Gly Phe Ser Gly Arg Ala Pro Ala			
	405	410	415
Glu Arg Cys Ile Ile Lys Ile Ser Pro Asp Leu Pro Asp Thr Ile Tyr			
	420	425	430
Val Leu Ala Leu Thr Tyr Asp Ser Ala Arg Leu Trp Trp Tyr Phe Gly			
	435	440	445
Cys Tyr Phe Cys Leu Pro Thr Leu Phe Thr Ile Thr Cys Ser Leu Val			
	450	455	460
Thr Ala Arg Lys Ile Arg Lys Ala Glu Lys Ala Cys Thr Arg Gly Asn			
	465	470	475
			480

310/518

Lys Arg Gln Ile Gln Leu Glu Ser Gln Met Asn Cys Thr Val Val Ala
 485 490 495
 Leu Thr Ile Leu Tyr Gly Phe Cys Ile Ile Pro Glu Asn Ile Cys Asn
 500 505 510
 Ile Val Thr Ala Tyr Met Ala Thr Gly Val Ser Gln Gln Thr Met Asp
 515 520 525
 Leu Leu Asn Ile Ile Ser Gln Phe Leu Leu Phe Phe Lys Ser Cys Val
 530 535 540
 Thr Pro Val Leu Leu Phe Cys Leu Cys Lys Pro Phe Ser Arg Ala Phe
 545 550 555 560
 Met Glu Cys Cys Cys Cys Cys Cys Glu Glu Cys Ile Gln Lys Ser Ser
 565 570 575
 Thr Val Thr Ser Asp Asp Asn Asp Asn Glu Tyr Thr Thr Glu Leu Glu
 580 585 590
 Leu Ser Pro Phe Ser Thr Ile Arg Arg Glu Met Ser Thr Phe Ala Ser
 595 600 605
 Val Gly Thr His Cys Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 610 615 620
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 625 630 635 640
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 645 650 655
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 660 665 670
 Leu Val Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 675 680 685
 Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 690 695 700
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys

311/518

705	710	715	720
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile			
	725	730	735
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His			
	740	745	750
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp			
	755	760	765
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile			
	770	775	780
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro			
785	790	795	800
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr			
	805	810	815
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val			
	820	825	830
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu			
	835	840	845
Leu Tyr Asn			
850			

<210> 117

<211> 719

<212> PRT

<213> Human

<400> 117

Met Arg Trp Leu Trp Pro Leu Ala Val Ser Leu Ala Val Ile Leu Ala		
	5	10
Val Gly Leu Ser Arg Val Ser Gly Gly Ala Pro Leu His Leu Gly Arg		15

312/518

20	25	30
His Arg Ala Glu Thr Gln Glu Gln Gln Ser Arg Ser Lys Arg Gly Thr		
35	40	45
Glu Asp Glu Glu Ala Lys Gly Val Gln Gln Tyr Val Pro Glu Glu Trp		
50	55	60
Ala Glu Tyr Pro Arg Pro Ile His Pro Ala Gly Leu Gln Pro Thr Lys		
65	70	75
Pro Leu Val Ala Thr Ser Pro Asn Pro Asp Lys Asp Gly Gly Thr Pro		
85	90	95
Asp Ser Gly Gln Glu Leu Arg Gly Asn Leu Thr Gly Ala Pro Gly Gln		
100	105	110
Arg Leu Gln Ile Gln Asn Pro Leu Tyr Pro Val Thr Glu Ser Ser Tyr		
115	120	125
Ser Ala Tyr Ala Ile Met Leu Leu Ala Leu Val Val Phe Ala Val Gly		
130	135	140
Ile Val Gly Asn Leu Ser Val Met Cys Ile Val Trp His Ser Tyr Tyr		
145	150	155
Leu Lys Ser Ala Trp Asn Ser Ile Leu Ala Ser Leu Ala Leu Trp Asp		
165	170	175
Phe Leu Val Leu Phe Phe Cys Leu Pro Ile Val Ile Phe Asn Glu Ile		
180	185	190
Thr Lys Gln Arg Leu Leu Gly Asp Val Ser Cys Arg Ala Val Pro Phe		
195	200	205
Met Glu Val Ser Ser Leu Gly Val Thr Thr Phe Ser Leu Cys Ala Leu		
210	215	220
Gly Ile Asp Arg Phe His Val Ala Thr Ser Thr Leu Pro Lys Val Arg		
225	230	235
Pro Ile Glu Arg Cys Gln Ser Ile Leu Ala Lys Leu Ala Val Ile Trp		
245	250	255

313/518

Val Gly Ser Met Thr Leu Ala Val Pro Glu Leu Leu Leu Trp Gln Leu
 260 265 270
 Ala Gln Glu Pro Ala Pro Thr Met Gly Thr Leu Asp Ser Cys Ile Met
 275 280 285
 Lys Pro Ser Ala Ser Leu Pro Glu Ser Leu Tyr Ser Leu Val Met Thr
 290 295 300
 Tyr Gln Asn Ala Arg Met Trp Trp Tyr Phe Gly Cys Tyr Phe Cys Leu
 305 310 315 320
 Pro Ile Leu Phe Thr Val Thr Cys Gln Leu Val Thr Trp Arg Val Arg
 325 330 335
 Gly Pro Pro Gly Arg Lys Ser Glu Cys Arg Ala Ser Lys His Glu Gln
 340 345 350
 Cys Glu Ser Gln Leu Asn Ser Thr Val Val Gly Leu Thr Val Val Tyr
 355 360 365
 Ala Phe Cys Thr Leu Pro Glu Asn Val Cys Asn Ile Val Val Ala Tyr
 370 375 380
 Leu Ser Thr Glu Leu Thr Arg Gln Thr Leu Asp Leu Leu Gly Leu Ile
 385 390 395 400
 Asn Gln Phe Ser Thr Phe Phe Lys Gly Ala Ile Thr Pro Val Leu Leu
 405 410 415
 Leu Cys Ile Cys Arg Pro Leu Gly Gln Ala Phe Leu Asp Cys Cys Cys
 420 425 430
 Cys Cys Cys Cys Glu Glu Cys Gly Gly Ala Ser Glu Ala Ser Ala Ala
 435 440 445
 Asn Gly Ser Asp Asn Lys Leu Lys Thr Glu Val Ser Ser Ser Ile Tyr
 450 455 460
 Phe His Lys Pro Arg Glu Ser Pro Pro Leu Leu Pro Leu Gly Thr Pro
 465 470 475 480
 Cys Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu

314/518

485	490	495
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly		
500	505	510
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile		
515	520	525
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr		
530	535	540
Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys		
545	550	555
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu		
565	570	575
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu		
580	585	590
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly		
595	600	605
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr		
610	615	620
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn		
625	630	635
Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser		
645	650	655
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly		
660	665	670
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu		
675	680	685
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe		
690	695	700
Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn		
705	710	715

315/518

<210> 118

<211> 591

<212> PRT

<213> Human

<400> 118

Met Glu Thr Asn Phe Ser Ile Pro Leu Asn Glu Thr Glu Glu Val Leu

5

10

15

Pro Glu Pro Ala Gly His Thr Val Leu Trp Ile Phe Ser Leu Leu Val

20

25

30

His Gly Val Thr Phe Val Phe Gly Val Leu Gly Asn Gly Leu Val Ile

35

40

45

Trp Val Ala Gly Phe Arg Met Thr Arg Thr Val Asn Thr Ile Cys Tyr

50

55

60

Leu Asn Leu Ala Leu Ala Asp Phe Ser Phe Ser Ala Ile Leu Pro Phe

65

70

75

80

Arg Met Val Ser Val Ala Met Arg Glu Lys Trp Pro Phe Gly Ser Phe

85

90

95

Leu Cys Lys Leu Val His Val Met Ile Asp Ile Asn Leu Phe Val Ser

100

105

110

Val Tyr Leu Ile Thr Ile Ile Ala Leu Asp Arg Cys Ile Cys Val Leu

115

120

125

His Pro Ala Trp Ala Gln Asn His Arg Thr Met Ser Leu Ala Lys Arg

130

135

140

Val Met Thr Gly Leu Trp Ile Phe Thr Ile Val Leu Thr Leu Pro Asn

145

150

155

160

Phe Ile Phe Trp Thr Thr Ile Ser Thr Thr Asn Gly Asp Thr Tyr Cys

165

170

175

316/518

Ile Phe Asn Phe Ala Phe Trp Gly Asp Thr Ala Val Glu Arg Leu Asn
 180 185 190
 Val Phe Ile Thr Met Ala Lys Val Phe Leu Ile Leu His Phe Ile Ile
 195 200 205
 Gly Phe Ser Val Pro Met Ser Ile Ile Thr Val Cys Tyr Gly Ile Ile
 210 215 220
 Ala Ala Lys Ile His Arg Asn His Met Ile Lys Ser Ser Arg Pro Leu
 225 230 235 240
 Arg Val Phe Ala Ala Val Val Ala Ser Phe Phe Ile Cys Trp Phe Pro
 245 250 255
 Tyr Glu Leu Ile Gly Ile Leu Met Ala Val Trp Leu Lys Glu Met Leu
 260 265 270
 Leu Asn Gly Lys Tyr Lys Ile Ile Leu Val Leu Ile Asn Pro Thr Ser
 275 280 285
 Ser Leu Ala Phe Phe Asn Ser Cys Leu Asn Pro Ile Leu Tyr Val Phe
 290 295 300
 Met Gly Arg Asn Phe Gln Glu Arg Leu Ile Arg Ser Leu Pro Thr Ser
 305 310 315 320
 Leu Glu Arg Ala Leu Thr Glu Val Pro Asp Ser Ala Gln Thr Ser Asn
 325 330 335
 Thr Asp Thr Thr Ser Ala Ser Pro Pro Glu Glu Thr Glu Leu Gln Ala
 340 345 350
 Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 355 360 365
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 370 375 380
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 385 390 395 400
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr

317/518

	405		410		415										
Leu	Cys	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys
	420		425		430										
Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu
	435		440		445										
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu
	450		455		460										
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly
	465		470		475										
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr
	485		490		495										
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn
	500		505		510										
Gly	Ile	Lys	Val	Asn	Phe	Lys	Thr	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser
	515		520		525										
Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly
	530		535		540										
Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu
	545		550		555										
Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe
	565		570		575										
Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	Leu	Tyr	Asn	
	580		585		590										

<210> 119

<211> 594

<212> PRT

<213> Human

318/518

<400> 119

Met	Asn	Gly	Val	Ser	Glu	Gly	Thr	Arg	Gly	Cys	Ser	Asp	Arg	Gln	Pro
				5					10					15	
Gly	Val	Leu	Thr	Arg	Asp	Arg	Ser	Cys	Ser	Arg	Lys	Met	Asn	Ser	Ser
				20				25					30		
Gly	Cys	Leu	Ser	Glu	Glu	Val	Gly	Ser	Leu	Arg	Pro	Leu	Thr	Val	Val
		35					40					45			
Ile	Leu	Ser	Ala	Ser	Ile	Val	Val	Gly	Val	Leu	Gly	Asn	Gly	Leu	Val
	50					55				60					
Leu	Trp	Met	Thr	Val	Phe	Arg	Met	Ala	Arg	Thr	Val	Ser	Thr	Val	Cys
	65				70					75				80	
Phe	Phe	His	Leu	Ala	Leu	Ala	Asp	Phe	Met	Leu	Ser	Leu	Ser	Leu	Pro
			85						90				95		
Ile	Ala	Met	Tyr	Tyr	Ile	Val	Ser	Arg	Gln	Trp	Leu	Leu	Gly	Glu	Trp
		100						105					110		
Ala	Cys	Lys	Leu	Tyr	Ile	Thr	Phe	Val	Phe	Leu	Ser	Tyr	Phe	Ala	Ser
		115					120					125			
Asn	Cys	Leu	Leu	Val	Phe	Ile	Ser	Val	Asp	Arg	Cys	Ile	Ser	Val	Leu
		130				135					140				
Tyr	Pro	Val	Trp	Ala	Leu	Asn	His	Arg	Thr	Val	Gln	Arg	Ala	Ser	Trp
	145				150					155				160	
Leu	Ala	Phe	Gly	Val	Trp	Leu	Leu	Ala	Ala	Ala	Leu	Cys	Ser	Ala	His
			165					170				175			
Leu	Lys	Phe	Arg	Thr	Thr	Arg	Lys	Trp	Asn	Gly	Cys	Thr	His	Cys	Tyr
		180					185					190			
Leu	Ala	Phe	Asn	Ser	Asp	Asn	Glu	Thr	Ala	Gln	Ile	Trp	Ile	Glu	Gly
		195					200					205			
Val	Val	Glu	Gly	His	Ile	Ile	Gly	Thr	Ile	Gly	His	Phe	Leu	Leu	Gly
	210					215						220			

319/518

Phe Leu Gly Pro Leu Ala Ile Ile Gly Thr Cys Ala His Leu Ile Arg
 225 230 235 240
 Ala Lys Leu Leu Arg Glu Gly Trp Val His Ala Asn Arg Pro Lys Arg
 245 250 255
 Leu Leu Leu Val Leu Val Ser Ala Phe Phe Ile Phe Trp Ser Pro Phe
 260 265 270
 Asn Val Val Leu Leu Val His Leu Trp Arg Arg Val Met Leu Lys Glu
 275 280 285
 Ile Tyr His Pro Arg Met Leu Leu Ile Leu Gln Ala Ser Phe Ala Leu
 290 295 300
 Gly Cys Val Asn Ser Ser Leu Asn Pro Phe Leu Tyr Val Phe Val Gly
 305 310 315 320
 Arg Asp Phe Gln Glu Lys Phe Phe Gln Ser Leu Thr Ser Ala Leu Ala
 325 330 335
 Arg Ala Phe Gly Glu Glu Glu Phe Leu Ser Ser Cys Pro Arg Gly Asn
 340 345 350
 Ala Pro Arg Glu Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val
 355 360 365
 Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser
 370 375 380
 Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu
 385 390 395 400
 Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu
 405 410 415
 Val Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp
 420 425 430
 His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr
 435 440 445
 Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr

320/518

450 455 460
 Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu
 465 470 475 480
 Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys
 485 490 495
 Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys
 500 505 510
 Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu
 515 520 525
 Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
 530 535 540
 Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln
 545 550 555 560
 Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
 565 570 575
 Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu
 580 585 590
 Tyr Asn

<210> 120

<211> 1459

<212> PRT

<213> Human

<400> 120

Met Met Phe Arg Ser Asp Arg Met Trp Ser Cys His Trp Lys Trp Lys
 5 10 15
 Pro Ser Pro Leu Leu Phe Leu Phe Ala Leu Tyr Ile Met Cys Val Pro
 20 25 30

321/518

His Ser Val Trp Gly Cys Ala Asn Cys Arg Val Val Leu Ser Asn Pro
 35 40 45
 Ser Gly Thr Phe Thr Ser Pro Cys Tyr Pro Asn Asp Tyr Pro Asn Ser
 50 55 60
 Gln Ala Cys Met Trp Thr Leu Arg Ala Pro Thr Gly Tyr Ile Ile Gln
 65 70 75 80
 Ile Thr Phe Asn Asp Phe Asp Ile Glu Glu Ala Pro Asn Cys Ile Tyr
 85 90 95
 Asp Ser Leu Ser Leu Asp Asn Gly Glu Ser Gln Thr Lys Phe Cys Gly
 100 105 110
 Ala Thr Ala Lys Gly Leu Ser Phe Asn Ser Ser Ala Asn Glu Met His
 115 120 125
 Val Ser Phe Ser Ser Asp Phe Ser Ile Gln Lys Lys Gly Phe Asn Ala
 130 135 140
 Ser Tyr Ile Arg Val Ala Val Ser Leu Arg Asn Gln Lys Val Ile Leu
 145 150 155 160
 Pro Gln Thr Ser Asp Ala Tyr Gln Val Ser Val Ala Lys Ser Ile Ser
 165 170 175
 Ile Pro Glu Leu Ser Ala Phe Thr Leu Cys Phe Glu Ala Thr Lys Val
 180 185 190
 Gly His Glu Asp Ser Asp Trp Thr Ala Phe Ser Tyr Ser Asn Ala Ser
 195 200 205
 Phe Thr Gln Leu Leu Ser Phe Gly Lys Ala Lys Ser Gly Tyr Phe Leu
 210 215 220
 Ser Ile Ser Asp Ser Lys Cys Leu Leu Asn Asn Ala Leu Pro Val Lys
 225 230 235 240
 Glu Lys Glu Asp Ile Phe Ala Glu Ser Phe Glu Gln Leu Cys Leu Val
 245 250 255
 Trp Asn Asn Ser Leu Gly Ser Ile Gly Val Asn Phe Lys Arg Asn Tyr

322/518

260	265	270
Glu Thr Val Pro Cys Asp Ser Thr Ile Ser Lys Val Ile Pro Gly Asn		
275	280	285
Gly Lys Leu Leu Leu Gly Ser Asn Gln Asn Glu Ile Val Ser Leu Lys		
290	295	300
Gly Asp Ile Tyr Asn Phe Arg Leu Trp Asn Phe Thr Met Asn Ala Lys		
305	310	315
Ile Leu Ser Asn Leu Ser Cys Asn Val Lys Gly Asn Val Val Asp Trp		
325	330	335
Gln Asn Asp Phe Trp Asn Ile Pro Asn Leu Ala Leu Lys Ala Glu Ser		
340	345	350
Asn Leu Ser Cys Gly Ser Tyr Leu Ile Pro Leu Pro Ala Ala Glu Leu		
355	360	365
Ala Ser Cys Ala Asp Leu Gly Thr Leu Cys Gln Ala Thr Val Asn Ser		
370	375	380
Pro Ser Thr Thr Pro Pro Thr Val Thr Thr Asn Met Pro Val Thr Asn		
385	390	395
Arg Ile Asp Lys Gln Arg Asn Asp Gly Ile Ile Tyr Arg Ile Ser Val		
405	410	415
Val Ile Gln Asn Ile Leu Arg His Pro Glu Val Lys Val Gln Ser Lys		
420	425	430
Val Ala Glu Trp Leu Asn Ser Thr Phe Gln Asn Trp Asn Tyr Thr Val		
435	440	445
Tyr Val Val Asn Ile Ser Phe His Leu Ser Ala Gly Glu Asp Lys Ile		
450	455	460
Lys Val Lys Arg Ser Leu Glu Asp Glu Pro Arg Leu Val Leu Trp Ala		
465	470	475
Leu Leu Val Tyr Asn Ala Thr Asn Asn Thr Asn Leu Glu Gly Lys Ile		
485	490	495

323/518

Ile Gln Gln Lys Leu Leu Lys Asn Asn Glu Ser Leu Asp Glu Gly Leu
 500 505 510
 Arg Leu His Thr Val Asn Val Arg Gln Leu Gly His Cys Leu Ala Met
 515 520 525
 Glu Glu Pro Lys Gly Tyr Tyr Trp Pro Ser Ile Gln Pro Ser Glu Tyr
 530 535 540
 Val Leu Pro Cys Pro Asp Lys Pro Gly Phe Ser Ala Ser Arg Ile Cys
 545 550 555 560
 Phe Tyr Asn Ala Thr Asn Pro Leu Val Thr Tyr Trp Gly Pro Val Asp
 565 570 575
 Ile Ser Asn Cys Leu Lys Glu Ala Asn Glu Val Ala Asn Gln Ile Leu
 580 585 590
 Asn Leu Thr Ala Asp Gly Gln Asn Leu Thr Ser Ala Asn Ile Thr Asn
 595 600 605
 Ile Val Glu Gln Val Lys Arg Ile Val Asn Lys Glu Glu Asn Ile Asp
 610 615 620
 Ile Thr Leu Gly Ser Thr Leu Met Asn Ile Phe Ser Asn Ile Leu Ser
 625 630 635 640
 Ser Ser Asp Ser Asp Leu Leu Glu Ser Ser Ser Glu Ala Leu Lys Thr
 645 650 655
 Ile Asp Glu Leu Ala Phe Lys Ile Asp Leu Asn Ser Thr Ser His Val
 660 665 670
 Asn Ile Thr Thr Arg Asn Leu Ala Leu Ser Val Ser Ser Leu Leu Pro
 675 680 685
 Gly Thr Asn Ala Ile Ser Asn Phe Ser Ile Gly Leu Pro Ser Asn Asn
 690 695 700
 Glu Ser Tyr Phe Gln Met Asp Phe Glu Ser Gly Gln Val Asp Pro Leu
 705 710 715 720
 Ala Ser Val Ile Leu Pro Pro Asn Leu Leu Glu Asn Leu Ser Pro Glu

324/518

725	730	735
Asp Ser Val Leu Val Arg Arg Ala Gln Phe Thr Phe Phe Asn Lys Thr		
740	745	750
Gly Leu Phe Gln Asp Val Gly Pro Gln Arg Lys Thr Leu Val Ser Tyr		
755	760	765
Val Met Ala Cys Ser Ile Gly Asn Ile Thr Ile Gln Asn Leu Lys Asp		
770	775	780
Pro Val Gln Ile Lys Ile Lys His Thr Arg Thr Gln Glu Val His His		
785	790	795
Pro Ile Cys Ala Phe Trp Asp Leu Asn Lys Asn Lys Ser Phe Gly Gly		
805	810	815
Trp Asn Thr Ser Gly Cys Val Ala His Arg Asp Ser Asp Ala Ser Glu		
820	825	830
Thr Val Cys Leu Cys Asn His Phe Thr His Phe Gly Val Leu Met Asp		
835	840	845
Leu Pro Arg Ser Ala Ser Gln Leu Asp Ala Arg Asn Thr Lys Val Leu		
850	855	860
Thr Phe Ile Ser Tyr Ile Gly Cys Gly Ile Ser Ala Ile Phe Ser Ala		
865	870	875
Ala Thr Leu Leu Thr Tyr Val Ala Phe Glu Lys Leu Arg Arg Asp Tyr		
885	890	895
Pro Ser Lys Ile Leu Met Asn Leu Ser Thr Ala Leu Leu Phe Leu Asn		
900	905	910
Leu Leu Phe Leu Leu Asp Gly Trp Ile Thr Ser Phe Asn Val Asp Gly		
915	920	925
Leu Cys Ile Ala Val Ala Val Leu Leu His Phe Phe Leu Leu Ala Thr		
930	935	940
Phe Thr Trp Met Gly Leu Glu Ala Ile His Met Tyr Ile Ala Leu Val		
945	950	955
		960

325/518

Lys Val Phe Asn Thr Tyr Ile Arg Arg Tyr Ile Leu Lys Phe Cys Ile
 965 970 975
 Ile Gly Trp Gly Leu Pro Ala Leu Val Val Ser Val Val Leu Ala Ser
 980 985 990
 Arg Asn Asn Asn Glu Val Tyr Gly Lys Glu Ser Tyr Gly Lys Glu Lys
 995 1000 1005
 Gly Asp Glu Phe Cys Trp Ile Gln Asp Pro Val Ile Phe Tyr Val Thr
 1010 1015 1020
 Cys Ala Gly Tyr Phe Gly Val Met Phe Phe Leu Asn Ile Ala Met Phe
 1025 1030 1035 1040
 Ile Val Val Met Val Gln Ile Cys Gly Arg Asn Gly Lys Arg Ser Asn
 1045 1050 1055
 Arg Thr Leu Arg Glu Glu Val Leu Arg Asn Leu Arg Ser Val Val Ser
 1060 1065 1070
 Leu Thr Phe Leu Leu Gly Met Thr Trp Gly Phe Ala Phe Phe Ala Trp
 1075 1080 1085
 Gly Pro Leu Asn Ile Pro Phe Met Tyr Leu Phe Ser Ile Phe Asn Ser
 1090 1095 1100
 Leu Gln Gly Leu Phe Ile Phe Ile Phe His Cys Ala Met Lys Glu Asn
 1105 1110 1115 1120
 Val Gln Lys Gln Trp Arg Arg His Leu Cys Cys Gly Arg Phe Arg Leu
 1125 1130 1135
 Ala Asp Asn Ser Asp Trp Ser Lys Thr Ala Thr Asn Ile Ile Lys Lys
 1140 1145 1150
 Ser Ser Asp Asn Leu Gly Lys Ser Leu Ser Ser Ser Ser Ile Gly Ser
 1155 1160 1165
 Asn Ser Thr Tyr Leu Thr Ser Lys Ser Lys Ser Ser Ser Thr Thr Tyr
 1170 1175 1180
 Phe Lys Arg Asn Ser His Thr Asp Asn Val Ser Tyr Glu His Ser Phe

326/518

1185	1190	1195	1200
Asn Lys Ser Gly Ser Leu Arg Gln Cys Phe His Gly Gln Val Leu Val			
1205	1210	1215	
Lys Thr Gly Pro Cys Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val			
1220	1225	1230	
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe			
1235	1240	1245	
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr			
1250	1255	1260	
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr			
1265	1270	1275	1280
Leu Val Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro			
1285	1290	1295	
Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly			
1300	1305	1310	
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys			
1315	1320	1325	
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile			
1330	1335	1340	
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His			
1345	1350	1355	1360
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp			
1365	1370	1375	
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile			
1380	1385	1390	
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro			
1395	1400	1405	
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr			
1410	1415	1420	

327/518

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 1425 1430 1435 1440
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 1445 1450 1455
 Leu Tyr Asn

<210> 121

<211> 637

<212> PRT

<213> Human

<400> 121

Met Ala Gln Arg Gln Pro His Ser Pro Asn Gln Thr Leu Ile Ser Ile
 5 10 15
 Thr Asn Asp Thr Glu Ser Ser Ser Ser Val Val Ser Asn Asp Asn Thr
 20 25 30
 Asn Lys Gly Trp Ser Gly Asp Asn Ser Pro Gly Ile Glu Ala Leu Cys
 35 40 45
 Ala Ile Tyr Ile Thr Tyr Ala Val Ile Ile Ser Val Gly Ile Leu Gly
 50 55 60
 Asn Ala Ile Leu Ile Lys Val Phe Phe Lys Thr Lys Ser Met Gln Thr
 65 70 75 80
 Val Pro Asn Ile Phe Ile Thr Ser Leu Ala Phe Gly Asp Leu Leu Leu
 85 90 95
 Leu Leu Thr Cys Val Pro Val Asp Ala Thr His Tyr Leu Ala Glu Gly
 100 105 110
 Trp Leu Phe Gly Arg Ile Gly Cys Lys Val Leu Ser Phe Ile Arg Leu
 115 120 125
 Thr Ser Val Gly Val Ser Val Phe Thr Leu Thr Ile Leu Ser Ala Asp

328/518

130	135	140	
Arg Tyr Lys Ala Val	Val Lys Pro Leu Glu Arg	Gln Pro Ser Asn Ala	
145	150	155	160
Ile Leu Lys Thr Cys	Val Lys Ala Gly Cys	Val Trp Ile Val Ser Met	
165	170	175	
Ile Phe Ala Leu Pro	Glu Ala Ile Phe Ser Asn	Val Tyr Thr Phe Arg	
180	185	190	
Asp Pro Asn Lys Asn	Met Thr Phe Glu Ser Cys	Thr Ser Tyr Pro Val	
195	200	205	
Ser Lys Lys Leu Leu	Gln Glu Ile His Ser Leu	Leu Cys Phe Leu Val	
210	215	220	
Phe Tyr Ile Ile Pro	Leu Ser Ile Ile Ser Val	Tyr Tyr Ser Leu Ile	
225	230	235	240
Ala Arg Thr Leu Tyr	Lys Ser Thr Leu Asn Ile	Pro Thr Glu Glu Gln	
245	250	255	
Ser His Ala Arg Lys	Gln Ile Glu Ser Arg Lys	Arg Ile Ala Arg Thr	
260	265	270	
Val Leu Val Leu Val	Ala Leu Phe Ala Leu Cys	Trp Leu Pro Asn His	
275	280	285	
Leu Leu Tyr Leu Tyr	His Ser Phe Thr Ser Gln	Thr Tyr Val Asp Pro	
290	295	300	
Ser Ala Met His Phe	Ile Phe Thr Ile Phe Ser	Arg Val Leu Ala Phe	
305	310	315	320
Ser Asn Ser Cys Val	Asn Pro Phe Ala Leu Tyr	Trp Leu Ser Lys Ser	
325	330	335	
Phe Gln Lys His Phe	Lys Ala Gln Leu Phe Cys	Cys Lys Ala Glu Arg	
340	345	350	
Pro Glu Pro Pro Val	Ala Asp Thr Ser Leu Thr	Thr Leu Ala Val Met	
355	360	365	

329/518

Gly Thr Val Pro Gly Thr Gly Ser Ile Gln Met Ser Glu Ile Ser Val
 370 375 380
 Thr Ser Phe Thr Gly Cys Ser Val Lys Gln Ala Glu Asp Arg Phe Ala
 385 390 395 400
 Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu
 405 410 415
 Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly
 420 425 430
 Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr
 435 440 445
 Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Cys
 450 455 460
 Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg His
 465 470 475 480
 Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr
 485 490 495
 Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys
 500 505 510
 Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp
 515 520 525
 Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr
 530 535 540
 Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile
 545 550 555 560
 Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser Val Gln
 565 570 575
 Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val
 580 585 590
 Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys

605

620

635

<213> Human

15

30

45

60

80

95

110

125

Leu Ser Phe Glu Arg Tyr Ile Ala Ile Cys His Pro Phe Arg Tyr Lys

331/518

130	135	140	
Ala Val Ser Gly Pro Cys Gln Val Lys Leu Leu Ile Gly Phe Val Trp			
145	150	155	160
Val Thr Ser Ala Leu Val Ala Leu Pro Leu Leu Phe Ala Met Gly Thr			
	165	170	175
Glu Tyr Pro Leu Val Asn Val Pro Ser His Arg Gly Leu Thr Cys Asn			
	180	185	190
Arg Ser Ser Thr Arg His His Glu Gln Pro Glu Thr Ser Asn Met Ser			
	195	200	205
Ile Cys Thr Asn Leu Ser Ser Arg Trp Thr Val Phe Gln Ser Ser Ile			
	210	215	220
Phe Gly Ala Phe Val Val Tyr Leu Val Val Leu Leu Ser Val Ala Phe			
225	230	235	240
Met Cys Trp Asn Met Met Gln Val Leu Met Lys Ser Gln Lys Gly Ser			
	245	250	255
Leu Ala Gly Gly Thr Arg Pro Pro Gln Leu Arg Lys Ser Glu Ser Glu			
	260	265	270
Glu Ser Arg Thr Ala Arg Arg Gln Thr Ile Ile Phe Leu Arg Leu Ile			
	275	280	285
Val Val Thr Leu Ala Val Cys Trp Met Pro Asn Gln Ile Arg Arg Ile			
	290	295	300
Met Ala Ala Ala Lys Pro Lys His Asp Trp Thr Arg Ser Tyr Phe Arg			
305	310	315	320
Ala Tyr Met Ile Leu Leu Pro Phe Ser Glu Thr Phe Phe Tyr Leu Ser			
	325	330	335
Ser Val Ile Asn Pro Leu Leu Tyr Thr Val Ser Ser Gln Gln Phe Arg			
	340	345	350
Arg Val Phe Val Gln Val Leu Cys Cys Arg Leu Ser Leu Gln His Ala			
	355	360	365

332/518

Asn His Glu Lys Arg Leu Arg Val His Ala His Ser Thr Thr Asp Ser
 370 375 380
 Ala Arg Phe Val Gln Arg Pro Leu Leu Phe Ala Ser Arg Arg Gln Ser
 385 390 395 400
 Ser Ala Arg Arg Thr Glu Lys Ile Phe Leu Ser Thr Phe Gln Ser Glu
 405 410 415
 Ala Glu Pro Gln Ser Lys Ser Gln Ser Leu Ser Leu Glu Ser Leu Glu
 420 425 430
 Pro Asn Ser Gly Ala Lys Pro Ala Asn Ser Ala Ala Glu Asn Gly Phe
 435 440 445
 Gln Glu His Glu Val Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 450 455 460
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 465 470 475 480
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 485 490 495
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 500 505 510
 Leu Val Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 515 520 525
 Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 530 535 540
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 545 550 555 560
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 565 570 575
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 580 585 590
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp

333/518

595 600 605
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile
 610 615 620
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 625 630 635 640
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 645 650 655
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 660 665 670
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 675 680 685
 Leu Tyr Asn
 690

<210> 123
 <211> 661
 <212> PRT
 <213> Human

<400> 123
 Met Val Pro His Leu Leu Leu Leu Cys Leu Leu Pro Leu Val Arg Ala
 5 10 15
 Thr Glu Pro His Glu Gly Arg Ala Asp Glu Gln Ser Ala Glu Ala Ala
 20 25 30
 Leu Ala Val Pro Asn Ala Ser His Phe Phe Ser Trp Asn Asn Tyr Thr
 35 40 45
 Phe Ser Asp Trp Gln Asn Phe Val Gly Arg Arg Arg Tyr Gly Ala Glu
 50 55 60
 Ser Gln Asn Pro Thr Val Lys Ala Leu Leu Ile Val Ala Tyr Ser Phe

334/518

65	70	75	80
Ile Ile Val Phe Ser Leu Phe Gly Asn Val Leu Val Cys His Val Ile			
	85	90	95
Phe Lys Asn Gln Arg Met His Ser Ala Thr Ser Leu Phe Ile Val Asn			
	100	105	110
Leu Ala Val Ala Asp Ile Met Ile Thr Leu Leu Asn Thr Pro Phe Thr			
	115	120	125
Leu Val Arg Phe Val Asn Ser Thr Trp Ile Phe Gly Lys Gly Met Cys			
	130	135	140
His Val Ser Arg Phe Ala Gln Tyr Cys Ser Leu His Val Ser Ala Leu			
145	150	155	160
Thr Leu Thr Ala Ile Ala Val Asp Arg His Gln Val Ile Met His Pro			
	165	170	175
Leu Lys Pro Arg Ile Ser Ile Thr Lys Gly Val Ile Tyr Ile Ala Val			
	180	185	190
Ile Trp Thr Met Ala Thr Phe Phe Ser Leu Pro His Ala Ile Cys Gln			
	195	200	205
Lys Leu Phe Thr Phe Lys Tyr Ser Glu Asp Ile Val Arg Ser Leu Cys			
	210	215	220
Leu Pro Asp Phe Pro Glu Pro Ala Asp Leu Phe Trp Lys Tyr Leu Asp			
225	230	235	240
Leu Ala Thr Phe Ile Leu Leu Tyr Ile Leu Pro Leu Leu Ile Ile Ser			
	245	250	255
Val Ala Tyr Ala Arg Val Ala Lys Lys Leu Trp Leu Cys Asn Met Ile			
	260	265	270
Gly Asp Val Thr Thr Glu Gln Tyr Phe Ala Leu Arg Arg Lys Lys Lys			
	275	280	285
Lys Thr Ile Lys Met Leu Met Leu Val Val Val Leu Phe Ala Leu Cys			
	290	295	300

335/518

Trp Phe Pro Leu Asn Cys Tyr Val Leu Leu Leu Ser Ser Lys Val Ile
 305 310 315 320
 Arg Thr Asn Asn Ala Leu Tyr Phe Ala Phe His Trp Phe Ala Met Ser
 325 330 335
 Ser Thr Cys Tyr Asn Pro Phe Ile Tyr Cys Trp Leu Asn Glu Asn Phe
 340 345 350
 Arg Ile Glu Leu Lys Ala Leu Leu Ser Met Cys Gln Arg Pro Pro Lys
 355 360 365
 Pro Gln Glu Asp Arg Pro Pro Ser Pro Val Pro Ser Phe Arg Val Ala
 370 375 380
 Trp Thr Glu Lys Asn Asp Gly Gln Arg Ala Pro Leu Ala Asn Asn Leu
 385 390 395 400
 Leu Pro Thr Ser Gln Leu Gln Ser Gly Lys Thr Asp Leu Ser Ser Val
 405 410 415
 Glu Pro Ile Val Thr Met Ser Ala Ser Lys Gly Glu Glu Leu Phe Thr
 420 425 430
 Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His
 435 440 445
 Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys
 450 455 460
 Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp
 465 470 475 480
 Pro Thr Leu Val Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg
 485 490 495
 Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro
 500 505 510
 Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn
 515 520 525
 Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn

336/518

530 535 540
 Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu
 545 550 555 560
 Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met
 565 570 575
 Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His
 580 585 590
 Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn
 595 600 605
 Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu
 610 615 620
 Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His
 625 630 635 640
 Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met
 645 650 655
 Asp Glu Leu Tyr Asn
 660

<210> 124

<211> 634

<212> PRT

<213> Human

<400> 124

Met Trp Asn Ser Ser Asp Ala Asn Phe Ser Cys Tyr His Glu Ser Val
 5 10 15
 Leu Gly Tyr Arg Tyr Val Ala Val Ser Trp Gly Val Val Val Ala Val
 20 25 30
 Thr Gly Thr Val Gly Asn Val Leu Thr Leu Leu Ala Leu Ala Ile Gln

337/518

35	40	45
Pro Lys Leu Arg Thr Arg Phe Asn Leu Leu Ile Ala Asn Leu Thr Leu		
50	55	60
Ala Asp Leu Leu Tyr Cys Thr Leu Leu Gln Pro Phe Ser Val Asp Thr		
65	70	75
Tyr Leu His Leu His Trp Arg Thr Gly Ala Thr Phe Cys Arg Val Phe		
85	90	95
Gly Leu Leu Leu Phe Ala Ser Asn Ser Val Ser Ile Leu Thr Leu Cys		
100	105	110
Leu Ile Ala Leu Gly Arg Tyr Leu Leu Ile Ala His Pro Lys Leu Phe		
115	120	125
Pro Gln Val Phe Ser Ala Lys Gly Ile Val Leu Ala Leu Val Ser Thr		
130	135	140
Trp Val Val Gly Val Ala Ser Phe Ala Pro Leu Trp Pro Ile Tyr Ile		
145	150	155
Leu Val Pro Val Val Cys Thr Cys Ser Phe Asp Arg Ile Arg Gly Arg		
165	170	175
Pro Tyr Thr Thr Ile Leu Met Gly Ile Tyr Phe Val Leu Gly Leu Ser		
180	185	190
Ser Val Gly Ile Phe Tyr Cys Leu Ile His Arg Gln Val Lys Arg Ala		
195	200	205
Ala Gln Ala Leu Asp Gln Tyr Lys Leu Arg Gln Ala Ser Ile His Ser		
210	215	220
Asn His Val Ala Arg Thr Asp Glu Ala Met Pro Gly Arg Phe Gln Glu		
225	230	235
Leu Asp Ser Arg Leu Ala Ser Gly Gly Pro Ser Glu Gly Ile Ser Ser		
245	250	255
Glu Pro Val Ser Ala Ala Thr Thr Gln Thr Leu Glu Gly Asp Ser Ser		
260	265	270

338/518

Glu Val Gly Asp Gln Ile Asn Ser Lys Arg Ala Lys Gln Met Ala Glu
 275 280 285
 Lys Ser Pro Pro Glu Ala Ser Ala Lys Ala Gln Pro Ile Lys Gly Ala
 290 295 300
 Arg Arg Ala Pro Asp Ser Ser Ser Glu Phe Gly Lys Val Thr Arg Met
 305 310 315 320
 Cys Phe Ala Val Phe Leu Cys Phe Ala Leu Ser Tyr Ile Pro Phe Leu
 325 330 335
 Leu Leu Asn Ile Leu Asp Ala Arg Val Gln Ala Pro Arg Val Val His
 340 345 350
 Met Leu Ala Ala Asn Leu Thr Trp Leu Asn Gly Cys Ile Asn Pro Val
 355 360 365
 Leu Tyr Ala Ala Met Asn Arg Gln Phe Arg Gln Ala Tyr Gly Ser Ile
 370 375 380
 Leu Lys Arg Gly Pro Arg Ser Phe His Arg Leu His Ala Ser Lys Gly
 385 390 395 400
 Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly
 405 410 415
 Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp
 420 425 430
 Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys
 435 440 445
 Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Cys Tyr Gly Val
 450 455 460
 Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe
 465 470 475 480
 Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe
 485 490 495
 Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly

339/518

500	505	510	
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu			
515	520	525	
Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His			
530	535	540	
Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn			
545	550	555	560
Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp			
565	570	575	
His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro			
580	585	590	
Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn			
595	600	605	
Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly			
610	615	620	
Ile Thr His Gly Met Asp Glu Leu Tyr Asn			
625	630		

<210> 125

<211> 587

<212> PRT

<213> Human

<400> 125

Met Asn Ser Thr Leu Asp Gly Asn Gln Ser Ser His Pro Phe Cys Leu		
5	10	15
Leu Ala Phe Gly Tyr Leu Glu Thr Val Asn Phe Cys Leu Leu Glu Val		
20	25	30
Leu Ile Ile Val Phe Leu Thr Val Leu Ile Ile Ser Gly Asn Ile Ile		

340/518

35	40	45	
Val Ile Phe Val Phe His Cys Ala Pro Leu Leu Asn His His Thr Thr			
50	55	60	
Ser Tyr Phe Ile Gln Thr Met Ala Tyr Ala Asp Leu Phe Val Gly Val			
65	70	75	80
Ser Cys Val Val Pro Ser Leu Ser Leu Leu His His Pro Leu Pro Val			
85	90	95	
Glu Glu Ser Leu Thr Cys Gln Ile Phe Gly Phe Val Val Ser Val Leu			
100	105	110	
Lys Ser Val Ser Met Ala Ser Leu Ala Cys Ile Ser Ile Asp Arg Tyr			
115	120	125	
Ile Ala Ile Thr Lys Pro Leu Thr Tyr Asn Thr Leu Val Thr Pro Trp			
130	135	140	
Arg Leu Arg Leu Cys Ile Phe Leu Ile Trp Leu Tyr Ser Thr Leu Val			
145	150	155	160
Phe Leu Pro Ser Phe Phe His Trp Gly Lys Pro Gly Tyr His Gly Asp			
165	170	175	
Val Phe Gln Trp Cys Ala Glu Ser Trp His Thr Asp Ser Tyr Phe Thr			
180	185	190	
Leu Phe Ile Val Met Met Leu Tyr Ala Pro Ala Ala Leu Ile Val Cys			
195	200	205	
Phe Thr Tyr Phe Asn Ile Phe Arg Ile Cys Gln Gln His Thr Lys Asp			
210	215	220	
Ile Ser Glu Arg Gln Ala Arg Phe Ser Ser Gln Ser Gly Glu Thr Gly			
225	230	235	240
Glu Val Gln Ala Cys Pro Asp Lys Arg Tyr Ala Met Val Leu Phe Arg			
245	250	255	
Ile Thr Ser Val Phe Tyr Ile Leu Trp Leu Pro Tyr Ile Ile Tyr Phe			
260	265	270	

341/518

Leu Leu Glu Ser Ser Thr Gly His Ser Asn Arg Phe Ala Ser Phe Leu
 275 280 285
 Thr Thr Trp Leu Ala Ile Ser Asn Ser Phe Cys Asn Cys Val Ile Tyr
 290 295 300
 Ser Leu Ser Asn Ser Val Phe Gln Arg Gly Leu Lys Arg Leu Ser Gly
 305 310 315 320
 Ala Met Cys Thr Ser Cys Ala Ser Gln Thr Thr Ala Asn Asp Pro Tyr
 325 330 335
 Thr Val Arg Ser Lys Gly Pro Leu Asn Gly Cys His Ile Ala Ser Lys
 340 345 350
 Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp
 355 360 365
 Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly
 370 375 380
 Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly
 385 390 395 400
 Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Cys Tyr Gly
 405 410 415
 Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg His Asp Phe
 420 425 430
 Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe
 435 440 445
 Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu
 450 455 460
 Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys
 465 470 475 480
 Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
 485 490 495
 His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val

342/518

500	505	510
Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala		
515	520	525
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu		
530	535	540
Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro		
545	550	555
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala		
565	570	575
Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn		
580	585	

<210> 126

<211> 1189

<212> PRT

<213> Human

<400> 126

Met Pro Gly Pro Leu Gly Leu Leu Cys Phe Leu Ala Leu Gly Leu Leu		
5	10	15
Gly Ser Ala Gly Pro Ser Gly Ala Ala Pro Pro Leu Cys Ala Ala Pro		
20	25	30
Cys Ser Cys Asp Gly Asp Arg Arg Val Asp Cys Ser Gly Lys Gly Leu		
35	40	45
Thr Ala Val Pro Glu Gly Leu Ser Ala Phe Thr Gln Ala Leu Asp Ile		
50	55	60
Ser Met Asn Asn Ile Thr Gln Leu Pro Glu Asp Ala Phe Lys Asn Phe		
65	70	75
Pro Phe Leu Glu Glu Leu Gln Leu Ala Gly Asn Asp Leu Ser Phe Ile		

343/518

	85	90	95
His Pro Lys Ala Leu Ser Gly Leu Lys Glu Leu Lys Val Leu Thr Leu			
	100	105	110
Gln Asn Asn Gln Leu Lys Thr Val Pro Ser Glu Ala Ile Arg Gly Leu			
	115	120	125
Ser Ala Leu Gln Ser Leu Arg Leu Asp Ala Asn His Ile Thr Ser Val			
	130	135	140
Pro Glu Asp Ser Phe Glu Gly Leu Val Gln Leu Arg His Leu Trp Leu			
	145	150	155
Asp Asp Asn Ser Leu Thr Glu Val Pro Val His Pro Leu Ser Asn Leu			
	165	170	175
Pro Thr Leu Gln Ala Leu Thr Leu Ala Leu Asn Lys Ile Ser Ser Ile			
	180	185	190
Pro Asp Phe Ala Phe Thr Asn Leu Ser Ser Leu Val Val Leu His Leu			
	195	200	205
His Asn Asn Lys Ile Arg Ser Leu Ser Gln His Cys Phe Asp Gly Leu			
	210	215	220
Asp Asn Leu Glu Thr Leu Asp Leu Asn Tyr Asn Asn Leu Gly Glu Phe			
	225	230	235
Pro Gln Ala Ile Lys Ala Leu Pro Ser Leu Lys Glu Leu Gly Phe His			
	245	250	255
Ser Asn Ser Ile Ser Val Ile Pro Asp Gly Ala Phe Asp Gly Asn Pro			
	260	265	270
Leu Leu Arg Thr Ile His Leu Tyr Asp Asn Pro Leu Ser Phe Val Gly			
	275	280	285
Asn Ser Ala Phe His Asn Leu Ser Asp Leu His Ser Leu Val Ile Arg			
	290	295	300
Gly Ala Ser Met Val Gln Gln Phe Pro Asn Leu Thr Gly Thr Val His			
	305	310	315
			320

344/518

Leu Glu Ser Leu Thr Leu Thr Gly Thr Lys Ile Ser Ser Ile Pro Asn

325

330

335

Asn Leu Cys Gln Glu Gln Lys Met Leu Arg Thr Leu Asp Leu Ser Tyr

340

345

350

Asn Asn Ile Arg Asp Leu Pro Ser Phe Asn Gly Cys His Ala Leu Glu

355

360

365

Glu Ile Ser Leu Gln Arg Asn Gln Ile Tyr Gln Ile Lys Glu Gly Thr

370

375

380

Phe Gln Gly Leu Ile Ser Leu Arg Ile Leu Asp Leu Ser Arg Asn Leu

385

390

395

400

Ile His Glu Ile His Ser Arg Ala Phe Ala Thr Leu Gly Pro Ile Thr

405

410

415

Asn Leu Asp Val Ser Phe Asn Glu Leu Thr Ser Phe Pro Thr Glu Gly

420

425

430

Leu Asn Gly Leu Asn Gln Leu Lys Leu Val Gly Asn Phe Lys Leu Lys

435

440

445

Glu Ala Leu Ala Ala Lys Asp Phe Val Asn Leu Arg Ser Leu Ser Val

450

455

460

Pro Tyr Ala Tyr Gln Cys Cys Ala Phe Trp Gly Cys Asp Ser Tyr Ala

465

470

475

480

Asn Leu Asn Thr Glu Asp Asn Ser Leu Gln Asp His Ser Val Ala Gln

485

490

495

Glu Lys Gly Thr Ala Asp Ala Ala Asn Val Thr Ser Thr Leu Glu Asn

500

505

510

Glu Glu His Ser Gln Ile Ile Ile His Cys Thr Pro Ser Thr Gly Ala

515

520

525

Phe Lys Pro Cys Glu Tyr Leu Leu Gly Ser Trp Met Ile Arg Leu Thr

530

535

540

Val Trp Phe Ile Phe Leu Val Ala Leu Phe Phe Asn Leu Leu Val Ile

345/518

545	550	555	560
Leu Thr Thr Phe Ala Ser Cys Thr Ser Leu Pro Ser Ser Lys Leu Phe			
	565	570	575
Ile Gly Leu Ile Ser Val Ser Asn Leu Phe Met Gly Ile Tyr Thr Gly			
	580	585	590
Ile Leu Thr Phe Leu Asp Ala Val Ser Trp Gly Arg Phe Ala Glu Phe			
	595	600	605
Gly Ile Trp Trp Gln Thr Gly Ser Gly Cys Lys Val Ala Gly Phe Leu			
	610	615	620
Ala Val Phe Ser Ser Glu Ser Ala Ile Phe Leu Leu Met Leu Ala Thr			
	625	630	635
Val Glu Arg Ser Leu Ser Ala Lys Asp Ile Met Lys Asn Gly Lys Ser			
	645	650	655
Asn His Leu Lys Gln Phe Arg Val Ala Ala Leu Leu Ala Phe Leu Gly			
	660	665	670
Ala Thr Val Ala Gly Cys Phe Pro Leu Phe His Arg Gly Glu Tyr Ser			
	675	680	685
Ala Ser Pro Leu Cys Leu Pro Phe Pro Thr Gly Glu Thr Pro Ser Leu			
	690	695	700
Gly Phe Thr Val Thr Leu Val Leu Leu Asn Ser Leu Ala Phe Leu Leu			
	705	710	715
Met Ala Val Ile Tyr Thr Lys Leu Tyr Cys Asn Leu Glu Lys Glu Asp			
	725	730	735
Leu Ser Glu Asn Ser Gln Ser Ser Met Ile Lys His Val Ala Trp Leu			
	740	745	750
Ile Phe Thr Asn Cys Ile Phe Phe Cys Pro Val Ala Phe Phe Ser Phe			
	755	760	765
Ala Pro Leu Ile Thr Ala Ile Ser Ile Ser Pro Glu Ile Met Lys Ser			
	770	775	780

346/518

Val Thr Leu Ile Phe Phe Pro Leu Pro Ala Cys Leu Asn Pro Val Leu
 785 790 795 800
 Tyr Val Phe Phe Asn Pro Lys Phe Lys Glu Asp Trp Lys Leu Leu Lys
 805 810 815
 Arg Arg Val Thr Lys Lys Ser Gly Ser Val Ser Val Ser Ile Ser Ser
 820 825 830
 Gln Gly Gly Cys Leu Glu Gln Asp Phe Tyr Tyr Asp Cys Gly Met Tyr
 835 840 845
 Ser His Leu Gln Gly Asn Leu Thr Val Cys Asp Cys Cys Glu Ser Phe
 850 855 860
 Leu Leu Thr Lys Pro Val Ser Cys Lys His Leu Ile Lys Ser His Ser
 865 870 875 880
 Cys Pro Ala Leu Ala Val Ala Ser Cys Gln Arg Pro Glu Gly Tyr Trp
 885 890 895
 Ser Asp Cys Gly Thr Gln Ser Ala His Ser Asp Tyr Ala Asp Glu Glu
 900 905 910
 Asp Ser Phe Val Ser Asp Ser Ser Asp Gln Val Gln Ala Cys Gly Arg
 915 920 925
 Ala Cys Phe Tyr Gln Ser Arg Gly Phe Pro Leu Val Arg Tyr Ala Tyr
 930 935 940
 Asn Leu Pro Arg Val Lys Asp Thr Ser Lys Gly Glu Glu Leu Phe Thr
 945 950 955 960
 Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His
 965 970 975
 Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys
 980 985 990
 Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp
 995 1000 1005
 Pro Thr Leu Val Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg

347/518

1010	1015	1020	
Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro			
1025	1030	1035	1040
Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn			
1045	1050	1055	
Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn			
1060	1065	1070	
Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu			
1075	1080	1085	
Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met			
1090	1095	1100	
Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His			
1105	1110	1115	1120
Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn			
1125	1130	1135	
Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu			
1140	1145	1150	
Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His			
1155	1160	1165	
Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met			
1170	1175	1180	
Asp Glu Leu Tyr Asn			
1185			

<210> 127

<211> 586

<212> PRT

<213> Human

348/518

<400> 127

Met Val Asn Asn Phe Ser Gln Ala Glu Ala Val Glu Leu Cys Tyr Lys

5

10

15

Asn Val Asn Glu Ser Cys Ile Lys Thr Pro Tyr Ser Pro Gly Pro Arg

20

25

30

Ser Ile Leu Tyr Ala Val Leu Gly Phe Gly Ala Val Leu Ala Ala Phe

35

40

45

Gly Asn Leu Leu Val Met Ile Ala Ile Leu His Phe Lys Gln Leu His

50

55

60

Thr Pro Thr Asn Phe Leu Ile Ala Ser Leu Ala Cys Ala Asp Phe Leu

65

70

75

80

Val Gly Val Thr Val Met Pro Phe Ser Thr Val Arg Ser Val Glu Ser

85

90

95

Cys Trp Tyr Phe Gly Asp Ser Tyr Cys Lys Phe His Thr Cys Phe Asp

100

105

110

Thr Ser Phe Cys Phe Ala Ser Leu Phe His Leu Cys Cys Ile Ser Val

115

120

125

Asp Arg Tyr Ile Ala Val Thr Asp Pro Leu Thr Tyr Pro Thr Lys Phe

130

135

140

Thr Val Ser Val Ser Gly Ile Cys Ile Val Leu Ser Trp Phe Phe Ser

145

150

155

160

Val Thr Tyr Ser Phe Ser Ile Phe Tyr Thr Gly Ala Asn Glu Glu Gly

165

170

175

Ile Glu Glu Leu Val Val Ala Leu Thr Cys Val Gly Gly Cys Gln Ala

180

185

190

Pro Leu Asn Gln Asn Trp Val Leu Leu Cys Phe Leu Leu Phe Phe Ile

195

200

205

Pro Asn Val Ala Met Val Phe Ile Tyr Ser Lys Ile Phe Leu Val Ala

210

215

220

349/518

Lys His Gln Ala Arg Lys Ile Glu Ser Thr Ala Ser Gln Ala Gln Ser
 225 230 235 240
 Ser Ser Glu Ser Tyr Lys Glu Arg Val Ala Lys Arg Glu Arg Lys Ala
 245 250 255
 Ala Lys Thr Leu Gly Ile Ala Met Ala Ala Phe Leu Val Ser Trp Leu
 260 265 270
 Pro Tyr Leu Val Asp Ala Val Ile Asp Ala Tyr Met Asn Phe Ile Thr
 275 280 285
 Pro Pro Tyr Val Tyr Glu Ile Leu Val Trp Cys Val Tyr Tyr Asn Ser
 290 295 300
 Ala Met Asn Pro Leu Ile Tyr Ala Phe Phe Tyr Gln Trp Phe Gly Lys
 305 310 315 320
 Ala Ile Lys Leu Ile Val Ser Gly Lys Val Leu Arg Thr Asp Ser Ser
 325 330 335
 Thr Thr Asn Leu Phe Ser Glu Glu Val Glu Thr Asp Ala Ser Lys Gly
 340 345 350
 Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly
 355 360 365
 Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp
 370 375 380
 Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys
 385 390 395 400
 Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Cys Tyr Gly Val
 405 410 415
 Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe
 420 425 430
 Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe
 435 440 445
 Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly

350/518

450 455 460
 Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
 465 470 475 480
 Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His
 485 490 495
 Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn
 500 505 510
 Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp
 515 520 525
 His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro
 530 535 540
 Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn
 545 550 555 560
 Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly
 565 570 575
 Ile Thr His Gly Met Asp Glu Leu Tyr Asn
 580 585

<210> 128

<211> 1810

<212> PRT

<213> Human

<400> 128

Met Thr Pro Ala Cys Pro Leu Leu Leu Ser Val Ile Leu Ser Leu Arg
 5 10 15
 Leu Ala Thr Ala Phe Asp Pro Ala Pro Ser Ala Cys Ser Ala Leu Ala
 20 25 30
 Ser Gly Val Leu Tyr Gly Ala Phe Ser Leu Gln Asp Leu Phe Pro Thr

351/518

35	40	45			
Ile	Ala	Ser	Gly	Cys	Ser
Trp	Thr	Leu	Glu	Asn	Pro
Asp	Pro	Thr	Lys		
50	55	60			
Tyr	Ser	Leu	Tyr	Leu	Arg
Phe	Asn	Arg	Gln	Glu	Gln
Val	Cys	Ala	His		
65	70	75	80		
Phe	Ala	Pro	Arg	Leu	Leu
Pro	Leu	Asp	His	Tyr	Leu
Val	Asn	Phe	Thr		
85	90	95			
Cys	Leu	Arg	Pro	Ser	Pro
Glu	Glu	Ala	Val	Ala	Gln
Ala	Glu	Ser	Glu		
100	105	110			
Val	Gly	Arg	Pro	Glu	Glu
Glu	Glu	Ala	Glu	Ala	Ala
Ala	Gly	Leu	Glu		
115	120	125			
Leu	Cys	Ser	Gly	Ser	Gly
Pro	Phe	Thr	Phe	Leu	His
Phe	Asp	Lys	Asn		
130	135	140			
Phe	Val	Gln	Leu	Cys	Leu
Ser	Ala	Glu	Pro	Ser	Glu
Ala	Pro	Arg	Leu		
145	150	155	160		
Leu	Ala	Pro	Ala	Ala	Leu
Ala	Phe	Arg	Phe	Val	Glu
Val	Leu	Leu	Ile		
165	170	175			
Asn	Asn	Asn	Asn	Ser	Ser
Gln	Phe	Thr	Cys	Gly	Val
Leu	Cys	Arg	Trp		
180	185	190			
Ser	Glu	Glu	Cys	Gly	Arg
Ala	Ala	Gly	Arg	Ala	Cys
Gly	Phe	Ala	Gln		
195	200	205			
Pro	Gly	Cys	Ser	Cys	Pro
Gly	Glu	Ala	Gly	Ala	Gly
Ser	Thr	Thr	Thr		
210	215	220			
Thr	Ser	Pro	Gly	Pro	Pro
Ala	Ala	His	Thr	Leu	Ser
Asn	Ala	Leu	Val		
225	230	235	240		
Pro	Gly	Gly	Pro	Ala	Pro
Pro	Ala	Glu	Ala	Asp	Leu
His	Ser	Gly	Ser		
245	250	255			
Ser	Asn	Asp	Leu	Phe	Thr
Thr	Glu	Met	Arg	Tyr	Gly
Glu	Glu	Pro	Glu		
260	265	270			

352/518

Glu Glu Pro Lys Val Lys Thr Gln Trp Pro Arg Ser Ala Asp Glu Pro
 275 280 285
 Gly Leu Tyr Met Ala Gln Thr Gly Asp Pro Ala Ala Glu Glu Trp Ser
 290 295 300
 Pro Trp Ser Val Cys Ser Leu Thr Cys Gly Gln Gly Leu Gln Val Arg
 305 310 315 320
 Thr Arg Ser Cys Val Ser Ser Pro Tyr Gly Thr Leu Cys Ser Gly Pro
 325 330 335
 Leu Arg Glu Thr Arg Pro Cys Asn Asn Ser Ala Thr Cys Pro Val His
 340 345 350
 Gly Val Trp Glu Glu Trp Gly Ser Trp Ser Leu Cys Ser Arg Ser Cys
 355 360 365
 Gly Arg Gly Ser Arg Ser Arg Met Arg Thr Cys Val Pro Pro Gln His
 370 375 380
 Gly Gly Lys Ala Cys Glu Gly Pro Glu Leu Gln Thr Lys Leu Cys Ser
 385 390 395 400
 Met Ala Ala Cys Pro Val Glu Gly Gln Trp Leu Glu Trp Gly Pro Trp
 405 410 415
 Gly Pro Cys Ser Thr Ser Cys Ala Asn Gly Thr Gln Gln Arg Ser Arg
 420 425 430
 Lys Cys Ser Val Ala Gly Pro Ala Trp Ala Thr Cys Thr Gly Ala Leu
 435 440 445
 Thr Asp Thr Arg Glu Cys Ser Asn Leu Glu Cys Pro Ala Thr Asp Ser
 450 455 460
 Lys Trp Gly Pro Trp Asn Ala Trp Ser Leu Cys Ser Lys Thr Cys Asp
 465 470 475 480
 Thr Gly Trp Gln Arg Arg Phe Arg Met Cys Gln Ala Thr Gly Thr Gln
 485 490 495
 Gly Tyr Pro Cys Glu Gly Thr Gly Glu Glu Val Lys Pro Cys Ser Glu

353/518

500	505	510
Lys Arg Cys Pro Ala Phe His Glu Met Cys Arg Asp Glu Tyr Val Met		
515	520	525
Leu Met Thr Trp Lys Lys Ala Ala Ala Gly Glu Ile Ile Tyr Asn Lys		
530	535	540
Cys Pro Pro Asn Ala Ser Gly Ser Ala Ser Arg Arg Cys Leu Leu Ser		
545	550	555
Ala Gln Gly Val Ala Tyr Trp Gly Leu Pro Ser Phe Ala Arg Cys Ile		
565	570	575
Ser His Glu Tyr Arg Tyr Leu Tyr Leu Ser Leu Arg Glu His Leu Ala		
580	585	590
Lys Gly Gln Arg Met Leu Ala Gly Glu Gly Met Ser Gln Val Val Arg		
595	600	605
Ser Leu Gln Glu Leu Leu Ala Arg Arg Thr Tyr Tyr Ser Gly Asp Leu		
610	615	620
Leu Phe Ser Val Asp Ile Leu Arg Asn Val Thr Asp Thr Phe Lys Arg		
625	630	635
Ala Thr Tyr Val Pro Ser Ala Asp Asp Val Gln Arg Phe Phe Gln Val		
645	650	655
Val Ser Phe Met Val Asp Ala Glu Asn Lys Glu Lys Trp Asp Asp Ala		
660	665	670
Gln Gln Val Ser Pro Gly Ser Val His Leu Leu Arg Val Val Glu Asp		
675	680	685
Phe Ile His Leu Val Gly Asp Ala Leu Lys Ala Phe Gln Ser Ser Leu		
690	695	700
Ile Val Thr Asp Asn Leu Val Ile Ser Ile Gln Arg Glu Pro Val Ser		
705	710	715
Ala Val Ser Ser Asp Ile Thr Phe Pro Met Arg Gly Arg Arg Gly Met		
725	730	735

354/518

Lys Asp Trp Val Arg His Ser Glu Asp Arg Leu Phe Leu Pro Lys Glu

740

745

750

Val Leu Ser Leu Ser Ser Pro Gly Lys Pro Ala Thr Ser Gly Ala Ala

755

760

765

Gly Ser Pro Gly Arg Gly Arg Gly Pro Gly Thr Val Pro Pro Gly Pro

770

775

780

Gly His Ser His Gln Arg Leu Leu Pro Ala Asp Pro Asp Glu Ser Ser

785

790

795

800

Tyr Phe Val Ile Gly Ala Val Leu Tyr Arg Thr Leu Gly Leu Ile Leu

805

810

815

Pro Pro Pro Arg Pro Pro Leu Ala Val Thr Ser Arg Val Met Thr Val

820

825

830

Thr Val Arg Pro Pro Thr Gln Pro Pro Ala Glu Pro Leu Ile Thr Val

835

840

845

Glu Leu Ser Tyr Ile Ile Asn Gly Thr Thr Asp Pro His Cys Ala Ser

850

855

860

Trp Asp Tyr Ser Arg Ala Asp Ala Ser Ser Gly Asp Trp Asp Thr Glu

865

870

875

880

Asn Cys Gln Thr Leu Glu Thr Gln Ala Ala His Thr Arg Cys Gln Cys

885

890

895

Gln His Leu Ser Thr Phe Ala Val Leu Ala Gln Pro Pro Lys Asp Leu

900

905

910

Thr Leu Glu Leu Ala Gly Ser Pro Ser Val Pro Leu Val Ile Gly Cys

915

920

925

Ala Val Ser Cys Met Ala Leu Leu Thr Leu Leu Ala Ile Tyr Ala Ala

930

935

940

Phe Trp Arg Phe Ile Lys Ser Glu Arg Ser Ile Ile Leu Leu Asn Phe

945

950

955

960

Cys Leu Ser Ile Leu Ala Ser Asn Ile Leu Ile Leu Val Gly Gln Ser

355/518

	965	970	975
Arg Val Leu Ser Lys Gly Val Cys Thr Met Thr Ala Ala Phe Leu His			
	980	985	990
Phe Phe Phe Leu Ser Ser Phe Cys Trp Val Leu Thr Glu Ala Trp Gln			
	995	1000	1005
Ser Tyr Leu Ala Val Ile Gly Arg Met Arg Thr Arg Leu Val Arg Lys			
	1010	1015	1020
Arg Phe Leu Cys Leu Gly Trp Gly Leu Pro Ala Leu Val Val Ala Val			
	1025	1030	1035
Ser Val Gly Phe Thr Arg Thr Lys Gly Tyr Gly Thr Ser Ser Tyr Cys			
	1045	1050	1055
Trp Leu Ser Leu Glu Gly Gly Leu Leu Tyr Ala Phe Val Gly Pro Ala			
	1060	1065	1070
Ala Val Ile Val Leu Val Asn Met Leu Ile Gly Ile Ile Val Phe Asn			
	1075	1080	1085
Lys Leu Met Ala Arg Asp Gly Ile Ser Asp Lys Ser Lys Lys Gln Arg			
	1090	1095	1100
Ala Gly Ser Glu Arg Cys Pro Trp Ala Ser Leu Leu Leu Pro Cys Ser			
	1105	1110	1115
Ala Cys Gly Ala Val Pro Ser Pro Leu Leu Ser Ser Ala Ser Ala Arg			
	1125	1130	1135
Asn Ala Met Ala Ser Leu Trp Ser Ser Cys Val Val Leu Pro Leu Leu			
	1140	1145	1150
Ala Leu Thr Trp Met Ser Ala Val Leu Ala Met Thr Asp Arg Arg Ser			
	1155	1160	1165
Val Leu Phe Gln Ala Leu Phe Ala Val Phe Asn Ser Ala Gln Gly Phe			
	1170	1175	1180
Val Ile Thr Ala Val His Cys Phe Leu Arg Arg Glu Val Gln Asp Val			
	1185	1190	1195
			1200

356/518

Val Lys Cys Gln Met Gly Val Cys Arg Ala Asp Glu Ser Glu Asp Ser
 1205 1210 1215
 Pro Asp Ser Cys Lys Asn Gly Gln Leu Gln Ile Leu Ser Asp Phe Glu
 1220 1225 1230
 Lys Asp Val Asp Leu Ala Cys Gln Thr Val Leu Phe Lys Glu Val Asn
 1235 1240 1245
 Thr Cys Asn Pro Ser Thr Ile Thr Gly Thr Leu Ser Arg Leu Ser Leu
 1250 1255 1260
 Asp Glu Asp Glu Glu Pro Lys Ser Cys Leu Val Gly Pro Glu Gly Ser
 1265 1270 1275 1280
 Leu Ser Phe Ser Pro Leu Pro Gly Asn Ile Leu Val Pro Met Ala Ala
 1285 1290 1295
 Ser Pro Gly Leu Gly Glu Pro Pro Pro Pro Gln Glu Ala Asn Pro Val
 1300 1305 1310
 Tyr Met Cys Gly Glu Gly Gly Leu Arg Gln Leu Asp Leu Thr Trp Leu
 1315 1320 1325
 Arg Pro Thr Glu Pro Gly Ser Glu Gly Asp Tyr Met Val Leu Pro Arg
 1330 1335 1340
 Arg Thr Leu Ser Leu Gln Pro Gly Gly Gly Gly Gly Gly Glu Asp
 1345 1350 1355 1360
 Ala Pro Arg Ala Arg Pro Glu Gly Thr Pro Arg Arg Ala Ala Lys Thr
 1365 1370 1375
 Val Ala His Thr Glu Gly Tyr Pro Ser Phe Leu Ser Val Asp His Ser
 1380 1385 1390
 Gly Leu Gly Leu Gly Pro Ala Tyr Gly Ser Leu Gln Asn Pro Tyr Gly
 1395 1400 1405
 Met Thr Phe Gln Pro Pro Pro Pro Thr Pro Ser Ala Arg Gln Val Pro
 1410 1415 1420
 Glu Pro Gly Glu Arg Ser Arg Thr Met Pro Arg Thr Val Pro Gly Ser

357/518

1425	1430	1435	1440
Thr Met Lys Met Gly Ser Leu Glu Arg Lys Lys Leu Arg Tyr Ser Asp			
	1445	1450	1455
Leu Asp Phe Glu Val Met His Thr Arg Lys Arg His Ser Glu Leu Tyr			
	1460	1465	1470
His Glu Leu Asn Gln Lys Phe His Thr Phe Asp Arg Tyr Arg Ser Gln			
	1475	1480	1485
Ser Thr Ala Lys Arg Glu Lys Arg Trp Ser Val Ser Ser Gly Gly Ala			
	1490	1495	1500
Ala Glu Arg Ser Val Cys Thr Asp Lys Pro Ser Pro Gly Glu Arg Pro			
1505	1510	1515	1520
Ser Leu Ser Gln His Arg Arg His Gln Ser Trp Ser Thr Phe Lys Ser			
	1525	1530	1535
Met Thr Leu Gly Ser Leu Pro Pro Lys Pro Arg Glu Arg Leu Thr Leu			
	1540	1545	1550
His Arg Ala Ala Ala Trp Glu Pro Thr Glu Pro Pro Asp Gly Asp Phe			
	1555	1560	1565
Gln Thr Glu Val Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val			
	1570	1575	1580
Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser			
1585	1590	1595	1600
Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu			
	1605	1610	1615
Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu			
	1620	1625	1630
Val Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp			
	1635	1640	1645
His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr			
	1650	1655	1660

358/518

Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr
 1665 1670 1675 1680
 Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu
 1685 1690 1695
 Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys
 1700 1705 1710
 Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys
 1715 1720 1725
 Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu
 1730 1735 1740
 Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
 1745 1750 1755 1760
 Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln
 1765 1770 1775
 Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
 1780 1785 1790
 Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu
 1795 1800 1805
 Tyr Asn
 1810

<210> 129

<211> 563

<212> PRT

<213> Human

<400> 129

Met Asp Gly Ser Asn Val Thr Ser Phe Val Val Glu Glu Pro Thr Asn

359/518

Ile Ser Thr Gly Arg Asn Ala Ser Val Gly Asn Ala His Arg Gln Ile
 20 25 30
 Pro Ile Val His Trp Val Ile Met Ser Ile Ser Pro Val Gly Phe Val
 35 40 45
 Glu Asn Gly Ile Leu Leu Trp Phe Leu Cys Phe Arg Met Arg Arg Asn
 50 55 60
 Pro Phe Thr Val Tyr Ile Thr His Leu Ser Ile Ala Asp Ile Ser Leu
 65 70 75 80
 Leu Phe Cys Ile Phe Ile Leu Ser Ile Asp Tyr Ala Leu Asp Tyr Glu
 85 90 95
 Leu Ser Ser Gly His Tyr Tyr Thr Ile Val Thr Leu Ser Val Thr Phe
 100 105 110
 Leu Phe Gly Tyr Asn Thr Gly Leu Tyr Leu Leu Thr Ala Ile Ser Val
 115 120 125
 Glu Arg Cys Leu Ser Val Leu Tyr Pro Ile Trp Tyr Arg Cys His Arg
 130 135 140
 Pro Lys Tyr Gln Ser Ala Leu Val Cys Ala Leu Leu Trp Ala Leu Ser
 145 150 155 160
 Cys Leu Val Thr Thr Met Glu Tyr Val Met Cys Ile Asp Arg Glu Glu
 165 170 175
 Glu Ser His Ser Arg Asn Asp Cys Arg Ala Val Ile Ile Phe Ile Ala
 180 185 190
 Ile Leu Ser Phe Leu Val Phe Thr Pro Leu Met Leu Val Ser Ser Thr
 195 200 205
 Ile Leu Val Val Lys Ile Arg Lys Asn Thr Trp Ala Ser His Ser Ser
 210 215 220
 Lys Leu Tyr Ile Val Ile Met Val Thr Ile Ile Ile Phe Leu Ile Phe
 225 230 235 240
 Ala Met Pro Met Arg Leu Leu Tyr Leu Leu Tyr Tyr Glu Tyr Trp Ser

360/518

	245	250	255
Thr Phe Gly Asn Leu His His Ile Ser Leu Leu Phe Ser Thr Ile Asn			
	260	265	270
Ser Ser Ala Asn Pro Phe Ile Tyr Phe Phe Val Gly Ser Ser Lys Lys			
	275	280	285
Lys Arg Phe Lys Glu Ser Leu Lys Val Val Leu Thr Arg Ala Phe Lys			
	290	295	300
Asp Glu Met Gln Pro Arg Arg Gln Lys Asp Asn Cys Asn Thr Val Thr			
305	310	315	320
Val Glu Thr Val Val Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val			
	325	330	335
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe			
	340	345	350
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr			
	355	360	365
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr			
	370	375	380
Leu Val Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro			
385	390	395	400
Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly			
	405	410	415
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys			
	420	425	430
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile			
	435	440	445
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His			
	450	455	460
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp			
465	470	475	480

361/518

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile
 485 490 495
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 500 505 510
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 515 520 525
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 530 535 540
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 545 550 555 560
 Leu Tyr Asn

<210> 130

<211> 707

<212> PRT

<213> Human

<400> 130

Met Gln Met Ala Asp Ala Ala Thr Ile Ala Thr Met Asn Lys Ala Ala
 5 10 15
 Gly Gly Asp Lys Leu Ala Glu Leu Phe Ser Leu Val Pro Asp Leu Leu
 20 25 30
 Glu Ala Ala Asn Thr Ser Gly Asn Ala Ser Leu Gln Leu Pro Asp Leu
 35 40 45
 Trp Trp Glu Leu Gly Leu Glu Leu Pro Asp Gly Ala Pro Pro Gly His
 50 55 60
 Pro Pro Gly Ser Gly Gly Ala Glu Ser Ala Asp Thr Glu Ala Arg Val
 65 70 75 80
 Arg Ile Leu Ile Ser Val Val Tyr Trp Val Val Cys Ala Leu Gly Leu

362/518

85	90	95
Ala Gly Asn Leu Leu Val Leu Tyr Leu Met Lys Ser Met Gln Gly Trp		
100	105	110
Arg Lys Ser Ser Ile Asn Leu Phe Val Thr Asn Leu Ala Leu Thr Asp		
115	120	125
Phe Gln Phe Val Leu Thr Leu Pro Phe Trp Ala Val Glu Asn Ala Leu		
130	135	140
Asp Phe Lys Trp Pro Phe Gly Lys Ala Met Cys Lys Ile Val Ser Met		
145	150	155
Val Thr Ser Met Asn Met Tyr Ala Ser Val Phe Phe Leu Thr Ala Met		
165	170	175
Ser Val Thr Arg Tyr His Ser Val Ala Ser Ala Leu Lys Ser His Arg		
180	185	190
Thr Arg Gly His Gly Arg Gly Asp Cys Cys Gly Arg Ser Leu Gly Asp		
195	200	205
Ser Cys Cys Phe Ser Ala Lys Ala Leu Cys Val Trp Ile Trp Ala Leu		
210	215	220
Ala Ala Leu Ala Ser Leu Pro Ser Ala Ile Phe Ser Thr Thr Val Lys		
225	230	235
Val Met Gly Glu Glu Leu Cys Leu Val Arg Phe Pro Asp Lys Leu Leu		
245	250	255
Gly Arg Asp Arg Gln Phe Trp Leu Gly Leu Tyr His Ser Gln Lys Val		
260	265	270
Leu Leu Gly Phe Val Leu Pro Leu Gly Ile Ile Ile Leu Cys Tyr Leu		
275	280	285
Leu Leu Val Arg Phe Ile Ala Asp Arg Arg Ala Ala Gly Thr Lys Gly		
290	295	300
Gly Ala Ala Val Ala Gly Gly Arg Pro Thr Gly Ala Ser Ala Arg Arg		
305	310	315
		320

363/518

Leu Ser Lys Val Thr Lys Ser Val Thr Ile Val Val Leu Ser Phe Phe
 325 330 335
 Leu Cys Trp Leu Pro Asn Gln Ala Leu Thr Thr Trp Ser Ile Leu Ile
 340 345 350
 Lys Phe Asn Ala Val Pro Phe Ser Gln Glu Tyr Phe Leu Cys Gln Val
 355 360 365
 Tyr Ala Phe Pro Val Ser Val Cys Leu Ala His Ser Asn Ser Cys Leu
 370 375 380
 Asn Pro Val Leu Tyr Cys Leu Val Arg Arg Glu Phe Arg Lys Ala Leu
 385 390 395 400
 Lys Ser Leu Leu Trp Arg Ile Ala Ser Pro Ser Ile Thr Ser Met Arg
 405 410 415
 Pro Phe Thr Ala Thr Thr Lys Pro Glu His Glu Asp Gln Gly Leu Gln
 420 425 430
 Ala Pro Ala Pro Pro His Ala Ala Ala Glu Pro Asp Leu Leu Tyr Tyr
 435 440 445
 Pro Pro Gly Val Val Val Tyr Ser Gly Gly Arg Tyr Asp Leu Leu Pro
 450 455 460
 Ser Ser Ser Ala Tyr Thr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 465 470 475 480
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 485 490 495
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 500 505 510
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 515 520 525
 Leu Val Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 530 535 540
 Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly

364/518

545 550 555 560
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 565 570 575
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 580 585 590
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 595 600 605
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 610 615 620
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile
 625 630 635 640
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 645 650 655
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 660 665 670
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 675 680 685
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 690 695 700
 Leu Tyr Asn
 705

<210> 131

<211> 746

<212> PRT

<213> Human

<400> 131

Met Thr Ser Thr Cys Thr Asn Ser Thr Arg Glu Ser Asn Ser Ser His

365/518

	5	10	15
Thr Cys Met Pro Leu Ser Lys Met Pro Ile Ser Leu Ala His Gly Ile			
	20	25	30
Ile Arg Ser Thr Val Leu Val Ile Phe Leu Ala Ala Ser Phe Val Gly			
	35	40	45
Asn Ile Val Leu Ala Leu Val Leu Gln Arg Lys Pro Gln Leu Leu Gln			
	50	55	60
Val Thr Asn Arg Phe Ile Phe Asn Leu Leu Val Thr Asp Leu Leu Gln			
	65	70	75
Ile Ser Leu Val Ala Pro Trp Val Val Ala Thr Ser Val Pro Leu Phe			
	85	90	95
Trp Pro Leu Asn Ser His Phe Cys Thr Ala Leu Val Ser Leu Thr His			
	100	105	110
Leu Phe Ala Phe Ala Ser Val Asn Thr Ile Val Leu Val Ser Val Asp			
	115	120	125
Arg Tyr Leu Ser Ile Ile His Pro Leu Ser Tyr Pro Ser Lys Met Thr			
	130	135	140
Gln Arg Arg Gly Tyr Leu Leu Leu Tyr Gly Thr Trp Ile Val Ala Ile			
	145	150	155
Leu Gln Ser Thr Pro Pro Leu Tyr Gly Trp Gly Gln Ala Ala Phe Asp			
	165	170	175
Glu Arg Asn Ala Leu Cys Ser Met Ile Trp Gly Ala Ser Pro Ser Tyr			
	180	185	190
Thr Ile Leu Ser Val Val Ser Phe Ile Val Ile Pro Leu Ile Val Met			
	195	200	205
Ile Ala Cys Tyr Ser Val Val Phe Cys Ala Ala Arg Arg Gln His Ala			
	210	215	220
Leu Leu Tyr Asn Val Lys Arg His Ser Leu Glu Val Arg Val Lys Asp			
	225	230	235
			240

366/518

Cys Val Glu Asn Glu Asp Glu Glu Gly Ala Glu Lys Lys Glu Glu Phe
 245 250 255
 Gln Asp Glu Ser Glu Phe Arg Arg Gln His Glu Gly Glu Val Lys Ala
 260 265 270
 Lys Glu Gly Arg Met Glu Ala Lys Asp Gly Ser Leu Lys Ala Lys Glu
 275 280 285
 Gly Ser Thr Gly Thr Ser Glu Ser Ser Val Glu Ala Arg Gly Ser Glu
 290 295 300
 Glu Val Arg Glu Ser Ser Thr Val Ala Ser Asp Gly Ser Met Glu Gly
 305 310 315 320
 Lys Glu Gly Ser Thr Lys Val Glu Glu Asn Ser Met Lys Ala Asp Lys
 325 330 335
 Gly Arg Thr Glu Val Asn Gln Cys Ser Ile Asp Leu Gly Glu Asp Asp
 340 345 350
 Met Glu Phe Gly Glu Asp Asp Ile Asn Phe Ser Glu Asp Asp Val Glu
 355 360 365
 Ala Val Asn Ile Pro Glu Ser Leu Pro Pro Ser Arg Arg Asn Ser Asn
 370 375 380
 Ser Asn Pro Pro Leu Pro Arg Cys Tyr Gln Cys Lys Ala Ala Lys Val
 385 390 395 400
 Ile Phe Ile Ile Ile Phe Ser Tyr Val Leu Ser Leu Gly Pro Tyr Cys
 405 410 415
 Phe Leu Ala Val Leu Ala Val Trp Val Asp Val Glu Thr Gln Val Pro
 420 425 430
 Gln Trp Val Ile Thr Ile Ile Ile Trp Leu Phe Phe Leu Gln Cys Cys
 435 440 445
 Ile His Pro Tyr Val Tyr Gly Tyr Met His Lys Thr Ile Lys Lys Glu
 450 455 460
 Ile Gln Asp Met Leu Lys Lys Phe Phe Cys Lys Glu Lys Pro Pro Lys

367/518

465	470	475	480
Glu Asp Ser His Pro Asp Leu Pro Gly Thr Glu Gly Gly Thr Glu Gly			
	485	490	495
Lys Ile Val Pro Ser Tyr Asp Ser Ala Thr Phe Pro Ala Ser Lys Gly			
	500	505	510
Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly			
	515	520	525
Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp			
	530	535	540
Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys			
545	550	555	560
Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Cys Tyr Gly Val			
	565	570	575
Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe			
	580	585	590
Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe			
	595	600	605
Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly			
	610	615	620
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu			
625	630	635	640
Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His			
	645	650	655
Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn			
	660	665	670
Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp			
	675	680	685
His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro			
	690	695	700

368/518

Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn
 705 710 715 720
 Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly
 725 730 735
 Ile Thr His Gly Met Asp Glu Leu Tyr Asn
 740 745

<210> 132

<211> 1635

<212> DNA

<213> Human

<400> 132

atgtattcat ttatggcagg atccatattc atcacaatat ttggcaatct tgccatgata 60
 atttccattt cctacttcaa gcagcttcac acaccaacca acttccctcat cctctccatg 120
 gccatcactg atttccctct gggattcacc atcatgccat atagtatgat cagatcggtg 180
 gagaactgct ggtatttttg gcttacattt tgcaagattt attatagttt tgacctgatg 240
 cttagcataa catccatttt tcattcttgc tcagtggcca ttgatagatt ttatgctata 300
 tgttaccat tactttattc caccaaaata actattccag tcattaaaag attgctactt 360
 ctatgttggc cgggtccctgg agcatttgcc ttccgggttg tcttctcaga ggcctatgca 420
 gatggaatag agggctatga catcttggtt gcttgttcca gtctctgccc agtgatgttc 480
 aacaagctat gggggaccac ctgtttatg gcaggtttct tcactcctgg gtcctatgatg 540
 gtggggattt atggcaaaat ttttgagta tccagaaaac atgctcatgc catcaataac 600
 ttgcgagaaa atcaaaataa tcaagtgaag aaagacaaaa aagctgcca aacttttagga 660
 atagtgatag gagttttctt attatgttgg tttccttggt tcttcacaat tttattggat 720
 cccittttga acttctctac tcctgtagtt ttgtttgatg ccttgacatg gtttggctat 780
 ttttaactcca catgtaatcc gtttaatat ggtttcttct atccctgggt tcgcagagca 840
 ctgaagtaca ttttgctagg taaaattttc agctcatgtt tccataatac tatttttgtt 900
 atgcaaaaag aaagtgaggc tagcaaagga gaagaactct tcactggagt tgtcccaatt 960

369/518

ctgttgaat tagatggiga tgtaacggc cacaagttct ctgtcagtg agagggtgaa 1020
 ggigatgcaa calacggaaa acttaccctg aagttcatct gcactactgg caaacigcct 1080
 gtccatggc caacactagt cactactctg tgctatggig ttcaatgctt ttcaagatac 1140
 ccggatcata tgaaacggca tgactttttc aagagtgcc aagccgaagg ttaigtacag 1200
 gaaaggacca tcttcttcaa agatgacggc aactacaaga cacgtgctga agtcaagttt 1260
 gaaggigata cccttggtta tagaatcgag ttaaaaggta ttgacttcaa ggaagatggc 1320
 aacattctgg gacacaaatt ggaatacaac tataactcac acaatgtata catcatggca 1380
 gacaaacaaa agaattggaat caaagtgaac ttcaagaccc gccacaacat tgaagatgga 1440
 agcgttcaac tagcagacca ttatcaacaa aatactccaa ttggcgatgg ccctgtcctt 1500
 ttaccagaca accattacct gtccacacaa tctgcccttt cgaaagatcc caacgaaaag 1560
 agagaccaca tggctcttct tgagtttgta acagctgctg ggattacaca tggcatggat 1620
 gaactgtaca actga 1635

<210> 133

<211> 1839

<212> DNA

<213> Human

<400> 133

atgccacac tcaatacttc tgcctctcca cccacattct tctgggcca tgcctccgga 60
 ggcagtgtgc tgagtgtga tgaigtccg atgctgtca aattcctagc cctgaggctc 120
 atggttgccc tggcctatgg gcitgtgggg gccattggct tgcigggaaa tttggcggtg 180
 ctgtgggtac tgagtaactg tggcggaga gcccctggcc caccttcaga caccttcgtc 240
 ttcaacctgg ctctggcgga cctgggactg gcactcactc tccccctttg ggcagccgag 300
 tcggcactgg actttactg gcccttcgga ggtgccctct gcaagatggt tctgacggcc 360
 actgtcctca acgtctatgc cagcatcttc ctcatcacag cgctgagcgt tgctcgctac 420
 tgggigggtg ccatggctgc ggggccaggc acccacctct cactcttctg ggcccgaata 480
 gccaccctgg cagtgtgggc ggcggctgcc ctggtgacgg tggccacagc tgtcttcggg 540
 gtggagggtg aggtgtgtgg tgtgcgcctt tgcctgctgc gtttccccag caggtactgg 600

370/518

ctgggggcct accagctgca gagggtggtg ctggccttca tggtgccctt gggcgctatc 660
 accaccagct acctgctgct gctggccttc ctgcagcggc ggcaacggcg gcggcaggac 720
 agcagggctg tggcccgtc tgtccgcatc ctggctggctt ccttcttctt ctgctggttt 780
 cccaacctg tggcactct ctggggtgtc ctggctgaagt ttgacctggt gccctggaac 840
 agtactttct atactatcca gacgtatgtc ttccctgtca ctacttgctt ggcacacagc 900
 aatagctgcc tcaacctgt gctgtactgt ctccctgaggc gggagccccg gcaggctctg 960
 gcaggcacct tcagggatct gcggctgagg ctgtggcccc agggcggagg ctgggtgcaa 1020
 caggtggccc taaagcaggt aggcaggcgg tgggtcgcaa gcaacccccg ggagagccgc 1080
 ccttctaccc tgcacacaa cctggacaga gggacacccg gggctagcaa aggagaagaa 1140
 ctcttctactg gagtgtctcc aattcttgtt gaattagatg gtgatgttaa cggccacaag 1200
 ttctctgtca gtggagagg tgaaggatg gcaacatagc gaaaacttac cctgaagttc 1260
 atctgcacta ctggcaaact gccgtgtcca tggccaacac tagtactac tctgtgtat 1320
 ggtgttcaat gcttttcaag ataccggat catatgaaac ggcatgactt tttcaagagt 1380
 gccatgcccc aaggttatgt acaggaaagg accatcttct tcaaagatga cggcaactac 1440
 aagacacgtg ctgaagtcaa gtttgaaggt gatacccttg ttaatagaat cgagttaaaa 1500
 ggtattgact tcaaggaaga tggcaacatt ctgggacaca aattggaata caactataac 1560
 tcacacaatg tatacatcat ggcagacaaa caaaagaatg gaatcaaagt gaacttcaag 1620
 acccgccaca acattgaaga tggaaagctt caactagcag accattatca acaaaatact 1680
 ccaattggcg atggccctgt ccttttacca gacaaccatt acctgtccac acaatctgcc 1740
 ctctcgaaag atcccaacga aaagagagac cacatggtcc ttcttgagtt tgtaacagct 1800
 gctgggatta cacatggcat ggalgaactg tacaactga 1839

<210> 134

<211> 1800

<212> DNA

<213> Human

<400> 134

atgtccccctg aatgcgcgcg ggcagcgggc gacgcgccct tgcgcagcct ggagcaagcc 60

371/518

aaccgcaccc gctttccctt ctctccgac gtcaaggcg accaccggct ggtgctggcc 120
gcggiggaga caaccgtgt ggtgctcgc ttgacagtgt cgtgctggg caacgtgtgc 180
gccctggigc tggggcgcg ccgacgacgc cgcggcgga ctgctgcct ggtactcaac 240
ctctctgcg cggacctgt ctcatcagc gctatccctc tgggctggc cgtgcgtgg 300
actgaggcct ggtgctggg ccccggtgc tggacctgc tctctacgt gatgacctg 360
agcggcagcg tcaccatcct cagctggcc gcggtcagcc tggagcgat ggtgtgcatc 420
gtgcacctgc agcggcggt gcgggtcct ggcggcggg cgcggcgagt gctgctggcg 480
ctcatctggg gctattcggc ggtcgccgt ctgcctctct gcgtctctt ccgagtcgtc 540
ccgcaacggc tccccggcg cgaccaggaa atttcgattt gcacacgat ttggcccacc 600
attcctggag agatctcgtg ggtgtctct tttgttactt tgaacttctt ggtgccagga 660
ctggtcattg tgatcagta ctccaaaatt ttacagatca caaaggcatc aaggaagagg 720
ctcacggtaa gcctggccta ctggagagc caccagatcc gcgtgtccca gcaggacttc 780
cggtcttcc gcacctctt cctctcatg gtctctctt tcatcatgtg gagccccatc 840
atcatcacca tctctctcat cctgatccag aacttcaagc aagacctgt catctggccg 900
tccctcttct tctgggtgtt ggcttcaca ttgtctaatt cagccctaaa ccccatcctc 960
tacaacatga cactgtgcag gaatgagtgg aagaaaattt ttgtctgtt ctggttccca 1020
gaaaaggag ccattttaac agacacatct gtcaaaagaa atgacttgc gattatttct 1080
ggcgttagca aaggagaaga actcttact ggagtgtcc caattctgt tgaattagat 1140
ggtgatgta acggccacaa gtctctgtc agtggagagg gtgaaggta tgcaacatac 1200
ggaaaactta cctgaagtt catctgcact actggcaaac tgcctgttcc atggccaaca 1260
ctagtcacta ctctgtgcta tgggtgtcaa tgctttcaa gataccgga tcatatgaaa 1320
cgcatgact tttcaagag tgccatgcc gaaggttatg tacaggaaag gaccatctc 1380
ttcaaagatg acggcaacta caagacagc gctgaagtca agtttgaagg tgataccctt 1440
gttaatagaa tcgagttaaa aggtattgac ttcaaggaag atggcaacat tctgggacac 1500
aaattggaat acaactataa ctacacaaat gtatacatca iggcagacaa aaaaaagaat 1560
ggaatcaaag tgaacttcaa gaccgccac aacattgaag atggaagcgt tcaactagca 1620
gaccattatc aaaaaatac tccaattggc gatggccctg tcttttacc agacaacat 1680
tacctgtcca cacaatctgc ctttcgaaa gatcccaacg aaaagagaga ccacatggtc 1740
ctcttgagt ttgtaacagc tgcgggatt acacatggca tggatgaact gtacaactga 1800

372/518

<210> 135

<211> 2673

<212> DNA

<213> Human

<400> 135

atgcaggac cattgcttct tccaggcctc tgctttctgc tgagcctctt tggagctgtg 60
actcagaaaa ccaaaacttc ctgtgctaag tgcccccaa atgcttcctg tgtcaataac 120
actcactgca cctgcaacca tggatatact tctggatctg ggcagaaact attcacattc 180
cccttggaga catgtaacga cattaatgaa tgcacaccac cctatagtgt atattgtgga 240
ttaaagctg tgtgttaca tgcgaagga agtttctact gtcaatgtgt cccaggatat 300
agactgcatt ctgggaatga acaattcagt aattccaatg agaacacctg tcaggacacc 360
acctctcaa agacaacca gggcaggaaa gagctgcaaa agattgtgga caaatttgag 420
tcacttctca ccaatcagac ttatggaga acagaaggga gacaagaaat ctcatccaca 480
gtaccacta ttctccggga tgtggaatcg aaagttctag aaactgccit gaaagatcca 540
gaacaaaaag tctgaaaaat ccaaaacgat agttagcta ttgaaactca agcgattaca 600
gacaattgct ctgaagaaag aaagacattc aacttgaacg tccaaatgaa ctcaatggac 660
atccgttgca gtgacatcat ccaggagac acacaaggtc ccagtgccat tgcctttatc 720
tcataattct ctcttgaaa catcataaat gcaacttttt ttgaagagat ggataagaaa 780
gatcaagtgt atctgaactc tcaggttgtg agtgctgcta ttggaccaa aaggaacgtg 840
tctctctcca agtctgtgac gctgacttgc cagcacgtga agatgacccc cagtacaaa 900
aaggtcttct gtgtctactg gaagagcaca gggcagggca gccagtgtc cagggatggc 960
tgcttctga tacacgtgaa caagagtcac accatgtgta attgcagtca cctgtccagc 1020
ttcgctgtcc tgatggccct gaccagccag gaggaggatc ccgtgtgac tgtcatcacc 1080
tacgtggggc tgagcgtctc tctgtgtgc ctctcctgg cggccctcac ttttctcctg 1140
tgtaaagcca tccagaacac cagcacctca ctgcatctgc agctctcgct ctgcctcttc 1200
ctggcccacc tctcttctct cgtggggatt gatcgaactg aaccaaggt gctgtgtcc 1260
atcatgccc gtgctttgca ctatctctac ctggccgctt tcacctggat gctgtgtgag 1320

373/518

ggigtgcacc tcttcctcac tgcacggaac ctgacagigg tcaactactc aagcatcaat 1380
 agactcatga agtggatcat gttcccagtc ggctatggcg ttcccgcgtg gactgtggcc 1440
 atttctgcag cctcctggcc tcacctttat ggaactgctg atcgatgctg gctccacctg 1500
 gaccagggat tcatgtggag tticcttggc ccagtcctgt ccatittctc tgcgaattta 1560
 gtattgttta tcttggcttt ttggattttg aaaagaaaac tticctccct caatagttaa 1620
 gtgtcaacca tccagaacac aaggatgctg gctttcaaag caacagctca gctcttcac 1680
 ctgggctgca catggtgtct gggcttggta cagggtgggtc cagctgcccc ggtcatggcc 1740
 tacctcttca ccatcatcaa cagcctccaa ggcttcttca tcttcttggc ctactgcctc 1800
 ctccagccagc aggtccagaa acaatatcaa aagtggttta gagagatcgt aaaatcaaaa 1860
 tctgagcttg agacatacac actttccagc aagatgggtc ctgactcaa acccagtgag 1920
 ggggatgttt ttccaggaca agtgaagaga aaataigcta gcaaaggaga agaactcttc 1980
 actggagtig tccaattct tgtgaatta gatggtgatg ttaacggcca caagtictct 2040
 gtcagtggag agggatgaagg tgatgaaca tacggaaaac ttaccctgaa gticactgctc 2100
 actactggca aacigcctgt tccatggcca acactagtca ctactctgtg ctatggtgtt 2160
 caatgcittt caagataccc ggalcatatg aaacggcatg actttttcaa gagtgccatg 2220
 cccgaagggt atgtacagga aaggaccatc ttcttcaaag atgacggcaa ctacaagaca 2280
 cgtgctgaag tcaagtttga aggtgatacc cttgttaata gaatcgagtt aaaaggtatt 2340
 gacttcaagg aagatggcaa cattctggga cacaattgg aatacaacta taactcacac 2400
 aatgtatata tcatggcaga caaacaaaag aatggaatca aagtgaactt caagaccgc 2460
 cacaacattg aagatggaag cgttcaacta gcagaccatt atcaacaaaa tactccaatt 2520
 ggcatggcc ctgtcctttt accagacaac cattacctgt ccacacaatc tgccctttcg 2580
 aaagatccca acgaaaagag agaccacatg gtccttcttg agtttgtaac agctgctggg 2640
 attacacatg gcatggatga actgtacaac tga 2673

<210> 136

<211> 1797

<212> DNA

<213> Human

374/518

<400> 136

atggacccag aagaaacttc agtttatttg gattattact atgctacgag cccaaactct 60
gacatcaggg agaccacatc ccatgttcct tacacctctg tcttccctcc agtcttttac 120
acagctgtgt tcttgactgg agtgctgggg aaccttggtc tcatgggagc gttgcatttc 180
aaacccggca gccgaagact gatcgacatc tttatcatca atctggctgc ctctgacttc 240
atttttcttg tcacattgcc tctctgggtg gataaagaag catctctagg actgtggagg 300
acgggctcct tectgtgcaa agggagctcc tacatgatct cegtcaatat gcactgcagt 360
gtcctccctgc tcaattgcat gagtgttgac cgctacctgg ccattgtgtg gccagtcgta 420
tccaggaaat tcagaaggac agactgtgca tatgtagtct gtgccagcat ctggttttac 480
tcttcctgc tggggttgcc tactctcttg tccagggagc tcacgtgat tgatgataag 540
ccatactgtg cagagaaaaa ggcaactcca attaaactca tatggctcct ggtggcctta 600
attttacct tttttgtccc tttgttgagc attgtgacct gctactgttg cattgcaagg 660
aagctgtgtg ccattacca gcaatcagga aagcacaaca aaaagctgaa gaaatctata 720
aagatcatct ttattgtcgt ggcagccttt ctgtctcct ggctgccctt caatactttc 780
aagttccctgg ccattgtctc tgggttgagg caagaacact atttaccctc agctattctt 840
cagcttggtg tggagggtgag tggacccttg gcatttgcca acagctgtgt caacccttc 900
atttactata tcttcgacag ctacatccgc cgggccattg tccactgctt gtgcccttgc 960
ctgaaaaact atgacttttg gagtagcact gagacatcag atagtcacct cactaaggct 1020
ctctccacct tcattcatgc agaagatctt gccaggagga ggaagaggtc tgtgtcactc 1080
gctagcaaag gagaagaact cttcactgga gttgtcccaa ttcttgttga attagatggt 1140
gatgttaacg gccacaagtt ctctgtcagt ggagagggtg aaggtgatgc aacatacggg 1200
aaacttaccg tgaagttcat ctgcactact ggcaaacctgc ctgttccatg gccaacacta 1260
gtcactactc tgtgctatgg tgttcaatgc ttttcaagat acccgatca tatgaaacgg 1320
catgactttt tcaagagtgc catgccgaa gggtatgtac aggaaaggac catcttcttc 1380
aaagatgacg gcaactacaa gacacgtgct gaagtcaagt ttgaaggiga tacccttggt 1440
aatagaatcg agttaaagg tattgacttc aaggaagatg gcaacattct gggacacaaa 1500
ttggaataca actataactc acacaatgta tacatcatgg cagacaaaca aaagaatgga 1560
atcaaagtga acttcaagac ccgccacaac attgaagatg gaagcgttca actagcagac 1620
cattatcaac aaaatactcc aattggcgat ggccctgtcc ttttaccaga caaccattac 1680

375/518

ctgtccacac aatctgccct ttcgaaagat cccaacgaaa agagagacca catggtcctt 1740
 cttgagittg taacagctgc tgggattaca catggcatgg atgaactgia caactga 1797

<210> 137

<211> 1674

<212> DNA

<213> Human

<400> 137

atgccattcc caaactgctc agccccagc actgtggtag ccacagctgt ggggtgtctt 60
 ctggggctgg agtgtgggt gggctctgtg ggcaacgcgg tggcgctgtg gaccttctg 120
 ttccgggtca ggggtgtgaa gccgtacgt gctacctgc tcaacctggc cctggctgac 180
 ctgtgttgg ctgcgtgcct gcccttctg gccgccttct acctgagcct ccaggcttgg 240
 catctgggcc gtgtgggctg ctgggcctg cgttctctg tggacctcag ccgcagcgtg 300
 gggatggcct tcttggccgc cgtggcttgg gaccggtacc tccgtgtggt ccacctcgg 360
 cttaaggta acctgctgtc tctcaggcg gccctggggg tctcgggcct cgtctggctc 420
 ctgatggctg cctcaccctg cccgggctt ctcattctg aggccgcca gaactccacc 480
 aggtgccaca gtttctactc cagggcagac ggctccttca gcatcatctg gcaggaagca 540
 ctctcttgc ttcagtttgt cctccccctt ggctcatcg tgttctgcaa tgcaggcatc 600
 atcagggtc tccagaaaag actccgggag cctgagaaac agcccaagct tcagcgggcc 660
 caggcactgg tcaccttggg ggtgggtgtg ttgtctgtg gctttctgcc ctgcttctg 720
 gccagagtc tgatgcacat ctccagaat ctggggagct gcagggccct ttgtgcagt 780
 gctataacct cggatgtcac gggcagcctc acctacctg acagtgtgt caacccctg 840
 gtatactgt tctccagccc caccctcagg agctcctatc ggagggtctt ccacaccctc 900
 cgaggcaaag ggcaggcagc agagcccca gatttcaacc ccagagactc ctattccgt 960
 agcaaaggag aagaactctt cactggagtt gtcccaattc ttgttgaatt agatggtgat 1020
 gttacggcc acaagtctc tgtcagtga gagggtgaag gtgatgcaac atacgaaaa 1080
 cttaacctga agttcatctg cactactggc aaactgcctg ttccatggcc aacactagt 1140
 actactctgt gctatgggtg tcaatgctt tcaagatacc cggatcatat gaaacggcat 1200

376/518

gactttttca agagtgccat gcccgaaggt tatgtacagg aaaggacat cttcttcaaa 1260
 gatgacggca actacaagac acgtgctgaa gtcaagtttg aagtgatac cttgttaat 1320
 agaatcgagt taaaaggat tgacttcaag gaagatggca acattctggg acacaaattg 1380
 gaatacaact ataactcaca caatgtatac atcatggcag acaaacaaaa gaatggaatc 1440
 aaagtgaact tcaagaccgg ccacaacatt gaagatggaa gcgttcaact agcagacat 1500
 tatcaacaaa atactccaat tggcgtggc cctgtccttt taccagacaa ccattacctg 1560
 tccacacaat ctgccctttc gaaagatccc aacgaaaaga gagaccacat ggtccttctt 1620
 gagtttgtaa cagctgctgg gattacacat ggcatggaig aactgtacaa ctga 1674

<210> 138

<211> 1926

<212> DNA

<213> Human

<400> 138

atgttcgtgg catcagagag aaagatgaga gctcaccagg tgctcacctt cctcctgctc 60
 ttctgtatca cctcggctggc ctctgaaaac gccagcacat cccgaggctg tgggctggac 120
 ctccctccctc agtacgtgtc cctgtgcgac ctggacgcca tctggggcat tgtgggtggag 180
 gcgggtggccg gggcggggcg cctgatcaca ctgctcctga tgcctatcct cctgggtgcgg 240
 ctgcccttca tcaaggagaa ggagaagaag agccctgtgg gcctccactt tctgttctc 300
 ctgggggacc tgggcctctt tgggctgacg ttgacctca tcatccagga ggacgagacc 360
 atctgctctg tccgccgctt cctctggggc gtcctctttg cgctctgctt ctccctgctg 420
 ctgagccagg catggcgctt gcggaggctg gtgcggcatg gcacggggcc cgcgggctgg 480
 cagctggctg gcctggcgct gtgcctgatg ctgggtgcaag tcatcatcgc tgtggagtgg 540
 ctgggtgctca ccgtgctgcg tgacacaagg ccagcctgcg cctacgagcc catggacttt 600
 gtgatggccc tcatctacga catggtactg cttgtggtea ccctggggct ggccctcttc 660
 actctgtgcg gcaagttaa gaggtggaag ctgaacgggg ccttctctct catcacagcc 720
 ttctctctct tgcctatctg gttggcctgg atgacatgt acctcttcgg caatgtcaag 780
 ctgcagcagg gggatgcctg gaacgacccc accttgcca tcacgtggc ggccagcggc 840

377/518

```

tgggtcttcg tcattttcca cgccatccct gagatccact gcacccttct gccagccctg 900
caggagaaca cgcccaacta cticgacacg tcgcagccca ggaatgcggga gacggccttc 960
gaggaggacg tgcagctgcc gcgggcctat atggagaaca aggccttctc catggatgaa 1020
cacaatgcag ctctccgaac agcaggattt cccaacggca gcttgggaaa aagaccaggt 1080
ggcagcttgg ggaaaagacc cagcgctccg tttagaagca acgtgtatca gccaaactgag 1140
atggccgtcg tgcicaacgg tgggaccatc ccaactgctc cgccaagtca cacaggaaga 1200
caccttggg ctagcaaagg agaagaactc ttcactggag ttgtcccaat tcttgttgaa 1260
ttagatggig atgitaacgg ccacaagttc tctgtcagtg gagagggtga aggtgatgca 1320
acatacggaa aactiaccct gaagttcatc tgcactacig gcaaactgcc tgttccatgg 1380
ccaacactag tcactactct gtgctatggt gttcaatgct tttcaagata cccggatcat 1440
atgaaacggc atgacttttt caagagtgcc atgcccgaag gttatgtaca ggaaaggacc 1500
atcttttica aagatgacgg caactacaag acacgtgctg aagtcaagti tgaaggigat 1560
acccttgta atagaatcga gttaaaaggt attgacttca aggaagatgg caacattctg 1620
ggacacaaat tggaatacaa ctataactca cacaatgtat acatcatggc agacaaacaa 1680
aagaatggaa tcaaagtga cttcaagacc cgccacaaca ttgaagatgg aagcgttcaa 1740
ctagcagacc attatcaaca aaatactcca attggcgatg gccctgtcct tttaccagac 1800
aaccattacc tgtccacaca atctgccctt tcgaaagatc ccaacgaaaa gagagaccac 1860
atggtccttc ttgagtttgt aacagctgct gggattacac atggcatgga tgaactgiac 1920
aactga 1926

```

<210> 139

<211> 1746

<212> DNA

<213> Human

<400> 139

```

atggctggaa actgctcctg ggaggcccat cccggcaaca ggaacaggat gtgccctggc 60
ctgagcgagg ccccgaact ctacagccgg ggcttcciga ccatcgagca gatcgcgatg 120
ctgccgcctc cggccgcat gaactacatc ttctgtctcc tctgccctgtg tggcctggig 180

```


378/518

```

ggcaacgggc tggcctctg gtttttcggc ttctccatca agaggaaccc cttctccatc 240
tacttccctgc acctggccag cgccgatgtg ggctacctct tcagcaaggc ggtgttctcc 300
atcctgaaca cggggggcctt cctgggcacg ttgtccgact acatccgcag cgtgtgccgg 360
gtcctggggc tctgcatgtt ccttacggc gtgagcctcc tgcgggccgt cagcgccgag 420
cgttgcgcct cggtcacttt ccccgctgg tactggcgcc ggcgggccaa gcgcctgtcg 480
gccgtgggtg gcgcctgtg gtgggtcctg tccctccctg tcacctgcct gcacaactac 540
ttctgcgtgt tcttgggccg cggggccccc ggcgcgccct gcaggcacat ggacatcttc 600
ctgggcatcc tctgttctt gctctgtgc ccgtcatgg tgtgccctg cctggccctc 660
atcctgcacg tggagtgcg ggcccgcag cgccagcgt ctgccaagct caaccacgtc 720
atcctggcca tgggtctcgt cttcctgggt tcctccatct acttaggat cgactggttc 780
ctcttctggg tcttccagat cccggccccc tccccgagt acgtcactga cctgtgcatc 840
tgcataaca gcagcgccaa gcccatgtc tacttccctg ccgggaggga caagtcgcag 900
cggctgtggg agccgctcag ggtggtcttc cagcgggccc tgcgggacgg cgtgagctg 960
ggggaggccg ggggcagcac gcccaacaca gtcaccatgg agatgcagtg tccccgggg 1020
aacgcctccg ctagcaaagg agaagaactc ttacttggag ttgtccaat tctgttgaa 1080
ttagatgggt atgttaacgg ccacaagttc tctgtcagt gagagggtga aggtgatgca 1140
acatacgga aacttacct gaagttcatc tgcactactg gcaaactgcc tgttccatgg 1200
ccaacactag tctactctt gtgctatgtt gttcaatgtt ttcaagata cccgatcat 1260
atgaaacggc atgacttttt caagagtgc atgcccgaag gttatgtaca ggaaaggacc 1320
atcttcttca aagatgacgg caactacaag acacgtgctg aagtcaagtt tgaaggatg 1380
accettgita atagaatcga gttaaaaggt attgacttca aggaagatgg caacattctg 1440
ggacacaaat tggaatacaa ctataactca cacaatgtat acatcatggc agacaaaca 1500
aagaatggaa tcaaagtga cttcaagacc cgccacaaca ttgaagatgg aagcgttcaa 1560
ctagcagacc attatcaaca aaatactcca attggcgatg gccctgtcct ttaccagac 1620
aaccattacc tgtccacaca atctgccctt tcgaaagatc ccaacgaaaa gagagaccac 1680
atggctcttc ttgagtttgt aacagctgct gggattacac atggcatgga tgaactgtac 1740
aactga 1746

```

379/518

<211> 3759

<212> DNA

<213> Human

<400> 140

```

atggttttct ctgtcaggca gtgtggccat gtggcagaa ctgaagaagt tt tactgacg    60
ttcaagatat tccttgtcat catttgtctt catgtcgttc tggtaacatc cctggaagaa    120
gatactgata attccagttt gtcaccacca cctgctaaat tatctgttgt cagttttgcc    180
ccctctcca atgaggttga aacaacaagc ctcaatgatg ttactttaag cttactccct    240
tcaaacgaaa cagaaaaaac taaaatcact atagtaaaaa ccttcaatgc atcaggcgtc    300
aaaccccgaa gaaatatctg caatttgtca tctatttgca atgactcagc attttttaga    360
ggtagatca tgtttcaata tgataaagaa agcacgttc cccagaatca acatataacg    420
aatggcacct taactggagt cctgtctcta agtgaattaa aacgctcaga gctcaacaaa    480
accttgcaaa ccctaagtga gacttacttt ataatgtgtg ctacagcaga ggcccaaagc    540
acattaaatt gtacattcac aataaaactg aataatacaa tgaatgcatg tgcgtgaata    600
gctgccttgg aaagagtaaa gattcgacca atggaacact gctgcgttc tgcaggata    660
ccctgccctt cctccccaga agagtiggaa aagcttcagt gtgacctgca ggatcccat    720
gtctgtcttg ctgaccatcc acgtggccca ccattttctt ccagccaatc catcccagtg    780
gtgcctcggg ccactgtgtt tcccaggtc ccaaagcta cctcttttgc tgagcctcca    840
gattattcac ctgtgacca caatgttccc tctccaatag gggagattca accccttica    900
ccccagcctt cagctcccat agcttcacgc cctgccattg acatgcccc acagtctgaa    960
acgatctctt cccctatgcc ccaaaccat gctccggca cccacctcc tgtgaaagcc    1020
tcattttctt ctcccaccgt gtctgccct gcgaatgtca acactaccag cgcacctcct    1080
gtccagacag acatcgtcaa caccagcagt attctgac ttgagaacca agtgttcag    1140
atggagaagg ctctgtcctt gggcagcctg gaccctaacc tcgcaggaga aatgatcaac    1200
caagtcagca gactccttca ttccccgcct gacatgtctg cccctctggc tcaaagattg    1260
ctgaaagtag tggatgacat tggcctacag ctgaactttt caaacacgac tataagtcta    1320
acctccccct cttggctctt ggcgtgac agagtgaatg ccagtagttt caacacaact    1380
acctttgttg cccaagacce tgcaaatctt caggtttctc tggaaacca agctcctgag    1440

```

380/518

aacagiattg gcacaattac tcttccttca tcgctgatga ataatttacc agctcatgac 1500
atggagctag cttccagggt tcagttcaat ttttttgaac cacctgcttt gtttcaggat 1560
ccttccttgg agaacctctc tctgatcagc tacgtcatat catcgagtgt tgcaaacctg 1620
accgtcagga acttgacaag aaacgtgaca gtcacattaa agcacatcaa cccgagccag 1680
gatgagttaa cagtgagatg tgtatttttg gacttgggca gaaatggtgg cagaggaggc 1740
tggtcagaca atggctgctc tgtcaaagac aggagattga atgaaacat ctgtacctgt 1800
agccatctaa caagcttcgg cgttcgtctg gacctatcta ggacatctgt gctgcctgct 1860
caaatgatgg ctctgacgtt cattacatat attggtttgt ggctttcatc aatttttctg 1920
tcagtgactc ttgtaacctc catagctttt gaaaagatcc ggagggatta cccttccaaa 1980
atcctcatcc agctgtgtgc tgcctgtctt ctgctgaacc tggctcttct cctggactcg 2040
tggtttgctc tgtataagat gcaaggcctc tgcattcagc tggctgtatt tcttcattat 2100
tttctcttgg tctcattcac atggatgggc ctagaagcat tccatatgta cctggccctt 2160
gtcaaagtat ttaatactta catccgaaaa tacatcctta aattctgcat tgtcggttgg 2220
gggttaccag ctgtggttgt gaccatcatc ctgactatat cccagataa ctatgggctt 2280
ggatcctatg ggaaattccc caatggttca ccggtgact tctgctggat caacaacaat 2340
gcagtattct acattacggt ggtgggatat ttctgtgtga tatttttgcg gaacgtcagc 2400
atgttcattg tggctctgtt tcagctctgt cgaattaaaa agaagaagca actgggagcc 2460
cagcgaaaaa ccagtattca agacctcagg agtatcgctg gccttacatt tttactggga 2520
ataacttggg gctttgcctt ctttgccctg ggaccagtta acgtgacctt catgtatctg 2580
tttgccatct ttaatacctt acaaggattt ttcattattca tcttttactg tgtggccaaa 2640
gaaaatgtca ggaagcaatg gaggcggtat cttgttgttg gaaagttagc gctggctgaa 2700
aattctgact ggagtataac tgcataaat gggttaaaga agcagactgt aaaccaagga 2760
gtgtccagct ctccaattc ctacagtca agcagtaact ccactaactc caccacactg 2820
ctagtgaata atgattgctc agtacacgca agcgggaatg gaaatgcttc tacagagagg 2880
aatggggtct cttttagtgt tcagaatgga gatgtgtgcc ttacagattt cactggaaaa 2940
cagcacatgt ttaacgagaa ggaagattcc tgcaatggga aaggccgtat ggctctcaga 3000
aggacttcaa agcggggaag ctacacttt attagcaaa tgcctagcaa aggagaagaa 3060
ctcttcactg gatttgtccc aattcttgtt gaattagatg gtgatgttaa cggccacaag 3120
ttctctgtca gtggagaggg tgaaggatg gcaacatacg gaaaacttac cctgaagttc 3180

381/518

atctgcacta ctggcaaact gcctgttcca tggccaacac tagtcactac tctgtgctat 3240
 gggtttcaat gcttttcaag ataccggat catatgaaac ggcatgactt tttaagagt 3300
 gccatgcccg aaggttatgt acaggaaagg accatcttct tcaaagatga cggcaactac 3360
 aagacacgtg ctgaagtcaa gtttgaaggt gatacccttg ttaatagaat cgagttaaaa 3420
 ggtattgact tcaaggaaga tggcaacatt ctgggacaca aattggaata caactataac 3480
 tcacacaatg tatacatcat ggcagacaaa caaaagaatg gaatcaaagt gaacttcaag 3540
 acccgccaca acattgaaga tggaagcgtt caactagcag accattatca aaaaaiaact 3600
 ccaattggcg atggccctgt ccttttacca gacaaccatt acctgtccac acaatctgcc 3660
 ctttcgaaag atcccaacga aaagagagac cacatgggcc ttcttgagtt tgtaacagct 3720
 gctgggattia cacatggcat ggaigaactg tacaactga 3759

<210> 141

<211> 1968

<212> DNA

<213> Human

<400> 141

atggagtcct cacccatccc ccagtcatca gggaactctt ccactttggg gagggtcctt 60
 caaaccacag gtccctctac tgccagtggg gtcccgagg tggggctacg ggaigtgtgt 120
 tcggaatctg tggccctctt ctcatgtc ctgctggact tgactgctgt ggctggcaat 180
 gccgctgtga tggccgtgat cgccaagacg cctgccctcc gaaaatttgt ctctgtcttc 240
 cacctctgcc tgggtggacct gctggctgcc ctgacctca tgccctggc catgctctcc 300
 agctctgccc tctttgacca cgccctctt ggggagggtg cctgccgcct ctactgtttt 360
 ctgagcgtgt gctttgtcag cctggccatc ctctcgggt cagccatcaa tgtggagcgc 420
 tactattacg tagtccaccc catgcgtac gaggtgcgca tgacgtggg gctgggtggc 480
 tctgtgctgg tgggtgtgtg ggtgaaggcc ttggccatgg ctctgtgcc agtgttggga 540
 agggctctct gggaggaagg agctcccagt gtccccacag gctgttact ccagtggagc 600
 cacagtgcct actgccagct ttttgtgtg gtctttgtg tctttactt tctgttggcc 660
 ctgctctca tacttgtgt ctactgcagc atgttccgag tggcccgct ggctgccatg 720

382/518

cagcacgggc cgctgcccac gttgatggag acaccccggc aacgctccga atctctcagc 780
 agccgctcca cgatggtcac cagctcgggg gccccccaga ccacccaca ccggacgttt 840
 gggggaggga aagcagcagt ggttctcctg gctgtggggg gacagttcct gctctgttgg 900
 ttgccctact tctctttcca cctctatgtt gccctgagtg ctacagccat ttcaactggg 960
 caggtggaga gtgtggtcac ctggattggc tacttttgct tcacttccaa ccttttcttc 1020
 tatggatgtc tcaaccggca gatccggggg gagctcagca agcagtttgt ctgcttcttc 1080
 aagccagctc cagaggagga gctgaggctg cctagccggg agggctccat tgaggagaac 1140
 ttcctgcagt tccttcaggg gactggctgt ccttctgagt cctgggtttc ccgacccta 1200
 ccagcccca agcaggagcc acctgctgtt gactttcgaa tccaggccag agctagcaaa 1260
 ggagaagaac tcttcactgg agttgtccca attcttgttg aattagatgg tgatgtaaac 1320
 ggccacaagt tctctgtcag tggagagggt gaaggatg caacatacgg aaaacttacc 1380
 ctgaagtcca tctgcactac tggcaaacctg cctgttccat ggccaacact agtcactact 1440
 ctgtgctatg gtgttcaatg cttttcaaga taccggatc atatgaaacg gcâtgacttt 1500
 ttcaagagtg ccâtgccga aggttatgta caggaaagga ccâtcttctt caaagatgac 1560
 ggcaactaca agacacgtgc tgaagtcaag tttgaagggtg atacccttgt taatagaatc 1620
 gagttaaag gtattgactt caaggaagat ggcaacattc tgggacacaa attggaatac 1680
 aactataact cacacaatgt atacatcatg gcagacaaac aaaagaatgg aatcaaagtg 1740
 aacttcaaga cccgccacaa cattgaagat ggaagcgttc aactagcaga ccattatcaa 1800
 caaaatactc caattggcga tggccctgtc cttttaccag acaaccatta cctgtccaca 1860
 caatctgccc tttcgaaaga tcccaacgaa aagagagacc acatggctct tcttgagttt 1920
 gtaacagctg ctgggattac acatggcatg gatgaactgt acaactga 1968

<210> 142

<211> 1722

<212> DNA

<213> Human

<400> 142

atgcagccgt ccccgccgcc caccgagctg gtgccgtcgg agcgcgccgt ggtgctgctg 60

383/518

tcgtgcgcac tctccgcgct cggctcgggc ctgctgggtg ccacgcacgc cctgtggccc	120
gacctgcgca gccgggcacg gcgcctgtg ctcttccgtg cgtggccga cctgctctcg	180
gccgcctcct acitctacgg agtgcgcag aacttcgcgg gcccgctgtg ggactgcgtg	240
ctgcagggcg cgctgtccac cttcgccaac accagctcct tcttctggac cgtggccatt	300
gcgctctact tgtacctcag catcgtccgc gccgcgcgcg gccctgcac agatcgctg	360
ctttgggcci tccatgtgt cagctggggg gtcccgttg tcatcactgt ggcagccgtc	420
gccctgaaga agattggcta tgacgcctcg gacgtgtctg tgggtgtgtg ctggatcgac	480
ctggaggcca aggacctgt cctgtggaag ctgtgacgg ggaagctgtg ggagatgtg	540
gcataatgtc tgcctgctt gctgtacctc ctggtccgga agcacatcaa cagagcgac	600
acggcactct ctgagtaccg gccatcctc tcccaggagc accgcctgtc gcgccactcc	660
tccatggcgg acaagaagct ggtgtcatc ccgctcatct tcatcggcct cagggctgtg	720
agcaccgtgc ggctcgtgt gacctctgt ggctccccg ccgtgcagac gccggtgtg	780
gtggttctgc atggtatcgg gaacacgtt caggagggtg ccaactgcat catgttcgtc	840
ctctgcaccc gcgcgtccg aactcggctc ttctctctct gtgtgtgtg ctgctcttct	900
cagcttccca ccaagagccc ggctggcact cccaaggctc ccgcgccttc caagccagga	960
gaatctcagg aatcccaagg gaccccagg gaacttccaa gcactgctag caaaggagaa	1020
gaactcttca ctggagtgt cccaattct gtggaattag atggtgatgt taacggccac	1080
aagtctctct tcagtgga gggigaaggt gatgcaacat acggaaaact taccctgaag	1140
ttcatctgca ctactggcaa actgcctgtt ccatggccaa cactagtcac tactctgtgc	1200
tatggtgttc aatgctttc aagatacccg gatcatatga aacggcatga ctttttcaag	1260
agtgccatgc ccgaaggta tgtacaggaa aggacctct tcttcaaaga tgacggcaac	1320
tacaagacac gigtgaagt caagtttgaa ggtgatacc ttgttaatag aatcgagta	1380
aaaggtattg acttcaagga agatggcaac attciggac acaaattgga atacaactat	1440
aactcacaca atgtatacat catggcagac aaacaaaaga atggaatcaa agtgaacttc	1500
aagacccgcc acaacattga agatggaagc gttaactag cagaccatta tcaacaaaat	1560
actccaattg gcgatggccc tgtcctttta ccagacaacc attacctgtc cacacaatct	1620
gccctttcga aagatcccaa cgaaaagaga gaccacatgg tccttcttga gtttgtaaca	1680
gctgctggga ttacacatgg catggatgaa ctgtacaact ga	1722

384/518

<210> 143

<211> 2763

<212> DNA

<213> Human

<400> 143

```

atggcagtcc ggttgtgcag tctctctcta tatggagaga tagaattaca aaaagtgaca    60
ataggaaatt gcaatgaaaa tctggaaacc ctggaaaagc aggtaaagga tgtcacagca    120
ccacttaata acatttcttc tgaagtcagc attttaacat ctgatgccaa taaattaact    180
gctgagaaca tcaactagtc tacgcgagtg gttggacaga tattcaacac ttccagaaat    240
gcttcacctg aggcaaagaa agttgccata gtaacagtga gtcaactcct agatgccagt    300
gaagaigctt ttcaaagagt tgcgtctact gctaataatg atgcccttac aacgcttatt    360
gagcaaatgg agacttattc ctgtcttttg ggtaatacat cagtgggtga acctaacata    420
gcaatacagt cagcaaatct ctcttcagaa aatgcggtgg ggccttcaaa tgttcgcttc    480
tctgtgcaga aaggagctag cagttctcta gtttctagtt caacatttat acatacaaat    540
gtggatggcc ttaaccacaga tgcacagact gagcttcagg tcttgcttaa tatgacgaaa    600
aattacacca agacatgcgg cttttagatt tatcaaaatg acaagctttt ccaatcaaaa    660
acttttacag ctaaatcgga ttttagtcaa aaaattatct caagcaaac tgatgaaaat    720
gagcaagatc agagtgttc tgttgacatg gtctttagtc caagtacaa ccaaaaagaa    780
tttcaactct attcctatgc ctgtgtctat tggaaattgt cagcgaagga ctgggacaca    840
tatggctgtc aaaaagacaa gggcactgat ggattcctgc gctgccgctg caaccatact    900
actaattttg ctgtattaat gactttcaaa aaggattatc aatatcccaa atcacttgac    960
atattatcca acgttggatg tgcactgtct gttactggtc tggctctcac agttatattt   1020
cagattgtca ccaggaaagt cagaaaaacc tcagtaacct gggtttttgt caatctgtgc   1080
atatcaatgt tgattttcaa cctcctcttt gtgtttggaa ttgaaaactc caataagaac   1140
ttgcagacaa gtgatggatg catcaataat attgacittg acaataatga cataccagg   1200
acagacacca ttaacatccc gaatcceatg tgcactgcga ttgccgcctt actgcactat   1260
tttctgttag tgacatttac ctggaacgca ctcagcgtg cacagctcta ttaccttcta   1320
ataaggacca tgaagccctt tcctcgcatc ttcatctttt tcatctcatt aattggatgg   1380

```

385/518

```

ggagtcccag ctatagtagt ggctataaca gtgggagtta tttattctca gaatggaaat 1440
aatccacagt gggaattaga ctaccggcaa gagaaaatct gctggctggc aattccagaa 1500
cccaatggtg ttataaaaag tccgctgttg tggtcattca tcgtacctgt aaccattatc 1560
ctcatcagca atgttgttat gtttattaca atctcgatca aagtgtgtg gaagaataac 1620
cagaacctga caagcacaaa aaaagtittca tccatgaaga agattgtag cacattatct 1680
gttcagttg tttttggaat tacctggatt ctagcatacc tgatgctagt taatgaigat 1740
agcatcagga tcgtcttcag ctacatattc tgccttttca acactacaca gggattgcaa 1800
atttttatcc tgiacactgt tagaacaaaa gtcttcaga gtgaagcttc caaagtgtg 1860
atgttgctat cgtctattgg gagaaggaag tcattgccct cagtgcgcg gccgaggctg 1920
cgtgtaaaga tgtataattt cctcaggtca ttgccaacct tacatgaacg ctttaggcta 1980
ctggaaacct ctccgagtag tgaggaaatc acactctctg aaagtgacaa tgcaaaggaa 2040
agcatcgcta gcaaaggaga agaactcttc actggagttg tcccaattct tgttgaatta 2100
gatggtgatg ttaacggcca caagtctct gtcagtggag agggatgaagg tgatgcaaca 2160
tacggaaaac ttacctgaa gtcatctgc actactggca aactgcctgt tccatggcca 2220
acactagtca ctactctgtg ctatggtgtt caatgctttt caagatacc ggatcatatg 2280
aaacggcatg actttttcaa gagtgccatg cccgaaggtt atgtacagga aaggaccatc 2340
ttcttcaaag atgacggcaa ctacaagaca cgtgctgaag tcaagtttga aggtgatacc 2400
cttgtaata gaatcgagtt aaaaggtatt gacttcaagg aagatggcaa cattctggga 2460
cacaattgg aatacaacta taactcacac aatgtatata tcatggcaga caaacaaaag 2520
aatggaatca aagtgaactt caagaccgc cacaacattg aagatggaag cgttcaacta 2580
gcagaccatt atcaacaaaa tactccaatt ggcatggcc ctgtcctttt accagacaac 2640
cattacctgt ccacacaatc tgccttttcg aaagatccca acgaaaagag agaccacatg 2700
gtccttcttg agtttgtaac agctgtggg attacacatg gcatggatga actgtacaac 2760
tga 2763

```

<210> 144

<211> 2301

<212> DNA

<213> Human

386/518

<400> 144

atggatcact gtggtgccct tttcctgtgc ctgtgccctt tgactttgca gaatgcaaca	60
acagagacat gggaagaact cctgagctac atggagaata tgcaggtgtc caggggccgg	120
agctcagttt tttcctctcg tcaactccac cagctggagc agatgctact gaacaccagc	180
ttcccaggct acaacctgac ctgtcagaca cccaccatcc agtctctggc ctccaagctg	240
agctgtgact tctctggcct ctgctgacc agtgccactc tgaagcgggt gcccaggca	300
ggaggtcagc atgccccggg tcagcacgcc atgcagttcc ccgccgagct gacccgggac	360
gcttgaaga cccgccccag ggagctgcgg ctcatctgta tctacttctc caacaccac	420
ttttcaagg atgaaaaca ctcactctcg ctgaataact acgtcctggg ggcccagctg	480
agtcatgggc acgtgaaca cctcagggat cctgtgaaca tcagcttctg gcacaacaa	540
agcctggaag gctacacct gacctgtgc tcttggagg agggagccag gaaacagccc	600
tggggggct ggagccctga gggctgtcgt acagagcagc cctccactc tcaggtgtc	660
tggcgtgca accacctcac ctactttgct gttctcatgc aactctccc agccctgtc	720
ctgcagagt tgcctggacc tcttacgtac atctccctcg tggcctgcag catctccatc	780
gtggcctcgc tgatcacagt cctgctgcac ttccatttca ggaagcagag tgactcctta	840
acacgcattc acatgaacct gcatgccctc gtgctgtcct tgaacatgc ctctctgtg	900
agccccgcat tcgcaatgtc tctgtgtccc gggctagcat gcacggctct ggccgtgcc	960
ctgcactacg cgtgtctcag ctgcctcacc tggatggcca tcgaggctt caacctctac	1020
ctctctctcg ggcgtgtcta caacatctac atccgcagat atgtgttcaa gcttgggtgtg	1080
ctaggctggg gggccccagc cctcctgggt ctgctttccc tctctgtcaa gagctcggtta	1140
tacggacct gcacaatccc cgtcttcgac agctgggaga atggcacagg cttccagaac	1200
atgtccatat gctgggtgcg gagccccgtg gtgcacagtg tcctgggtcat gggctacggc	1260
ggcctcacgt cctctttcaa cctgggtgtg ctggcctggg cgctgtggac cctgcgcagg	1320
ctgcgggagc gggcggatgc accaagtgtc agggcctgcc atgacactgt cactgtgtgtg	1380
ggcctcaccg tgcctgtggg aaccacctgg gccttggcct tcttttctt tggcgtcttc	1440
ctgtgtcccc agctgttctt cttcaccatc ttaaactcgc tctacggttt cttcttttc	1500
ctgtggttct gctcccagcg gtgccgtca gaagcagagg ccaaggcaca gatagaggcc	1560
ttcagctcct cccaaacaac acaggctagc aaaggagaag aactcttcac tggagtgtc	1620

387/518

```

ccaattcttg ttgaattaga tggatgatgt aacggccaca agttctctgt cagtggagag 1680
ggtgaagggt atgcaacata cggaaaactt accctgaagt tcctctgcac tactggcaaa 1740
ctgacctgtc catggccaac actagtcact actctgtgct atgggtgtca atgcttttca 1800
agatacccggt atcataatgaa acggcatgac tttttcaaga gtgccatgcc cgaaggttat 1860
gtacaggaaa ggaccatctt ctccaagat gacggcaact acaagacacg tgcgtgaagtc 1920
aagtttgaag gtgataccct tggttaataga atcgagttaa aaggtattga ctccaaggaa 1980
gatggcaaca ttctgggaca caaattggaa tacaactata actcacacaa tgtatacatc 2040
atggcagaca aacaaaagaa tggaatcaaa gtgaacttca agaccgcca caacattgaa 2100
gatggaagcg ttcaactagc agaccattat caacaaaata ctccaattgg cgatggccct 2160
gtccttttac cagacaacca ttacctgtcc acacaatcig ccttttcgaa agatcccaac 2220
gaaaagagag accacatggt ccttcttgag ttgttaacag ctgctgggat tacacatggc 2280
atggatgaac tgtacaactg a 2301

```

<210> 145

<211> 3375

<212> DNA

<213> Human

<400> 145

```

atgcgtggct tcaacctgct cctcttcctg ggaatgtgtg ttatgcacag ctgggaaggg 60
cacataagac ccacacggaa accaaacaca aagggttaata actgtagaga cagtaccttg 120
tgcccagctt atgccacctg caccaatata gtggacagtt actattgcac ttgcaaacaa 180
ggcttctgt ccagcaatgg gcaaaatcac ttcaaggatc caggagtgcg atgcaaagat 240
attgatgaat gttctcaaag cccccagccc tgggttccta actcatcctg caaaaacctg 300
tcaggaggtt acaagtgcag ctgtttagat ggtttctctt ctccacttgg aaatgacttg 360
gtcccaggaa agccgggcaa ttcttctgt actgatatca atgagtcctt caccagcagg 420
gtctgccctg agcatcttga ctgtgtcaac tccatgggaa gctacagtig cagctgtcaa 480
gttggattca tctctagaaa ctccacctgt gaagacgtga atgaatgtgc agatccaaga 540
gcttgcccag agcatgcaac ttgtataaac actgttggaa actactcttg tttctgcaac 600

```

388/518

ccaggatttg aatccagcag tggccacttg agtttccagg gtctcaaagc atcgtgtgaa 660
 gatattgatg aatgcactga aatgtgcccc atcaattcaa catgcaccaa cactcctggg 720
 agctactttt gcacctgcca ccctggcttt gcaccaagca gtggacagtt gaatttcaca 780
 gaccaaggag tggaaatgtag agatatgatg gagtgccgcc aagatccatc aacctgtggt 840
 cctaattcta tcigcaccaa tgccctgggc tcctacagct gtggctgcat tgtaggcttt 900
 cateccaatc cagaaggctc ccagaaagat ggcaacttca gctgccaaag ggttctcttc 960
 aatgtaagg aagatgtgat acccgataat aagcagatcc agcaatgcca agagggaacc 1020
 gcagtgaaac ctgcataigt ctctttttgt gcacaaataa ataacatctt cagcgttctg 1080
 gacaaagigt gtgaaaataa aacgaccgta gtttctctga agaatacaac tgagagcttt 1140
 gtccctgtgc ttaaacaaat atccacgtgg actaaattca ccaaggaaga gacgtcctcc 1200
 ctggccacag tcttcttgga gagtgtggaa agcatgacac tggcatcttt ttggaaaccc 1260
 tcagcaaagt tcaactccggc tgttcggacg gaatacttag acattgagag caaagttatc 1320
 aacaaagaat gcagtgaaga gaatgtgacg ttggacttgg tagccaaggg ggataagatg 1380
 aagatcgggt gticcacaat tgaggaatct gaatccacag agaccactgg tgtggctttt 1440
 gtctcctttg tgggcatgga atcggtttta aatgagcgtt tcttccaaga ccaccaggct 1500
 ccttgacca cctctgagat caagctgaag atgaattctc gagtcgttgg gggcataatg 1560
 actggagaga agaaagacgg ctcttcagat ccaatcatct acactctgga gaacgttcag 1620
 ccaaagcaga agtttgagag gcccatctgt gtttcttgga gcactgatgt gaagggtgga 1680
 agatggacat cctttggctg tgtgatcctg gaagcttctg agacatatac catctgcagc 1740
 tgtaatcaga tggcaaatct tgccgttata atggcgtctg gggagctcac gatggacttt 1800
 tccttgtaca tcattagcca tgtaggcatt atcatctcct tgggtgacct cgtcttggcc 1860
 atgccacct ttctgtgtg tcgtccatc cgaaatcaca acacctacct ccacctgcac 1920
 ctctgcgtgt gtctcctctt ggcaagact ctcttctcg ccgtataca caagactgac 1980
 aacaagacgg gctgcgcat catcggggc ttcttgcact accttttctt tgcctgttc 2040
 ttctggatgc tggtaggagc tgtgatactg ttcttgatgg tcagaaacct gaagggtgtg 2100
 aattacttca gctctcgcaa catcaagatg ctgcacatct gtgcctttgg ttatgggctg 2160
 ccgatgctgg tggtagtgat ctctgccagt gtgcagccac agggctatgg aatgcataat 2220
 cgctgctggc tgaatacaga gacagggttc atctggagtt tcttggggcc agtttgaca 2280
 gttatagtga tcaactccct tctcctgacc tggaccttgt ggatcctgag gcagaggctt 2340

389/518

tccagtgta atgccgaagt ctcaacgcta aaagacacca ggttactgac cttcaaggcc 2400
 ttigcccagc tcttcatcct gggctgctcc tgggtgctgg gcatttttca gattggacct 2460
 gtggcagggtg tcatggctta cctgttcacc atcatcaaca gcctgcaggg ggccttcac 2520
 ttccatcatcc actgtctgct caacggccag gtacgagaag aatacaagag gtggatcact 2580
 gggaagacga agcccagctc ccagtcaccag acctcaagga tcttgctgtc ctccatgcc 2640
 tccgcttcca agacgggtgc tagcaaagga gaagaactct tcactggagt tgcaccaatt 2700
 ctgtttgaat tagatggta gttaacggc cacaagtict ctgtcagtg agagggtgaa 2760
 ggtgatgcaa catacggaaa acttaccctg aagttcatct gcactactgg caaactgcct 2820
 gtccatggc caacactagt cactactctg tgctaagggt ttcaatgcct ttcaagatac 2880
 ccggatcata tgaacggca tgaacttttc aagagtgcca tgcccgaagg ttaigtacag 2940
 gaaaggacca tcttcttcaa agatgacggc aactacaaga cacgtgctga agtcaagttt 3000
 gaaggtgata ccttgttaa tagaatcgag ttaaaaggta ttgacttcaa ggaagatggc 3060
 aacattctgg gacacaaatt ggaatacaac tataactcac acaatgtata catcatggca 3120
 gacaaacaaa agaattggaat caaagtgaac ttcaagacc gccacaacat tgaagatgga 3180
 agcgttcaac tagcagacca ttatcaacaa aatactccaa ttggcgatgg ccctgtcctt 3240
 ttaccagaca accattacct gtccacaaa tctgcccttt cgaaagatcc caacgaaaag 3300
 agagaccaca tggctcttct tgagtttgta acagctgctg ggattacaca tggcatggat 3360
 gaactgtaca actga 3375

<210> 146

<211> 1800

<212> DNA

<213> Human

<400> 146

atggcccca cagagccctg gagccccagc ccggggtcag cgccctggga ctactcgggg 60
 ttggacggcc tggaggagct ggagctgtgt ccggccgggg accigcccta cggctacgtc 120
 tacatccccg cgctctacct ggcggccttc gccgtgggcc tgcctgggcaa cgcccttctg 180
 gctgtggctgc tggccgggcg gcggggcccg cggcggctgg tggatacctt cgtgctgcac 240

390/518

ctggcggcag ctgacctggg ctctgtgctc acgtgcccgc tgtgggccgc ggcggcggcg 300
 ctaggcggcc gctggccgtt cggcgatggc ctctgcaagc tcagcagctt cgcgctggcg 360
 ggcacgcgct gcgcggggcg gctgctgctg gcgggcatga gctggaccg ctacctggcc 420
 gtggtgaagc tgctcgaggc gaggccactg cgcaccccg cgtgcgcgct ggcctcgtgc 480
 tgcggcgctt gggccgtggc gctgctggcc ggcctgccct ccttggtcta ccgggggttg 540
 cagccctgc ctggggggcca ggacagccag tgcggcgagg agccctccca cgccttccag 600
 ggcctcagct tgctgctgct gctgctgacc ttcgtgctgc ccttggtcgt caccctcttc 660
 tgctactgcc gcatctcgcg ccgccigcga cggccgcgc acgtgggtcg ggcccggagg 720
 aactcgctgc gcatcatctt cgccatcgag agcacgtttg tggcctcctg gctgcccttc 780
 agcgccctgc gggccgtctt ccacctggcg cgtctggggg cgtgccgct gccgtgcccc 840
 ctgctgctgg cgctgcgctg gggcctcacc attgccacct gccctggcctt cgtcaacagc 900
 tgcgccaacc cgctcatcta cctcctgctg gaccgctcat tccgagcccg ggcgctggac 960
 ggggcctgcg ggcgcaccgg ccgctggcg cgaaggatca gtcagcctc ctgctctcc 1020
 aggagcagaca gtcccggtgt cgttgccgg gccaggccg cgaacactgc ctggcctcc 1080
 tgggctagca aaggagaaga actcttact ggagtgtcc caattcttgt tgaattagat 1140
 ggtgatgta acggccacaa gtctctgtc agtggagagg gtgaaggta tgcaacatac 1200
 ggaaaactta cctgaagtt catctgcact actggcaaac tgcctgttc atggccaaca 1260
 ctagtacta ctctgtgcta tgggtttcaa tgcttttcaa gatacccga tcatagaaa 1320
 cggcatgact ttttcaagag tgccatgccc gaaggttatg tacaggaaag gaccatcttc 1380
 ttcaaagatg acggcaacta caagacacgt gctgaagtca agtttgaagg tgataccctt 1440
 gttaatagaa tcgagttaaa aggtattgac ttcaaggaag atggcaacat tctgggacac 1500
 aaattggaat acaactataa ctacacaaat gtatacatca tggcagacaa acaaaagaat 1560
 ggaatcaaag tgaacttcaa gacccgccac aacattgaag atggaagcgt tcaactagca 1620
 gaccattatc aacaaaatac tccaattggc gatggccctg tccttttacc agacaacat 1680
 tactgtcca cacaatctgc ccttcgaaa gatcccaacg aaaagagaga ccacatggtc 1740
 ctcttgagt ttgtaacagc tgctgggatt acacatggca tggatgaact gtacaactga 1800

<210> 147

<211> 1674

391/518

<212> DNA

<213> Human

<400> 147

```
atgagtcagc aaaacaccag tggggactgc ctgtttgacg gtgtcaacga gctgatgaaa 60
accctacagt ttgcagtgca catccccacc ttctgtcttg gccgtctcct caacctgctg 120
gccatccatg gcttcagcac cttccttaag aacaggltgg ccgattatgc tgccacctcc 180
atctacatga tcaacctggc agtcittgac ctgctgctgg tgctctccct cccattcaag 240
atggtccctgt cccaggltaca gtcccccttc ccgtccctgt gcaccttggt ggagtgccct 300
tacttcgtca gcatgtacgg aagcgtcttc accatctgct tcatcagcat ggaccggttc 360
ttggccatcc gttaccgct acttggtgagc cacctccgtt ccccaggaa gatctttggg 420
atctgtgca ccatctgggt cctggtgtgg accggaagca tccctatcta cagtttccat 480
gggaaagtgg aaaaatacat gtgtctccac aacatgtctg atgatactg gagcgccaag 540
gtctttcttc cgctggaggt gtttggttc ctccttccca tgggcatcat gggcttctgc 600
tgctccagga gcatccacat cctgctgggc cgccgagacc acaccagga ctgggtgcag 660
cagaaagcct gcatctacag catcgcagcc agcctggctg tcttcgtggt ctccttctc 720
ccagtcacc tgggtttctt cctgcagttc ctggtgagaa acagctttat cgtagagtgc 780
agagccaagc agagcatcag cttcttcttg caattgtcca tgtgtttctc caacgtcaac 840
tgctgcctgg atgtttctg ctactacttt gtcatcaaag aattccgcat gaacatcagg 900
gcccaccggc ctccagggt ccagctggtc ctgcaggaca ccacgatctc ccggggcgct 960
agcaaaggag aagaactctt cactggagtt gtcccaattc ttgttgaatt agatggtgat 1020
gttaacggcc acaagtctc tgcagtgga gaggtgaag gtgatgcaac atacggaaaa 1080
cttaccctga agttcatctg cactactggc aaactgcctg ttccatggcc aacactagtc 1140
actactctgt gctatggtgt tcaatgcttt tcaagatacc cggatcataat gaaacggcat 1200
gactttttca agagtccat gccgaaggt tatgtacagg aaaggacat cttcttcaaa 1260
gatgacggca actacaagac acgtgtgaa gtcaagttg aaggtgatac cttgttaat 1320
agaatcgagt taaaaggtat tgacttcaag gaagatggca acattctggg acacaaattg 1380
gaatacaact ataactcaca caatgtatac atcatggcag acaaacaaaa gaatggaatc 1440
aaagtgaact tcaagacctg ccacaacatt gaagatggaa gcgttcaact agcagacct 1500
```

392/518

tatcaacaaa atactccaat tggcgatggc cctgtccttt taccagacaa ccattacctg 1560
 tccacacaat ctgccctttc gaaagatccc aacgaaaaga gagaccacat ggctccttctt 1620
 gagtttgtaa cagctgctgg gattacacat ggcatggatg aactgtacaa ctga 1674

<210> 148

<211> 2127

<212> DNA

<213> Human

<400> 148

atggacacta ccatggaagc tgacctgggt gccactggcc acaggccccg cacagagctt 60
 gatgatgagg actcctaccc ccaaggtggc tgggacacgg ttttcttggg ggccctgctg 120
 ctcccttgggc tgccagccaa tgggttgatg gcgtggctgg cgggtccca ggcccggcat 180
 ggagctggca cgcgtctggc gctgtccttg ctacgctgg ccctctctga cttcttgctc 240
 ctggcagcag cggccttcca gaccttagag atccggcatg ggggacacig gccgctgggg 300
 acagctgcct gccgttcta ctacttcta tggggcgtgt cctactcctc cggcctcttc 360
 ctgctggccg ccctcagcct cgaccgtgc ctgctggcgc tgtgccaca ctggtaccct 420
 gggcaccgcc cagtccgctt gcccctctgg gtctgcgccg gtgtctgggt gctggccaca 480
 ctcttcagcg tgccctggct ggtcttcccc gaggtgccg tctggtggtg cgacctggtc 540
 atctgccttg acttctggga cagcgaggag ctgtcgtga ggatgctgga ggtcctgggg 600
 ggcttctctg ctttctctct gctgtctgtc tgccacgtgc tcaccaggc cacagcctgt 660
 cgcacctgcc accgccaaca gcagcccga gcctgccggg gcttcgcccg tgtggccagg 720
 accattctgt cagcctatgt ggtcctgagg ctgccctacc agctggccca gctgctctac 780
 ctggccttcc tggggacgt ctactctggc tacctgtctt gggaggccct ggtctactcc 840
 gactacctga tctactcaa cagctgcctc agccccttcc tctgccatcat ggccagtgcc 900
 gacctccgga ccctgctgcg ctccgtgctc tcgtccttcg cggcagctct ctgcgaggag 960
 cggccgggca gcttcagcc cactagacca cagaccagc tagattctga ggtccaact 1020
 ctgccagagc cgatggcaga ggcccagtc cagatggatc ctgtggcca gcctcagggt 1080
 aacccacac tccagccag atcggtatcc acagctcagc cacagctgaa ccctacggcc 1140

393/518

cagccacagt cggatccac agcccagcca cagctgaacc tcatggccca gccacagtca 1200
 gattctgtgg cccagccaca ggcagacact aacgtccaga cccctgcacc tgcctgccagt 1260
 tctgtgcca gtccctgiga tgaagcttcc ccaaccccat cctcgcatcc taccacaggg 1320
 gcccttgagg acccagccac acctcctgcc tctgaaggag aaagcccag cagcaccg 1380
 ccagaggcgg ccccgggcgc agggcccacg gctagcaaag gagaagaact cttcactgga 1440
 gttgtcccaa ttcttgttga attagatggt gatgttaacg gccacaagtt ctctgtcagt 1500
 ggagagggtg aaggtgatgc aacatacgga aaacttacc tgaagttcat ctgcactact 1560
 ggcaaatgct ctgttccatg gccaaacta gtcactactc tgtgctatgg tgttcaatgc 1620
 ttttcaagat acccggtatca tatgaaacgg catgactttt tcaagagtgc catgcccga 1680
 ggttatgtac aggaaggac catcttcttc aaagatgacg gcaactacaa gacacgtgct 1740
 gaagticaagt ttgaaggatg tacccttggt aatagaatcg agttaaaagg tattgacttc 1800
 aaggaagatg gcaacattct gggacacaaa ttggaatata actataactc acacaatgta 1860
 tacatcatgg cagacaaaca aaagaatgga atcaaagtga acttcaagac cggccacaac 1920
 attgaagatg gaagcgttca actagcagac cattatcaac aaaatactcc aattggcgat 1980
 ggccctgtcc ttttaccaga caaccattac ctgtccacac aatctgccct ttcgaaagat 2040
 cccaacgaaa agagagacca catggctcct cttgagtttg taacagctgc tgggattaca 2100
 catggcatgg atgaactgta caactga 2127

<210> 149

<211> 1914

<212> DNA

<213> Human

<400> 149

atgaggcccc agcgtccccc gccgcgcggc agcgcccccg gcccgatgga gacccccggc 60
 tgggaccag cccgcaacga ctgcctgccg cccagctga ccccgccgt gccccctac 120
 gtgaagcttg gcctaccgt cgtctacac ggttctacg cgtgctctt cgtgttcac 180
 tacgtgcagc tctggctggt gctgcgttac cgccacaagc ggctcagcta ccagagcgtc 240
 ttctctttc tctgctctt ctgggcctcc ctgcggaccg tctcttctc cttctacttc 300

394/518

aaagacttcg tggcggccaa ttgcctcagc cccctcgtct tctggctgct ctactgcttc 360
 cctgtgtgcc tgcagttttt caccctcagc ctgatgaact tgtacttcac gcagggtgatt 420
 ttcaaagcca agtcaaaata ttctccagaa ttactcaaat accggttgcc cctctacctg 480
 gcctccctct tcatcagcct tgttttcctg ttggatgaatt taacctgtgc tgtgctggta 540
 aagacgggaa attgaggagag gaaggttatc gtctctgtgc gagtggccat taatgacacg 600
 ctcttcgtgc tgtgtgccgt ctctctctcc atctgtctct acaaaatctc taagatgtcc 660
 tttagccaaca ttactttgga gtccaagggc tctccgtgt gtcaagtgc tgccatcggt 720
 gtcaccgtga tactgcttta caccctcctgg gcctgctaca acctgttcat cctgtcattt 780
 tctcagaaca agagcgtcca ttcccttgat tatgactggg acaatgtatc agaccaggca 840
 gatttgaaga atcagctggg agatgctgga tacgtattat ttggagtggt gttatttggt 900
 tgggaactct tactaccac cttagtcgtt tatttcttcc gagttagaaa tcctacaaag 960
 gaccctacca accttggaat ggtccccagc catggattca gtcccagatc ttatttcttt 1020
 gacaaccctc gaagatatga cagtatgat gaccttgcct ggaacattgc ccctcaggga 1080
 cttcaggagg gttttgctcc agattactat gatitggggac aacaaactaa cagcttcctg 1140
 gcacaagcag gaactttgca agactcaact ttggatcctg acaaaccaag ccttggggct 1200
 agcaaaggag aagaactctt cactggagtt gtcccaattc ttgttgaatt agatggatgat 1260
 gttaacggcc acaagttctc tgtcagtgga gaggtgaag gtgatgcaac atacggaaaa 1320
 cttaccctga agttcatctg cactactggc aaactgcctg ttccatggcc aacactagtc 1380
 actactctgt gctatgggtg tcaatgcctt tcaagatacc cggatcatac gaaacggcat 1440
 gactttttca agagtggcat gcccgaaggc tatgtacagg aaaggacat cttcttcaaa 1500
 gatgacggca actacaagac acgtgctgaa gtcaagtttg aaggatgatac ccttggtaat 1560
 agaatcgagt taaaaggat tgcattcaag gaagatggca acattctggg acacaaattg 1620
 gaatacaact ataactcaca caatgtatac atcatggcag acaaacaaaa gaatggaatc 1680
 aaagtgaact tcaagacccg ccacaacatt gaagatggaa gcgttcaact agcagacat 1740
 tatcaacaaa atactccaat tggcgtggc cctgtccttt taccagacaa ccattacctg 1800
 tccacacaat ctgccccttc gaaagatccc aacgaaaaga gagaccacat ggtccttctt 1860
 gagtttgtaa cagctgctgg gattacacat ggcatggatg aactgtacaa ctga 1914

<210> 150

395/518

<211> 1974

<212> DNA

<213> Human

<400> 150

atggtcttct cggcagtgit gactgcgttc cataccggga catccaacac aacatttgtc	60
gtgtatgaaa acacctacat gaalattaca ctccctccac cattccagca tcctgacctc	120
agtccattgc ttagatatag ttttgaaacc atggctccca ctggtttgag ttccttgacc	180
gtgaatagta cagctigtc cacaacacca gcagcattta agagcciaaa ctgacctctt	240
cagatcaccc tttctgctat aatgatattc attctgtttg tgtcttttct tgggaacttg	300
gttgtttgcc tcatggttta ccaaaaagct gccatgaggt ctgcaattaa catcttcctt	360
gccagcctag cttttgcaga catgttgctt gcagtgctga acatgccctt tgccciggtg	420
actattctta ctaccgaig gatttttggg aaattcttct gtagggatc tgctaigttt	480
ttctggttat ttgtgataga aggagtagcc atcctgtca tcattagcat agataggttc	540
cttattatag tccagaggca ggataagcta aaccatata gagctaaggt tctgattgca	600
gtttcttggg caacttcctt ttgtgtagct tttcctttag ccgtaggaaa ccccgacctg	660
cagatacctt cccgagctcc ccagtgtgtg ttgggttaca caaccaatcc aggctaccag	720
gcttatgtga ttttgatttc tctcatttct ttcttcatac ccttcctggt aatactgtac	780
tcatttatgg gcatactcaa cacccttcgg cacaatgcct tgaggatcca tagctaccct	840
gaaggatatat gcctcagcca ggccagcaaa ctgggtctca tgagtctgca gagaccttc	900
cagatgagca ttgacatggg ctttaaaaca cgtgccctca ccactatitt gattctcttt	960
gctgtcttca ttgtctgtg ggccccattc accacttaca gccttggtgc aacattcagt	1020
aagcaccttt actatcagca caactttttt gagattagca cctggctact gtggctctgc	1080
tacctcaagt ctgcatggaa tccgctgac tactactgga ggattaagaa attccatgat	1140
gcttgcctgg acatgatgcc taagtccttc aagtttttgc cgcagctccc tggtcacaca	1200
aagcgacgga tacgtcctag tgctgtctat gtgtgtggg aacatcggac ggtgggtggct	1260
agcaaaggag aagaactctt cactggagtt gtcccaattc ttgtgaatt agatggtgat	1320
gttaacggcc acaagttctc tgcagtga gaggtgaag gtgatgcaac atacggaaaa	1380
cttacctga agttcatctg cactactggc aaactgcctg ttccatggcc aacactagtc	1440

396/518

actactctgt gctatgggtg tcaatgcitt tcaagatacc cggatcatat gaaacggcat 1500
gactttttca agagtgccat gccgaagggt tatgtacagg aaaggacat cttcttcaaa 1560
gatgacggca actacaagac acgtgctgaa gtcaagtttg aaggtagatac ccttgtaaat 1620
agaatcgagt taaaagggtat tgacttcaag gaagatggca acattctggg acacaaattg 1680
gaatacaact ataactcaca caatgtatac atcatggcag acaaacaaaa gaatggaatc 1740
aaagtgaact tcaagacccg ccacaacatt gaagatggaa gcgttcaact agcagacat 1800
tatcaacaaa atactccaat tggcgatggc cctgtccttt taccagacaa ccattacctg 1860
tccacacaat ctgccctttc gaaagatccc aacgaaaaga gagaccacat ggctccttctt 1920
gagtttgtaa cagctgctgg gattacacat ggcatggatg aactgtacaa ctga 1974

<210> 151

<211> 1836

<212> DNA

<213> Human

<400> 151

atggccaaca ctaccggaga gccagaggag gtgagcggcg ctctgtcccc accgtccgca 60
tcagcttatg tgaagctgggt actgctggga ctgattatgt gcgtgagcct ggcgggtaac 120
gccatcttgt cctgctgggt gctcaaggag cgtgccctgc acaaggctcc ttactacttc 180
ctgctggacc tgtgcctggc cgatggcata cgctctgccg tctgcttccc ctttgtgtgtg 240
gcttctgtgc gccacggctc ttcatggacc ttcatggcac tcagctgcaa gattgtggcc 300
tttatggcgg tgctcttttg ctccatgcg gccitcatgc tgttctgcat cagcgtcacc 360
cgctacatgg ccctcgccca ccaccgctc tacgccaagc gcatgacact ctggacatgc 420
gcggtgtgca tctgcatggc ctggaccctg tctgtggcca tggccttccc acctgtcttt 480
gacgtgggca cctacaagtt tattcgggag gaggaccagt gcatctttga gcatcgctac 540
ttcaaggcca atgacacgct gggcttcatg cttatgttgg ctgtgctcat ggcagctacc 600
catgtgtct acggcaagct gctcctcttc gattatcgtc accgcaagat gaagccagtg 660
cagatgggtg cagccatcag ccagaactgg acattccatg gtcccggggc caccggccag 720
gctgttgcca actggatcgc cggctttggc cgtggggcca tgccaccaac cctgctgggt 780

397/518

```

atccggcaga atgggcatgc agccagccgg cggctactgg gcatggacga ggtcaagggt 840
gaaaagcagc tgggccgcat gttctacgcg atcacactgc tctttctgct cctctgggtca 900
ccctacatcg tggcctgcta ctggcgagtg tttgtgaaag cctgtgctgt gccccaccgc 960
tacctggcca ctgctgtttg gatgagcttc gcccaggctg ccgtaaccc aattgtctgc 1020
ttcctgctca acaaggacct caagaagtcg ctgaggactc acgccccctg ctggggcaca 1080
ggagggtccc cggctcccag agaaccctac tgtgtcatgg ctagcaaagg agaagaactc 1140
ttcactggag ttgtcccaat tcttgttgaa ttagatggig atgttaacgg ccacaagttc 1200
tctgtcagig gagaggggtga aggtgatgca acatacgaa aacttacct gaagttcatc 1260
tgcactactg gcaaactgcc tgttccatgg ccaacactag tcaactactc gtgctatggt 1320
gttcaatgct tttcaagata cccggtatcat atgaaacggc atgacttttt caagagtgcc 1380
atgcccgaa gttatgtaca ggaaaggacc atcttcttca aagatgacgg caactacaag 1440
acacgtgctg aagtcaagtt tgaaggatg acccttgita atagaatcga gttaaaaggt 1500
attgacttca aggaagatgg caacattctg ggacacaaat tggaatacaa ctataactca 1560
cacaatgtat acatcatggc agacaaacaa aagaatggaa tcaaagtga cttcaagacc 1620
cgccacaaca ttgaagatgg aagcgttcaa ctagcagacc attatcaaca aaatactcca 1680
attggcgatg gccctgtcct tttaccagac aaccattacc tgtccacaca atctgccctt 1740
tcgaaagatc ccaacgaaaa gagagaccac atggtccttc ttgagtttgt aacagctgct 1800
gggattacac atggcatgga tgaactgtac aactga 1836

```

<210> 152

<211> 2397

<212> DNA

<213> Human

<400> 152

```

atggatctga agacagtgtc ctccctgccc cgctaccag gggagttcct gcaccccggt 60
gtgtacgctg gcacggccgt catgctgtc tgcctcctgg cctccttcgt cacctacatc 120
gtgcaccaga gcgccatccg catcagccgc aagggccggc acacgtcct gaatttctgc 180
ttccacgcgg ccttgacctt cactigtgtc gccggcggca tcaatgcac caagtacccc 240

```

398/518

atcctgtgcc	aggcgggtggg	catcgtgctg	cactattcta	cactgtccac	catgctgtgg	300
ataggagtga	ccgccaggaa	catctacaag	caggtagacca	agaaggcccc	tctgtgcctg	360
gacacagacc	agccaccgta	ccccaggcag	cccctgtcta	ggttttacct	cgtcagcgga	420
gggggtccct	ttatcatctg	tggggtcacg	gctgccacga	acatcaggaa	ttacgggaca	480
gaggacgagg	acacggcgta	ctgctggatg	gcctgggagc	ccagccctggg	cgcctttctac	540
ggcccagccg	ccatcatcac	ccgggtcacc	tgtgtgtact	tcctgggcac	ctacgtgcag	600
ctgcggcgcc	accagggcg	caggtagcag	ctgcgcacac	agcccaggga	gcagcgcgcg	660
ctggcgacac	ccgagggcg	ccgtgggatc	cggccaggca	ccccaccgc	acacgatgcc	720
cccggcgct	ccgtgctgca	gaacgagcac	tcatccagg	cacagctcg	cgcgcgcgc	780
ttcacgctgt	tccgtttcac	ggccacgtgg	gccttcgggg	cgttggcggt	gtcacagggc	840
cacttctctg	acatggctct	cagctgcctg	tacggcgct	tctgcgtgac	cctgggactc	900
ttcgtgtca	tccaccactg	cgccaagcgt	gaggacgtgt	ggcagtgtg	gtgggcatgc	960
tgcccgcgcc	gcaaggacgc	ccaccccgca	cttgacgcca	acggggccgc	gctggggccgc	1020
ggcgctgcc	tgcactcgcc	gggactgggc	cagccacggg	gcttcgcgca	cccaccgggc	1080
ccctgcaaga	tgaccaacct	gcaggccgcg	cagggccacg	ccagttgcct	gtcaccggcc	1140
accccgctgt	gcgccaagat	gcactgcgag	ccactgacgg	cggacgaggc	gcacgtgcac	1200
ctgcaggagg	aggcgccctt	cgggcacgac	ccccacctgc	acgggtgcct	tcagggcaga	1260
actaagccgc	cctactttag	ccggcaccca	gcagaggagc	ccgagtacgc	ctaccacatc	1320
ccatccagcc	tggatggcag	ccccgcagc	tcgcgcacag	acagcccccc	cagctctctg	1380
gatggcccg	cggggacaca	cacgctggcc	tgtgcaccc	agggcgaccc	cttccccatg	1440
gtcaccgagc	ccgagggcag	tgatgggagc	cctgccctct	acagctgcc	cacgcagccg	1500
ggcagggagg	cagcgctcgg	gcccggccac	ttggagatgc	tgcggaggac	acagtccctg	1560
ccctttggtg	gccccagcca	gaacgggctg	cccaagggtg	aattgctaga	aggcctgccg	1620
tttggcaccg	acgggaccgg	caacatccga	acgggaccct	ggaaaaacga	aactactgtg	1680
gctagcaaag	gagaagaact	cttcaactga	gttgtcccaa	ttcttgttga	attagatggt	1740
gatgttaacg	gccacaagtt	ctctgtcagt	ggagagggtg	aaggatgatc	aacatacgga	1800
aaacttaccc	tgaagttcat	ctgcactact	ggcaaactgc	ctgttccatg	gccaacacta	1860
gtcactactc	igtgtatgg	igtcaatgc	ttttcaagat	acccggatca	tatgaaacgg	1920
catgactttt	tcaagagtgc	catgcccga	ggttatgtac	aggaaaggac	catcttcttc	1980

399/518

aaagatgacg gcaactacaa gacacgtgct gaagtcaggt ttgaaggiga tacccttggt 2040
 aatagaatcg agttaaagg tattgacttc aaggaagatg gcaacattct gggacacaaa 2100
 ttggaatata actataactc acacaatgta tacatcatgg cagacaaaca aaagaatgga 2160
 atcaaagiga acttaagac cggccacaac attgaagatg gaagcgttca actagcagac 2220
 cattatcaac aaaatactcc aattggcgat ggccctgtcc ttttaccaga caaccattac 2280
 ctgtccacac aatctgccct ttcgaaagat cccaacgaaa agagagacca catggtcctt 2340
 cttgagtttg taacagctgc tgggattaca catggcatgg atgaactgta caactga 2397

<210> 153

<211> 1674

<212> DNA

<213> Human

<400> 153

atgacaaaca gtctgttctt ctgcccagtt tataaagatc tggagccatt cacgtatitt 60
 ttttatttag ttttcttgt tgggaattatt ggaagttgtt ttgcaacctg ggcttttata 120
 cagaagaata cgaatcacag gtgtgtgagc atctacttaa ttaatttgc taccagccgat 180
 ttcttgctta ctctggcatt accagtgaat attgttgttg acttgggtgt ggcaccttgg 240
 aagctgaaga tattccactg ccaagtaaca gcctgcctca tctatatcaa tatgtattta 300
 tcaattatct tcttagcatt tgtcagcatt gaccgtgtc ttacgtgac acacagctgc 360
 aagatctacc gaatacaaga acccgattt gccaaaatga tatcaaccgt tgtgtggcta 420
 atggtccttc ttataatggt gccaaatag atgattccca tcaaagacat caaggaaaag 480
 tcaaagtgtg gtgtatgga gtttaaaaag gaatttgga gaaattggca ttgtctgaca 540
 aatttcatat gttagcaat atttttaa tttcagcca tcatTTaat atccaattgc 600
 ctgtgaattc gacagctcta cagaaacaaa gataatgaaa attacccaaa tgtgaaaaag 660
 gctctcatca acatactttt agtgaccacg ggctacatca tatgcttgt tccttaccac 720
 atgtccgaa tcccgatac ctcagccag acagaagica taactgattg ctcaaccagg 780
 atttcactct tcaaagccaa agaggctaca ctgtccttg ctgtgtcgaa cctgtgcttt 840
 gatcctatcc tgtactatca cctctcaaaa gcatccgct caaaggcac tgagactttt 900

400/518

gcctcaccta aagagaccaa ggctcagaaa gaaaaattaa gatgtgaaaa taatgcagct 960
 agcaaaggag aagaactcct cactggagtt gtcccaattc ttgttgaatt agatggatgat 1020
 gttacggcc acaagttctc tgtcagtga gagggigaag gtgatgcaac atacggaaaa 1080
 cttacctga agttcatctg cactactggc aaactgcctg ttccatggcc aacactagtc 1140
 actactctgt gctatgggtg tcaatgcttt tcaagatacc cggatcataat gaaacggcat 1200
 gactttttca agagtggcat gcccgagggt tatgtacagg aaaggacat cttcttcaaa 1260
 gatgacggca actacaagac acgtgctgaa gtcaagtttg aaggatgatac ccttggttaat 1320
 agaatcgagt taaaagggtat tgacttcaag gaagatggca acattctggg acacaaattg 1380
 gaatacaact ataactcaca caatgtatac atcatggcag acaaacaaaa gaatggaatc 1440
 aaagtgaact tcaagaccgg ccacaacatt gaagatggaa gcgttcaact agcagacat 1500
 tatcaacaaa atactccaat tggcgatggc cctgtccttt taccagacaa ccattacctg 1560
 tccacacaat ctgcccttcc gaaagatccc aacgaaaaga gagaccacat ggtccttctt 1620
 gagtttgtaa cagctgctgg gattacacat ggcatggatg aactgtacaa ctga 1674

<210> 154

<211> 1791

<212> DNA

<213> Human

<400> 154

atggggttca acttgacgct tgcaaaatta ccaaataacg agctgcacgg ccaagagagt 60
 cacaattcag gcaacaggag cgacgggcca ggaaagaaca ccaccttca caatgaattt 120
 gacacaattg tcttgccggt gctttatctc attatatttg tggcaagcat cttgctgaat 180
 ggtttagcag tgtggatctt ctccacatt aggaataaaa ccagcttcat attctatctc 240
 aaaaacatag tggttgcaga cctcataatg acgtgacat ttccatttcg aatagtccat 300
 gatgcaggat ttggaccttg gtacttcaag tttattctct gcagatacac ttcagttttg 360
 ttttatgcaa acatgtatac ttccatcgtg ttccttgggc tgataagcat tgatcgctat 420
 ctgaagggtg tcaagccatt tggggactct cggatgtaca gcataacctt cacgaagggt 480
 ttatctgttt gtgtttgggt gatcatggct gttttgtctt tgccaaacat catcctgaca 540

401/518

```

aatggtcagc caacagagga caatatccat gactgctcaa aacttaaaag tcctttgggg 600
gtcaaattggc atacggcagt cacctatgtg aacagctgct tgtttgtggc cgtgctgggtg 660
attcigatcg gatgttacat agccatatcc aggtacatcc acaaatccag caggcaattc 720
ataagtcagt caagccgaaa gcgaaaacat aaccagagca tcagggttgt tgtggctgtg 780
ttttttacct gctttctacc atatcacttg tgcagaattc cttttacttt tagtcactta 840
gacaggcttt tagatgaatc tgcacaaaaa atcctatatt acigcaaaga aattacactt 900
ttcttgctcg cgtgtaatgt ttgcttgat ccaataattt actttttcat gtgtaggtca 960
ttttcaagaa ggctgttcaa aaaatcaaat atcagaacca ggagtgaag catcagatca 1020
cigcaaagtg tgagaagatc ggaagttcgc atatattatg attacactga tgtggctagc 1080
aaaggagaag aactcttcac tggagttgtc ccaattcttg ttgaattaga tggtagtgtt 1140
aacggccaca agttctctgt cagtgagagag ggtagaagggtg atgcaacata cggaaaactt 1200
acctgaagt tcactgcac tactggcaaa ctgctgttc catggccaac actagtcact 1260
actctgtgct atggtgttca atgcttttca agataccgg atcatatgaa acggcatgac 1320
ttttcaaga gtgcatgcc cgaaggttat gtacaggaaa ggaccatctt cttcaaagat 1380
gacggcaact acaagacacg tgcgaagtc aagtttgaag gtgataccct tgttaataga 1440
atcgagttaa aaggtattga cttcaaggaa gatggcaaca ttctgggaca caaattggaa 1500
tacaactata actcacacaa tgtatacatc atggcagaca aacaaaagaa tggaatcaaa 1560
gtgaacttca agaccgcca caacattgaa gatggaagcg ttcaactagc agaccattat 1620
caacaaaata ctccaattgg cgatggccct gtccttttac cagacaacca ttacctgtcc 1680
acacaatctg ccttttcgaa agatcccaac gaaaagagag accacatggt ccttcttgag 1740
tttgtaacag ctgctgggat tacacatggc atggatgaac tgtacaactg a 1791

```

<210> 155

<211> 1719

<212> DNA

<213> Human

<400> 155

```

atgctgggga tcatggcatg gaatgcaact igcaaaaact ggctggcagc agaggctgcc 60

```


402/518

ctggaaaagt actacctttc cattttttat gggattgagt tcgttgtggg agtccttggg 120
 aataccattg ttgtttacgg ctacatcttc tctctgaaga actggaacag cagtaatat 180
 tatctcttta acctctctgt ctctgactta gcttttctgt gcacctccc catgcigata 240
 aggagttaig ccaatggaaa ctggatataat ggagacgtgc tctgcataag caaccgatat 300
 gtgcttcattg ccaacctcta taccagcatt ctctttctca cttttatcag catagatcga 360
 tacttgataa ttaagtatcc ttcccgagaa caccttctgc aaaagaaaga gtttgcatt 420
 ttaatctcct tggccatttg ggtttttagta accttagagt tactacccat acttcccctt 480
 ataaatcctg ttataactga caatggcacc acctgtaatg attttgcaag ttctggagac 540
 cccaactaca acctcattta cagcatgtgt ctacactgt tggggttcct tattcctctt 600
 ttgtgatgt gtttctttta ttacaagatt gctctcttcc taaagcagag gaataggcag 660
 gttgctactg ctctgcccct tgaagagcct ctcaacttgg tcatcatggc agtggtaatc 720
 ttctctgtgc cttttacacc ctatcacgtc atcggaatg tgaggatcgc ttcacgcctg 780
 gggagtggga agcagtatca gtgcactcag gtcgtcatca actcctttta catttgaca 840
 cggccttttg cctttctgaa cagtgtcatc aacctgtct tctattttct ttggggagat 900
 cacttcaggg acatgctgat gaatcaactg agacacaact tcaaatccct tacatccttt 960
 agcagatggg ctcatgaact cctactttca ttcagagaaa aggctagcaa aggagaagaa 1020
 ctcttactg gagttgtccc aattcttgtt gaattagatg gtgatgttaa cggccacaag 1080
 ttctctgtca gtggagaggg tgaaggtgat gcaacatacg gaaaacttac cctgaagttc 1140
 atctgcacta ctggcaaact gccgtttcca tggccaacac tagtactac tctgtgctat 1200
 ggtgttcaat gcttttcaag ataccggat catatgaaac ggcatgactt tttcaagagt 1260
 gccatgccg aaggttatgt acaggaaagg accatcttct tcaaagatga cggcaactac 1320
 aagacacgtg ctgaagtcaa gtttgaaggt gatacccttg ttaatagaat cgagttaaaa 1380
 ggtattgact tcaaggaaga tggcaacatt ctgggacaca aattggaata caactataac 1440
 tcacacaatg tatacatcat ggagacaaa caaagaaatg gaatcaaagt gaacttcaag 1500
 acccgccaca acattgaaga tggaagcgtt caactagcag accattatca acaaaatact 1560
 ccaattggcg atggccctgt ccttttacca gacaaccatt acctgtccac acaatctgcc 1620
 ctttcgaaag atcccaacga aaagagagac cacatggctc ttcttgagtt tgtaacagct 1680
 gctgggatta cacatggcat ggatgaactg tacaactga 1719

403/518

<210> 156

<211> 1728

<212> DNA

<213> Human

<400> 156

```

atgagagctg tcttcatcca aggtgctgaa gaggaccctg cggcattctg ctaccaggig      60
aatgggtcct gccccaggac agtacatact ctgggcatcc agttggatcat ctacctggcc      120
tgtgcagcag gcatgctgat tatcgtgcta gggaatglat ttgtggcatt tgctgtgtcc      180
tacttcaaag cgcttcacac gccaccaaac ttctgtctgc tctccctggc cctggctgac      240
atgtttcttg gtctgtctgt gctgcccctc agcaccattc gctcagtga gagctgtctg      300
ttcttcgggg acttcctctg ccgcctgcac acctacctgg acacctctt ctgcctcacc      360
tccatcttcc atctctgttt catttccatt gaccgccact gtgccatctg tgacccccig      420
ctctatccct ccaagttcac agtgaggggt gctctcaggt acatcctggc aggatggggg      480
gtgcccgcag catacattc gttattcctc tacacagatg tggtagagac aaggctcagc      540
cagtggcttg aagagatgcc ttgtgtgggc agttgccagc tgctgtctaa taaattttgg      600
ggctgggttaa acttcccttt gttctttgtc ccctgcctca ttatgatcag ctgtgtatgt      660
aagatctttg tggttgctac cagacaggct cagcagatta ccacattgag caaaagcctg      720
gctggggctg ccaagcatga gagaaaagct gccaaagacc tgggcattgc tgtgggcata      780
tacctcttgt gctggctgcc ctacaccata gacacgatgg tcgacagcct ccttacctt      840
atcacacccc cactggtctt tgacatcttt atctggtttg cttacttcaa ctacgcctgc      900
aaccocatca tctatgtctt ttcttaccag tggtttcgga aggcactgaa actcacactg      960
agccagaagg tcttctcacc gcagacacgc actgttgatt tgtaccaaga agctagcaaa     1020
ggagaagaac tcttctactg agttgtccca attctgtttg aattagatgg tgatgttaac     1080
ggccacaagt tctctgtcag tggagagggt gaaggatgat caacatacgg aaaacttacc     1140
ctgaagtcca tctgcactac tggcaaactg cctgttccat ggccaacact agtcactact     1200
ctgtgctatg gtgttcaatg cttttcaaga taccggatc atatgaaacg gcatgacttt     1260
ttcaagagtg ccatgcccga aggttaigta caggaaagga ccatcttctt caaagatgac     1320
ggcaactaca agacacgtgc tgaagtcaag ttgaagggtg atacccctgt taatagaatc     1380

```

404/518

gagttaaag gtattgactt caaggaagat ggcaacattc tgggacacaa attggaatac 1440
 aactataact cacacaatgt atacatcatg gcagacaaac aaaagaatgg aatcaaagtg 1500
 aacttcaaga cccgccacaa cattgaagat ggaagcggtc aactagcaga ccattatcaa 1560
 caaaatactc caattggcga tggccctgtc cttttaccag acaaccatta cctgtccaca 1620
 caatctgccc ttctgaaaga tcccaacgaa aagagagacc acatggctct tcttgagttt 1680
 gtaacagctg ctgggattac acatggcatg gatgaactgt acaactga 1728

<210> 157

<211> 1743

<212> DNA

<213> Human

<400> 157

atgaccagca atttttccca accgtttgtg cagctttgct atgaggatgt gaatggatct 60
 tgtattgaaa ctccctattc tcttgggtcc cgggtaattc tgtacacggc gtttagcttt 120
 gggcttttgc tggctgtatt tggaaatctc ttagtaatga cttctgttct tcattttaag 180
 cagctgcact ctccaaccaa tttctcatt gcctctctgg cctgtgctga cttcttggtg 240
 ggtgtgactg tgaigctttt cagcatggtc aggacggctg agagctgctg gtattttgga 300
 gccaaatitt gtactcttca cagttgctgt gatgtggcat ttgtttactc ttctgtcctc 360
 cactigtgct tcacttgcac cgacaggtaac attgtggta ctgatccctt ggtctatgct 420
 accaagttca ccgtgtctgt gtcgggaatt tgcacagcg tgtccctggat tctgcctctc 480
 acgtacagcg gtgctgtgtt ctacacaggt gtcaatgatg atgggctgga ggaattagta 540
 agtgccttca actgcgtagg tggctgtcaa attattgtaa gtcaaggctg ggtgttgata 600
 gattttctgt tattcttcat acctaccctt gttatgataa ttctttacag taagattttt 660
 cttatagcta aacaacaagc tataaaaatt gaaactacta gtagcaaagt agaatcatcc 720
 tcagagagtt ataaaatcag agtggccaag agagagagga aagcagctaa aacctgggg 780
 gtcacggtaac tagcatttgt tatttcatgg ttaccgtata cagttgatat attaatgtat 840
 gcctttatgg gcttctgac cctgcctat atctatgaaa ttgtctgttg gactgcttat 900
 tataactcag ccatgaatcc ttgatttat gctctatitt atccttggtt taggaaagcc 960

405/518

ataaaacit ttttaagttg agatgtttta aaggctagtt catcaacat tagtttttt 1020
 ttagaagcta gcaaaggaga agaactcttc actggagttg tccaattct tgtigaatta 1080
 gatggtagt ttaacggcca caagtctct gtcagtggag agggatgaagg tgaatgaaca 1140
 tacggaaaac ttacctgaa gtatcatctg actactggca aactgcctgt tccatggcca 1200
 acactagica ctactctgtg ctatgggtgt caatgctttt caagataccc ggaatcatatg 1260
 aaacggcatg actttttcaa gaggccaatg cccgaagggt atgtacagga aaggaccatc 1320
 ttcttcaaag atgacggcaa ctacaagaca cgtgctgaag tcaagttiga aggtgatacc 1380
 cttgttaata gaatcgagtt aaaaggtatt gacttcaagg aagatggcaa cattctggga 1440
 cacaattgg aatacaacta taactcacac aatgtataca tcatggcaga caaacaaaag 1500
 aatggaatca aagtgaactt caagaccgc cacaacattg aagatggaag cgttcaacta 1560
 gcagaccatt atcaacaaaa tactccaatt ggcatggcc ctgtcctttt accagacaac 1620
 cattacctgt ccacacaatc tgccttttcg aaagatccca acgaaaagag agaccacatg 1680
 gtccttcttg agtttgtaac agctgctggg attacacatg gcatggatga actgtacaac 1740
 tga 1743

<210> 158

<211> 1752

<212> DNA

<213> Human

<400> 158

atgagcagca attcatccct gctgggtggc gtgcagctgt gctacgcgaa cgtgaatggg 60
 tcctgtgtga aaatccctt ctgccggga tccgggtga ttctgtacat agtgtttggc 120
 ttggggctg tgcctggctgt gtttggaac ctctgggtga tgatttcaat cctccatttc 180
 aagcagctgc actctccgac caattttctc gtgcctctc tggcctgcgc tgatttcttg 240
 gtgggtgtga ctgtgatgcc ctacagcatg gtcaggacgg tggagagctg ctggtatatt 300
 gggaggagtt ttgtacttt ccacacctgc tgtgatgtgg cattttgtta ctcttctctc 360
 ttactattgt gttcatctc catcgacagg tacattgcgg ttactgacct cctggcttat 420
 cctaccaagt tcaccgtatc tgtgtcagga atttgatca gcgtgtcctg gatcctgccc 480

406/518

```

ctcatgtaca gcggtgctgt gtcttacaca ggtgtctatg acgatgggct ggaggaatta 540
tctgatgcc taaactgtat aggaggttgt cagaccgttg taaatcaaaa ctgggtgttg 600
acagattttc tacccttctt tatacctacc tttattatga taattctgta tggtaacata 660
tttcttgtgg ctagacgaca ggcgaaaaag atagaaaata ctggtagcaa gacagaatca 720
tcctcagaga gttacaaagc cagagtggcc aggagagaga gaaaagcagc taaaaccctg 780
ggggtcacag tggtagcatt tatgatttca tggttacat atagcattga ttcatttaatt 840
gatgccttta tgggctttat aacccttgcc tgtatttatg agatttgctg ttggtgtgct 900
tattataact cagccatgaa tcctttgatt tatgctttat ttaccctatg gtttaggaaa 960
gcaataaaag ttattgtaac tggtcaggtt ttaaagaaca gttcagcaac catgaatttg 1020
ttttctgaac atatagctag caaaggagaa gaactcttca ctggagtgtg cccaattctt 1080
gttgaattag atgggtgatgt taacggccac aagtctcttg tcagtggaga gggtagaggt 1140
gatgcaacat acgaaaaact taccctgaag ttcatctgca ctactggcaa actgcctgtt 1200
ccatggccaa cactagtcac tactctgtgc tatgggtgtc aatgcttttc aagataccg 1260
gatcatatga aacggcatga ctttttcaag agtgccatgc ccgaaggtta tgtacaggaa 1320
aggaccatct tcttcaaaga tgacggcaac tacaagacac gtgctgaagt caagtttgaa 1380
ggtgataccc ttgittaatag aatcgagtta aaaggatttg acttcaagga agatggcaac 1440
attctgggac acaaatigga atacaactat aactcacaca atgtatacat catggcagac 1500
aaacaaaaga atggaatcaa agtgaacttc aagacccgcc acaacattga agatggaagc 1560
gttcaactag cagaccatta tcaacaaaat actccaattg gcgatggccc tgtcctttta 1620
ccagacaacc attacctgtc cacacaatct gccctttcga aagatcccaa cgaaaagaga 1680
gaccacatgg tccttcttga gtttgtaaca gctgctggga ttacacatgg catggatgaa 1740
ctgtacaact ga 1752

```

<210> 159

<211> 2556

<212> DNA

<213> Human

<400> 159

407/518

atggggccca ccctagcggg tcccaccccc tatggctgta ttggctgtaa gctaccccag	60
ccagaatacc caccggctct aatcatcttt atgttctgcg cgaatggtat caccatcggt	120
gtagacctaa tcggcaactc catggtcatt ttggctgiga cgaagaacaa gaagctccgg	180
aattctggca acatcttctg ggtcagtcct tctgtggccg atatgctggg ggccatctac	240
ccataccctt tgaigctgca tgccatgtcc atggggggct gggatctgag ccagttacag	300
tgccagatgg tcgggttcac cacagggctg agtgtggctg gctccatctt caacatcggt	360
gcaatcgcta tcaaccgtta ctgctacatc tgccacagcc tccagiacga acggatcttc	420
agtgtcgca atacctgcat ctacctggct atcacctgga tcatgaccgt cctggctgtc	480
ctgccaacaa tgtacattgg caccatcgag tacgatcctc gcacctacac ctgcatcttc	540
aactatctga acaacctgtt ctactgtt accatctctt gcatccactt cgtcctccct	600
ctcctcatcg tgggtttctg ctactgagg atctggacca aagtgciggc gggccgigac	660
cctgcagggc agaatcciga caaccaactt gctgaggctc gcaatttctt aacctgttt	720
gtgatcttcc tctctttgc agtgtgctgg tgccctatca acgtgctcac tgtcttggg	780
gctgtcagtc cgaaggagat ggagggcaag atccccaact ggctttatct tgcagcctac	840
ttcatagcct acttcaacag ctgcctcaac gctgtgatct acgggctcct caatgagaat	900
ttccgaagag aatactggac catcttccat gctatgcggc accctatcat attcttccct	960
ggcctcatca gtgatattcg tgagatgcag gaggcccgta ccttggcccg cgcccggtcc	1020
catgctcgcg accaagctcg tgaacaagac cgtgcccatt cctgtcctgc tgtggaggaa	1080
accccgatga atgtccgga tgttccatta cctgggtgat ctgcagctgg ccaccccgac	1140
cgtgcctctg gccaccctaa gcccattcc agatcctcct ctgcctatcg caaatctgcc	1200
tctaccacc acaagtctgt cttagccac tccaaggctg cctctggtca cctcaagcct	1260
gtctctggcc actccaagcc tgcccttggg caccccaagt ctgccactgt ctaccctaag	1320
cctgcctctg tccatttcaa ggggtgactt gtccatttca aggttgactc tgtccatttc	1380
aagcctgact ctgttcattt caagcctgct tccagcaacc ccaagcccat cactggccac	1440
catgtctctg ctggcagcca ctccaagtct gccttcagt ctgccaccag ccaccciaaa	1500
cccatcaagc cagctaccag ccatgctgag cccaccactg ctgactatcc caagcctgcc	1560
actaccagcc accctaagcc cgtgctgct gacaacctg agctctctgc ctccattgc	1620
cccagatcc ctgccattgc ccacctgtg tctgacgaca gtgacctccc tgagtcggcc	1680
tctagccctg ccgtcgggcc caccaagcct gctgccagcc agctggagtc tgacaccatc	1740

408/518

gctgaccttc ctgaccctac tglagtcact accagiacca atgattacca tgatgtcgtg 1800
 gtltgtgatg ttgaagatga tcctgatgaa atggctgtgg ctagcaaagg agaagaactc 1860
 ttcactggag ttgtcccaat tcttgttgaa ttagatgggtg atgttaacgg ccacaagttc 1920
 tctgtcagtg gagagggtga aggtgatgca acatacggaa aacttacctt gaagttcatc 1980
 tgcactactg gcaaactgcc tgttccatgg ccaacactag tcactactct gtgctatggt 2040
 gtccaatgct ttccaagata cccggatcat atgaaacggc atgacttttt caagagtgcc 2100
 atgcccgaag gttatgtaca ggaaaggacc atcttcttca aagatgacgg caactacaag 2160
 acacgtgctg aagtcaagtt tgaagggtgat acccttgtta atagaatcga gttaaaaggt 2220
 attgacttca aggaagatgg caacattctg ggacacaaat tggaatacaa ctataactca 2280
 cacaatgtat acatcatggc agacaaacaa aagaatggaa tcaaagtga cttcaagacc 2340
 cgccacaaca ttgaagatgg aagcgttcaa ctagcagacc attatcaaca aaatactcca 2400
 attggcgaatg gccctgtcct ttaccagac aaccattacc tgtccacaca atctgccctt 2460
 tcgaaagatc ccaacgaaaa gagagaccac atggtccttc ttgagtttgt aacagctgct 2520
 gggattacac atggcatgga tgaactgtac aactga 2556

<210> 160

<211> 2688

<212> DNA

<213> Human

<400> 160

atgaaaatga agtcccaggc aaccatgatt tgctgcttag tgttctttct gtccacagaa 60
 tgttcccact atagatccaa gattcaccta aaagctggag ataaacttca aagccctgaa 120
 gggaaaccca agactggaag gatccaagag aaatgcgaag gaccttgtat ttcttcttcc 180
 aactgcagcc agccctgtgc taaggacttt catggagaaa taggatttac atgtaatcaa 240
 aaaaagtggc aaaaatcagc tgaacatgt acaagccttt ctgtggaaaa actctttaag 300
 gactcaactg gtgcattctg cctttctgta gcagcaccat ctataacctt gcataattcta 360
 gactttcgag ctccagagac cattgagagt gtagtcaag gaatccgtaa gaactgcccc 420
 ttgattatg cctgcatcac tgacatgggtg aaatcatcag aaacaacatc tggaaatatt 480

409/518

gcatttatag tggagttatt aaaaaatatt tctacagact tgcctgataa tgttactcga 540
 gagaaaatga agagctatag tgaagtggcc aaccacatcc tcgacacagc agccatttca 600
 aactgggcctt tcattcccaa caaaaatgcc agctcggatt tgttcagtc agtgaatttg 660
 tttgccagac aactccacat ccacaataat tctgagaaca ttgtgaatga actcttcatt 720
 cagacaaaag ggtttcacat caaccataat acccagaga aaagcctcaa tttctccatg 780
 agcatgaaca ataccacaga agatatctta ggaatggtag agattcccag gcaagagcta 840
 aggaagctgt ggccaaatgc atcccaagcc attagcatag ctttcccaac cttgggggct 900
 atcctgagag aagcccactt gcaaaatgtg agtcttccca gacaggtaaa tggctcgttg 960
 ctatcagigg ttttaccaga aaggttgcaa gaaatcatac tcaccttcga aaagatcaat 1020
 aaaacccgca atgccagagc ccagtgtgtt ggctggcact ccaagaaaag gagatgggat 1080
 gagaaagcgt gccaaatgat gttggataac aggaacgaag tgaaatgccg ctgtaactac 1140
 accagtgttg tgatgtcttt ttccattctc atgtcctcca aatcagtagc cgacaaagtt 1200
 ctggactaca tcacctgcat tgggctcagc gtctcaatcc taagcttggt tctttgcctg 1260
 atcattgaag ccacagtgtg gtcccggttg gttgtgacgg agatatcata catgcgtcac 1320
 gtgtgcatcg tgaatatagc agtgtccctt ctgactgcca atgtgtggtt tatcataggc 1380
 tctcacttta acattaaggc ccaggactac aacatgtgtg ttgcagtac atttttcagc 1440
 cactttttct acctctctct gtttttcttg atgtcttca aagcattgct catcatttat 1500
 ggaatatttg tcattttccg taggatgatg aagtcgccga tgatggtcat tggctttgcc 1560
 attggctatg ggtgcccatt gatcattgct gtcactacag ttgctatcac agagccagag 1620
 aacggctaca tgagacctga ggctgttggt cttaactggg acaataccaa agccctttta 1680
 gcatttgcca tcccggcggt cgicattgtg gctgtaaatc tgattgtggt tttggttggt 1740
 gctgtcaaca ctcagaggcc ctctattggc agttccaagt ctcaggatgt ggtcataatt 1800
 atgaggatca gcaaaaatgt tgccatctc actccactgc tgggactgac ctggggtttt 1860
 ggaatagcca ctctcataga aggcacttcc ttgacgttcc atataatttt tgccttgctc 1920
 aatgccttcc aggttaagttc caagagggag acttttctgt gttactccga cgctagcaaa 1980
 ggagaagaac tcttcacttg agttgtccca attcttgttg aattagatgg tgatgttaac 2040
 ggccacaagt tctctgtcag tggagagggt gaaggtgatg caacatacgg aaaacttacc 2100
 ctgaagtcca tctgcactac tggcaaacctg cctgttccat ggccaacact agtcactact 2160
 ctgtgctatg gtgttcaatg cttttcaaga taccgggata atatgaaacg gcatgacttt 2220

410/518

```

ttcaagagtg ccatgccga aggttatgta caggaaagga ccatcttctt caaagatgac 2280
ggcaactaca agacacgtgc tgaagtcaag ttigaagggtg atacccttgt taatagaatc 2340
gagttaaaag gtattgactt caaggaagat ggcaacattc tgggacacaa attggaatac 2400
aactataact cacacaatgt atacatcatg gcagacaaac aaaagaatgg aatcaaagtg 2460
aacttcaaga cccgccacaa cattgaagat ggaagcggtc aactagcaga ccattatcaa 2520
caaaatactc caattggcga tggccctgtc cttttaccag acaaccatta cctgtccaca 2580
caatctgccc ttctgaaaga tccaacgaa aagagagacc acatggctct tcttgagttt 2640
gtaacagctg ctgggattac acatggcatg gatgaactgt acaactga 2688

```

<210> 161

<211> 3447

<212> DNA

<213> Human

<400> 161

```

atgaaagttg gaggctgtg gctcatttct ttcttcacct tcactgacgg ccacgggtggc 60
ttcctgggga aaaatgatgg catcaaaaca aaaaaagaac tcattgtgaa taagaaaaaa 120
catctaggcc cagtcgaaga atatcagctg ctgcttcagg tgacctatag agattccaag 180
gagaaaagag atttgagaaa tttctgaag ctcttgaagc ctccattatt atggtcacat 240
gggctaatta gaattatcag agcaaaggct accacagact gcaacagcct gaatggagtc 300
ctgcagtgtg cctgtgaaga cagctacacc tggtttcctc cctcatgcct tgatccccag 360
aactgctacc ttcacacggc tggagcactc ccaagctgtg aatgcatct caacaacctc 420
agccagagtg tcaatttctg tgagagaaca aagatttggg gcactttcaa aattaatgaa 480
aggtttacaa atgacctttt gaattcatct tctgctatat actccaaata tgcaaatgga 540
attgaaattc aacttaaaaa agcatatgaa agaattcaag gttttgagtc ggttcaggtc 600
acccaatttc gaaatggaag catcggtgtt gggtatgaag ttgttggtc cagcagtgca 660
tctgaactgc tgcagccat tgaacatgtt gccgagaagg ctaagacagc ccttcacaag 720
ctgtttccat tagaagacgg ctctttcaga gtgttcggaa aagcccagtg taatgacatt 780
gtctttggat ttgggtccaa ggaatgatgaa tataccctgc cctgcagcag tggctacagg 840

```

411/518

ggaaacatca cagccaagtg tgagtcctct ggggtggcagg tcatcagga gacttgtgtg 900
 ctctctctgc ttgaagaact gaacaagaat ttcagtatga ttgtaggcaa tgcactgag 960
 gcagctgtgt catccttcgt gcaaaatctt tctgtcatca ttcggcaaaa cccatcaacc 1020
 acagtgggga atctggcttc ggtgggtgtc attctgagca atatttcac tctgtcactg 1080
 gccagccatt tcagggtgtc caattcaaca atggaggatg tcatcaglat agctgacaat 1140
 atccttaatt cagcctcagt aaccaactgg acagtcttac tgcgggaaga aaagtatgcc 1200
 agctcacggt tactagagac attagaaaac atcagcactc tgggtgcctcc gacagctctt 1260
 cctctgaatt tttctcggaa attcattgac tggaaaggga ttccagtga caaaagccaa 1320
 ctcaaaagg gttacagcta tcagattaaa atgtgtcccc aaaatacatc tattcccatc 1380
 agaggccglt tgittaattgg gtcagaccaa ttccagagat cccttcaga aactattatc 1440
 agcatggcct cgttgactct ggggaacatt ctaccggtt ccaaaaatgg aaatgctcag 1500
 gtcaatggac ctgtgatac cacggttatt caaaactatt ccataaatga agttttccta 1560
 tttttttcca agatagagtc aaacctgagc cagcctcatt gtgtgttttg ggatttcagt 1620
 catttgcagt ggaacgatgc aggtgccac ctagtgaatg aaactcaaga catcgtgacg 1680
 tgccaatgta ctacttgac ctcttctcc atattgatgt cacctttgt cccctctaca 1740
 atcttccccg ttgtaaaatg gatcacctat gtgggactgg gtatctccat tggaaagtctc 1800
 attttatgcc tgatcatcga ggctttgttt tggaaagcaga ttaaaaaaag ccaaacctct 1860
 cacacacgtc gtatttgcatt ggtgaacata gccctgtccc tcttgattgc tgatgtctgg 1920
 tttattgttg gtgccacagt ggacaccacg gigaacctt ctggagtctg cacagctgct 1980
 gtgttcttta cacacttctt ctacctctt ttgttcttct ggatgctcat gcttggcatc 2040
 ctgctggctt accggatcat cctcgtgttc catcacatgg cccagcattt gatgatggct 2100
 gttggatttt gccctgggta tgggtgccct ctattatat ctgtcattac cattgcgtc 2160
 acgcaacctt gcaataccta caaaaggaaa gatgtgtgtt ggcttaactg gtccaatgga 2220
 agcaaaccac tcctggcttt tgtgttcct gcactggcta ttgtggctgt gaacttcgtt 2280
 gtgggtgtgc tagttctcac aaagctctgg aggccgactg ttggggaaag actgagtcgg 2340
 gatgacaagg ccaccatcat ccgcgtgggg aagagcctcc tcattctgac cctctgtcta 2400
 gggctcacct ggggccttgg aataggaaca atagtgga gccagaatct ggcttggcat 2460
 gttatTTTTT ctttactcaa tgcattccag ggatttttta tcttatgctt tggaaatactc 2520
 ttggacagta agctgcgaca acttctgttc aacaagttgt ctgccttaag ttcttgggaag 2580

412/518

caaacagaaa agcaaaactc atcagattta tctgccaaac ccaaattctc aaagcctttc 2640
 aaccctatgc aaaacaaagg ccattatgca ttttctcata ctggagattc ctccgacaac 2700
 atcatgctaa ctcatgttgt ctcaaataaa gctagcaaag gagaagaact ctctactgga 2760
 gttgtcccaa ttcttgttga attagatggt gatgttaacg gccacaagtt ctctgtcagt 2820
 ggagagggtg aaggtgatgc aacatacggg aaacttaccc tgaagttcat ctgcactact 2880
 ggcaaaactgc ctgttccatg gccaaactia gtcactactc tgtgctatgg tgttcaatgc 2940
 ttttcaagat acccggatca tatgaaacgg catgactttt tcaagagtgc catgcccga 3000
 ggttatgtac aggaaaggac catcttcttc aaagatgacg gcaactacaa gacacgtgct 3060
 gaagtcaagt ttgaaggatg tacccttgtt aatagaatcg agttaaaagg tatgtacttc 3120
 aaggaagatg gcaacattct gggacacaaa ttggaataca actataactc acacaatgta 3180
 tacatcatgg cagacaaaca aaagaatgga atcaaagtga acttcaagac ccgccacaac 3240
 attgaagatg gaagcgttca actagcagac cattatcaac aaaatactcc aattggcgat 3300
 ggccctgtcc ttttaccaga caaccattac ctgtccacac aatctgccct ttcgaaagat 3360
 cccaacgaaa agagagacca catggctcct cttagatttg taacagctgc tgggattaca 3420
 catggcatgg atgaactgta caactga 3447

<210> 162

<211> 1929

<212> DNA

<213> Human

<400> 162

atgtcagtga aaccagctg ggggcctggc cctcggagg gggtcaccgc agtgcctacc 60
 agtgaccttg gagagatcca caactggacc gagctgcttg acctctcaa ccacactttg 120
 tctgagtgcc acgtggagct cagccagagc accaagcgcg tggctccttt tgcctctac 180
 ctggccatgt ttgtggttgg gctgggtggg aacctcctgg tgatatgcgt caactggcgc 240
 ggctcaggcc gggcagggt gatgaacctc tacatctca acatggccat cgcggacctg 300
 ggcatgttcc tgtctctgcc cgtgtggaig ctggaggta cgctggacta cacctggctc 360
 tggggcagct tctcctgccg ctctactcac tactctact ttgtcaacat gtatagcagc 420

413/518

```

atcttcttcc tggigtgcct cagtgtcgac cgctatgcta ccctcaccag cgctccccc 480
tcctggcagc gttaccagca ccgagtgcgg cgggccatgt gtgcaggcat ctgggtccctc 540
tcggccatca tcccgtgcc tgagggtggtc cacatccagc tgggtggagg ccctgagccc 600
atgtgccctt tcatggcacc ttttgaaacg tacagcacct gggccctggc ggtggccctg 660
tcaccacca tcctgggctt cctgtgtccc ttccctctca tcacagtctt caatgtgtgtg 720
acagcctgcc ggctgcggca gccaggacaa cccaagagcc ggcgccactg cctgtgtgtg 780
tgcgcciacg tggccgtctt tgtcatgtgc tggctgccct atcatgtgac cctgtgtgtg 840
ctcacactgc atgggaccca catctccctc cactgccacc tgggtccact gctctacttc 900
ttctatgatg tcattgactg ctcttccatg ctgcactgtg tcatcaacct catcctttac 960
aactttctca gccacactt cggggccgg ctcctgaatg ctgtagtcca ttaccttctt 1020
aaggaccaga ccaaggcggg cacatgcgcc tctcttctt cctgtttccac ccagcattcc 1080
atcatcatca ccaagggtga tagccagcct gctgcagcag ccccccaccc tgagccaagc 1140
ctgagctttc aggcacacca ttgtcttcca aatacttccc ccatctctcc cactcagcct 1200
cttacacca gcgctagcaa aggagaagaa ctcttcactg gagttgtccc aattcttgtt 1260
gaattagatg gtgatgttaa cggccacaag ttctctgtca gtggagaggg tgaaggtgat 1320
gcaacatacg gaaaacttac cctgaagttc atctgcacta ctggcaaact gcctgtttcca 1380
tggccaacac tagtcactac tctgtgctat ggtgttcaat gcttttcaag ataccggat 1440
cataatgaaac ggcatgactt ttccaagagt gccatgcccg aaggttatgt acaggaaagg 1500
accatcttct tcaaagatga cggcaactac aagacacgtg ctgaagtcaa gtttgaaggt 1560
gatacccttg ttaatagaat cgagttaaaa ggtattgact tcaaggaaga tggcaacatt 1620
ctgggacaca aattiggaata caactataac tcacacaatg tatacatcat ggcagacaaa 1680
caaaagaatg gaatcaaagt gaacttcaag acccgccaca acattgaaga tggaaagcgtt 1740
caactagcag accattatca acaaaatact ccaattggcg atggccctgt ccttttacca 1800
gacaaccatt acctgtccac acaatctgcc ctctcgaaag atcccaacga aaagagagac 1860
cacatggctc ttcttgagtt tgaacagct gcitgggatta cacatggcat ggatgaactg 1920
tacaactga 1929

```

<210> 163

<211> 1962

414/518

<212> DNA

<213> Human

<400> 163

```

atggtttttg ctacacagaat ggataacagc aagccacatt tgattattcc tacacttctg   60
gtgcccctcc aaaaccgcag ctgcactgaa acagccacac ctctgccaag ccaataacctg   120
atggaattaa gtgaggagca cagttggatg agcaacaaaa cagaccttca ctatgtgctg   180
aaacccgggg aagtggccac agccagcadc ttctttggga ttctgtggtt gttttctatc   240
ttcggcaatt ccctggtttg ttgggtcadc cataggagta ggaggactca gtctaccacc   300
aactactttg tggcttccat ggcattgtct gaccttctca tcagcgttgc cagcacgcct   360
ttcgtcctgc tccagttcac cactggaagg tggacgctgg gtagtgaac gtgcaaggtt   420
gtgcgatatt ttcaatatct cactccaggt gtccagatct acgttctcct ctccatctgc   480
atagaccggt tctacacat cgtctatcct ctgagcttca aggtgtccag agaaaaagcc   540
aagaaaatga ttgcggcadc gtggatcttt gatgcaggct ttgtgacccc tgtgtctttt   600
ttctatggct ccaactggga cagtcattgt aactatttcc tcccctctc ttgggaaggc   660
actgcctaca ctgtcatcca ctctttggtg ggctttgtga ttccatctgt cctcataatt   720
ttattttacc aaaaggctat aaaatatatt tggagaatag gcacagatgg ccgaacggtg   780
aggaggacaa tgaacattgt ccctcggaca aaagtgaana ctatcaagat gttcctcatt   840
ttaaatctgt tgtttttgct ctcttggtg ccttttcatg tagctcagct atggcacccc   900
catgaacaag actataagaa aagttccctt gttttcacag ctatcacatg gatatccttt   960
agttcttcag cctctaaacc tactctgtat tcaatttata atgccaattt tcggagaggg  1020
atgaaagaga ctttttgcct gtcctctatg aaatgttacc gaagcaatgc ctatactatc  1080
acaacaagtt caaggatggc caaaaaaac tacgttggca tttcagaaat cccttccatg  1140
gccaaaacta ttaccaaaaga ctgatctat gactcatttg acagagaagc caaggaaaaa  1200
aagcttgctt ggccatttaa ctcaaatcca ccaaatactt ttgtcgctag caaaggagaa  1260
gaactcttca ctggagtgtt cccaattctt gttgaattag atggtgatgt taacggccac  1320
aagtctcttg tcagtggaga ggggaaggt gatgcaacat acggaanaact taccctgaag  1380
ttcatctgca ctactggcaa actgcctgtt ccatggccaa cactagtcac tactctgtgc  1440
tatggtgttc aatgtcttcc aagataccgc gatcatatga aacggcatga ctttttcaag  1500

```

415/518

agtgccatgc ccgaaggta tgtacaggaa aggaccatct tcttcaaaga tgacggcaac 1560
 tacaagacac gtgctgaagt caagttigaa ggtgataccc ttgttaatag aatcgagtta 1620
 aaaggtattg acttcaagga agatggcaac attctgggac acaaattgga atacaactat 1680
 aactcacaca atgtatacat catggcagac aaacaaaaga atggaatcaa agtgaacttc 1740
 aagacccgcc acaacattga agatggaagc gttcaactag cagaccatta tcaacaaaat 1800
 actccaattg gcgatggccc tgtcctttta ccagacaacc attacctgtc cacacaatct 1860
 gccctttcga aagatcccaa cgaaaagaga gaccacatgg tcttcttga gtttgaaca 1920
 gctgctggga ttacacatgg catggatgaa ctgtacaact ga 1962

<210> 164

<211> 1833

<212> DNA

<213> Human

<400> 164

atggcctgca acagcacgtc cctttaggct tacacatacc tgtgctgaa caccagcaac 60
 gcctcagact cgggggccac ccagttgccc gcacccctca ggatctcctt ggccatagtg 120
 atgtgctga tgaccgtggt ggggttctg ggcaacactg tggcttgcac catcgtgtac 180
 cagaggccgg ctatgcgtc ggccatcaac ctgtgctgg ccaccctggc ctctccgac 240
 atcatgtgt cctctgtgt catgccctc accgccgtca cctcatcac cgtgcgctgg 300
 cactttgggg accacttctg ccgccttca gccacgtct actggtttt tgcctggag 360
 ggcgtggcca tctgtctcat catcagcgtg gaccgttcc tcatcatcgt ccagcgccag 420
 gacaagctga acccgcgag ggccaagggt atcatcgcg tctctgggt gctgtcctc 480
 tgcacgcgg ggccctcgt cacgggctgg acgttggtg aggtgccggc gcgggcccc 540
 cagtgcgtgc tgggtacac ggagctccc gctgaccg cctacgtgt caccttggtg 600
 gtggccgtgt tcttcgccc ctttggcgt atgtgtgct cctacatgt catcctcaac 660
 acgttcgca agaacgccgt gcgctgcac aaccagtcg acagcctgga cctcggcgag 720
 ctcaccagg cgggctcgt gcgctgcag cggcagcaac aggtcagcgt ggacttgagc 780
 ttcaagacca aggccttcac caccatctg atcctcttc tgggtcttc cctctgctg 840

416/518

```

ctgccccact ccgctctacag cctcctgict gtggttagcc agcgcttita ctgcggttcc 900
tccttctacg ccaccagcac ctgcgtcctg tggctcagtt acctcaagtc cgtcttcaac 960
cccacgtctt actgctggag aatcaaaaaa ttccgcgagg cctgcataga gttgctgccc 1020
cagaccitcc aaatcctccc caaagtgcct gagcggaicc gaaggagaat ccagccaagc 1080
acagtctacg tgtgcaatga aaaccagict gcggttgcta gcaaaggaga agaactcttc 1140
actggagttg tcccaattct tgttgaatta gatggtgatg ttaacggcca caagttctct 1200
gtcagiggag agggatgaagg tgatgaaca tacgaaaac ttaccctgaa gttcatctgc 1260
actactggca aactgcctgt tccatggcca acactagtea ctactctgtg ctatggtgtt 1320
caatgctttt caagatacce ggatcatatg aaacggcatg actttttcaa gagtgccatg 1380
cccgaagggt atgtacagga aaggaccatc ttcttcaaag atgacggcaa ctacaagaca 1440
cgtgctgaag tcaagtttga aggtgatacc ctgtttaata gaatcgagtt aaaaggtatt 1500
gacttcaagg aagatggcaa cattctggga cacaattgg aatacaacta taactcacac 1560
aatgtatata tcatggcaga caaacaaaag aatggaatca aagtgaactt caagaccgcg 1620
cacaacattg aagatggaag cgttcaacta gcagaccatt atcaacaaaa tactccaatt 1680
ggcgatggcc ctgtcctttt accagacaac cattacctgt ccacacaatc tgccctttcg 1740
aaagatccca acgaaaagag agaccacatg gtccttcttg agtttgtaac agctgctggg 1800
attacacatg gcatggatga actgtacaac tga 1833

```

<210> 165

<211> 1752

<212> DNA

<213> Human

<400> 165

```

atgtacaagg actgcatcga gtccactgga gactattttc ttctctgtga cgccgagggg 60
ccatggggca tcattctgga gtccctggcc atacttggca tcgtggtcac aattctgcta 120
ctcttagcat ttctcttctt catgcgaaag atccaagact gcagccagtg gaatgtctc 180
cccacccagc tcctcttctt cctgagtgtc ctggggctct tcggactcgc ttttgcttc 240
atcatcgagc tcaatcaaca aactgcccc gtacgtact ttctctttgg ggttctctt 300

```

417/518

```

gctctctggt tctcatgctt cttagctcat gccccaatc tagtgaagct gggtcggggt 360
tgtgtctcct tctctggac gacaattctg tgcattgcta ttggttgcag tctgttgcaa 420
atcattattg ccactgagta tgtgactctc atcatgacca gaggtatgat gtttgtgaat 480
atgacaccct gccagctcaa tgtggacitt gttgtactcc tggctatgt cctcttctg 540
atggccctca cattcttctg ctccaaagcc accttctgtg gcccggtga gaactggaag 600
cagcatggaa ggctcatctt tatcactgtg ctcttctcca tcatcatctg ggtgggtggt 660
atctccatgc tctgagagg caaccgcag ttccagcgac agccccagtg ggatgacccg 720
gtcgtctgca ttgctctggt caccaacgca tgggttttcc tgcgtctgta catcgtccct 780
gagctctgca ttctctacag atcgtgtaga caggagtgcc ctttacaagg caatgcctgc 840
cccgtcacag cctaccaaca cagcttcaa gtggagaacc aggagctctc cagagcccga 900
gacagtgaig gagctgagga ggaigttagc ttaacttcat atggtactcc cattcagccg 960
cagactgttg atccacaca agagtgttc atccacagg ctaaactaag cccccagcaa 1020
gatgcaggag gagtagctag caaaggagaa gaactcttca ctggagtgt cccaattctt 1080
gttgaattag atggtgaigt taacggccac aagtctctg tcagtgga ggggtgaaggt 1140
gatgcaacat acggaact taccctgaag ttcatctgca ctactggcaa actgcctgtt 1200
ccatggccaa cactagtcac tactctgtgc tatggtgttc aatgctttc aagatacccg 1260
gatcatatga aacggcatga ctttttcaag agtgccatgc ccgaaggta tgtacaggaa 1320
aggaccatct tcttcaaaga tgacggcaac tacaagacac gtgctgaagt caagttgaa 1380
ggatgataccc ttgttaatag aatcgagta aaaggattg acttcaagga agatggcaac 1440
attctgggac acaaattgga atacaactat aactcacaca atgtatacat catggcagac 1500
aaacaaaaga atggaatcaa agtgaacttc aagaccgcc acaacattga agatggaagc 1560
gttcaactag cagaccatta tcaacaaaat actccaattg gcgatggccc tgcctttta 1620
ccagacaacc attacctgtc cacacaatct gccctttcga aagatcccaa cgaaaagaga 1680
gaccacatgg tccttcttga gtttgtaaca gctgctggga ttacacatgg catggatgaa 1740
ctgtacaact ga 1752

```

<210> 166

<211> 3618

<212> DNA

418/518

<213> Human

<400> 166

```

atgcccagcc cgccggggct ccgggcgcta tggctttgcg ccgcgctgtg cgcttcccgg 60
agggccggcg gcgcccccca gcccgggccc gggcccaccg cctgcccggc cccctgccac 120
tgccaggagg acggcatcat gctgtctgcc gactgtcttg agctcgggct gtccgccgtt 180
ccggggggacc tggacccccct gacggcttac ctggacctca gcatgaacaa cctcacagag 240
cttcagcctg gcctcttcca ccacctgcgc ttcttgagg agctgcgtct ctctgggaac 300
catctctcac acatcccagg acaagcattc tctggtctct acagcctgaa aatcctgatg 360
ctgcagaaca atcagctggg aggaatcccc gcagaggcgc tgtgggagct gccgagcctg 420
cagtcgtcgc gcctagatgc caacctcacc tccctggtcc cggagaggag ctttgagggg 480
ctgtcctccc tccgccacct ctggctggac gacaatgcac tcacggagat cctgtcagg 540
gccctcaaca acctccctgc cctgcaggcc atgaccttg ccctcaaccg catcagccac 600
atccccgact acgcgttcca gaatctcacc agccttgttg tgctgcattt gcataacaac 660
cgcattccagc atctggggac ccacagcttc gaggggctgc acaatctgga gacactagac 720
ctgaattata acaagctgca ggagttccct gtggccatcc ggacctggg cagactgcag 780
gaactgggggt tccataacaa caacatcaag gccatcccag aaaaggcctt catggggaac 840
cctctgtctac agacgataca cttttatgat aacccaatcc agtttgtggg aagatcgga 900
ttccagtacc tgcctaaact ccacacacta tctctgaatg gtgccatgga catccaggag 960
tttccagatc tcaaaggcac caccagcctg gagatcctga cctgaccgg cgcaggcatc 1020
cggctgtctc catcggggat gtgccaacag ctgcccaggc tccgagtcct ggaactgtct 1080
cacaatcaaa ttgaggagct gccagcctg cacagggtgc agaaattgga ggaaatcggc 1140
ctccaacaca accgcatctg ggaaattgga gctgacacct tcagccagct gagctccctg 1200
caagccctgg atcttagctg gaacgccatc cggtcacatc accccgaggc cttctccacc 1260
ctgcactccc tggtaagct ggacctgaca gacaaccagc tgaccacact gcccctggct 1320
ggacttgggg gcttgatgca tctgaagctc aaagggaacc ttgctctctc ccaggccttc 1380
tccaaggaca gtttcccaa actgaggatc ctggagggtc cttatgccta ccagtgtgt 1440
ccctatggga tgtgtgccag ctcttcaag gcctctgggc agtgggaggc tgaagacctt 1500
caccttgatg atgaggagtc ttcaaaaagg cccctgggcc tccttgccag acaagcagag 1560

```

419/518

aaccactatg accaggacct ggatgagctc cagctggaga tggaggactc aaagccacac 1620
cccagtgicc agttagagccc tactccaggc cccitcaagc cctgtgagta cctctttgaa 1680
agctggggca tccgcctggc cgtgtgggcc atcgtgttgc tctccgtgct ctgcaatgga 1740
ctgggtgctgc tgaccgtgtt cgctggcggg cctgtccccc tgcggcggt caagtttgtg 1800
gtaggtgcga ttgcaggcgc caacaccttg actggcattt cctgtggcct tctagcctca 1860
gtcgatgccc tgacctttgg tcagttctct gagiaggag cccgctggga gacggggcta 1920
ggctgccggg ccactggctt cctggcagta cttgggtcgg aggcacgggt gctgctgctc 1980
actctggccg cagtgcagtg cagcgtctcc gtctcctgig tccgggccta tgggaagtcc 2040
ccctccctgg gcagcgttcg agcaggggtc ctaggctgcc tggcactggc agggctggcc 2100
gccgcgtgc cctggcctc agtgggagaa tacggggcct cccactctg cctgccctac 2160
gcgccacctg agggtcagcc agcagccctg ggcttcaccg tggccctggt gatgatgaac 2220
tccttctgtt tcttggtcgt ggccggtgcc tacatcaaac tgtactgtga cctgccgcgg 2280
ggcgactttg aggccgtgtg ggactgcgcc atggtgaggc acgtggcctg gctcatcttc 2340
gcagacgggc tcctctactg tcccgtggcc ttccctcagct ttgcctccat gctgggcctc 2400
ttccctgtca cggccgaggc cgtcaagtct gtccctgtgg tgggtgtgcc cctgcctgcc 2460
tgctcaacc cactgtgtga cctgccttc aacccccact tccgggatga ccttcggcgg 2520
cttcggcccc gcgcagggga ctcagggccc ctagcctatg ctgcggccgg ggagctggag 2580
aagagctcct gtgattctac ccaggccctg gtagccttct ctgatgtgga tctattctg 2640
gaagcttctg aagctgggcg gccccctggg ctggagacct atggcttccc ctcagtacc 2700
ctcatctcct gtcagcagcc aggggcccc aggtcggagg gcagccattg tglagagcca 2760
gaggggaacc actttgggaa cccccaacct tccatggatg gagaactgct gctgagggca 2820
gagggatcta cgccagcagg tggaggcttg tcaggggtg gcggctttca gcccctggc 2880
ttggcctttg ctacacagt ggctagcaaa ggagaagaac tcttactgg agttgtcca 2940
attcttgttg aattagatgg tgatgtaac ggccacaagt tctctgtcag tggagagggt 3000
gaaggtgatg caacatacgg aaaacttacc ctgaagtta tctgcactac tggcaaactg 3060
cctgttccat ggccaacact agtcactact ctgtgctatg gtgttcaatg cttttcaaga 3120
taccggatc atatgaaacg gcatgacitt ttcaagagt ccatgccga aggttatgta 3180
caggaaagga ccatcttctt caaagatgac ggcaactaca agacacgtgc tgaagtcaag 3240
tttgaagggtg ataccttgt taatagaatc gagttaaag gtattgactt caaggaagat 3300

420/518

ggcaacattc tgggacacaa attggaatac aactataact cacacaatgt atacatcatg 3360
 gcagacaaac aaaagaatgg aatcaaagtg aacttcaaga cccgccacaa cattgaagat 3420
 ggaagcgttc aactagcaga ccattatcaa caaaatactc caattggcga tggccctgtc 3480
 cttttaccag acaaccatta cctgtccaca caatctgccc ttctgaaaga tcccaacgaa 3540
 aagagagacc acatggctct tcttgagttt gtaacagctg ctgggattac acatggcatg 3600
 gatgaactgt acaactga 3618

<210> 167

<211> 1722

<212> DNA

<213> Human

<400> 167

atggaatcat ctttctcatt tggagtgate cttgtgtgcc tggcctccct catcattgct 60
 actaacacac tagtggctgt ggctgtgctg ctgttgatcc acaagaatga tgggtgtcagt 120
 ctctgcttca ccttgaatct ggctgtggct gacacctga ttggtgtggc catctctggc 180
 ctactcacag accagctctc cagcccttct cgGCCcAcac agaagacct gtgcagcctg 240
 cggatggcat ttgtcacttc ctccgcagct gcctctgtcc tcacggtcac gctgatcacc 300
 ttgacaggt accttgccat caagcagccc ttccgtact tgaagatcat gagtgggttc 360
 gtggccgggg cctgcatigc cgggctgtgg ttagtgtctt acctcattgg cttcctccca 420
 ctcggaatcc ccatgttcca gcagactgcc tacaagggc agtgcagctt ctttctgtga 480
 tttcaccctc acttctgtgt gacctctcc tgcgttggct tcttcccagc catgctcttc 540
 ttgtcttct tctactgca catgtcaag attgcctcca tgcacagcca gcagattcga 600
 aagatggaac atgcaggagc catggctgga ggttatcat cccacggac tcccagcgac 660
 ttcaaagctc tccgtactgt gtctgttctc attgggagct ttgctctatc ctggaccccc 720
 ttccittatca ctggcattgt gcaggtgcc tgcaggagt gtcacctta cctagtgtgt 780
 gaacggatcc tgtggctgtc cggcgtgggc aactccctgc tcaaccact catctatgcc 840
 tattggcaga aggagggtgc actgcagctc taccacatgg ccctaggagt gaagaagggt 900
 ctcacctcat tctctctctt tctctcgcc aggaattgtg gccagagag gccagggaa 960

421/518

agttcctgtc acatcgtcac tatctccagc tcagagtttg atggcgctag caaaggagaa 1020
 gaactcttca ctggagtgtt cccaattctt gtigaattag atggatgatg taacggccac 1080
 aagttctctg tcagtgagga gggatgaagg gatgcaacat acggaaaact taccctgaag 1140
 ttcatctgca ctactggcaa actgcctgtt ccatggccaa cactagtcac tactctgtgc 1200
 tatgggtgtc aatgcctttc aagataccgc gatcataaga aacggcatga ctttttcaag 1260
 agtcccatgc ccgaagggtt tgtacaggaa aggaccatct tcttcaaaga tgacggcaac 1320
 tacaagacac gtgctgaagt caagtttgaa ggtgataccc ttgttaatat aatcgagtta 1380
 aaaggtattg acttcaagga agatggcaac attctgggac acaaattgga atacaactat 1440
 aactcacaca atgtatacat catggcagac aaacaaaaga atggaatcaa agtgaacttc 1500
 aagacccgcc acaacatiga agatggaagc gttcaactag cagaccatta tcaacaaaat 1560
 actccaattg gcgatggccc tgtcctttta ccagacaacc attacctgtc cacacaatct 1620
 gccctttcga aagatcccaa cgaaaagaga gaccacatgg tccttcttga gtttgtaaca 1680
 gctgctggga ttacacatgg catggatgaa ctgtacaact ga 1722

<210> 168

<211> 1839

<212> DNA

<213> Human

<400> 168

atgtgacag ggagctgcgg ggaccctcag aaaaagccac aggtgaccca ggactcaggg 60
 ccccagagca tggggcttga gggacgagag acagctggcc agccacgagt gaccctgtctg 120
 cccacgcca acgtcagcgg gctgagccag gagtttgaag gccactggcc agagatcgca 180
 gagaggctcc cgtgtgtggc tggcgtcatc cctgtcatct actacagtgt cctgtctggc 240
 ttggggctgc ctgtcagcct cctgaccgca gtggcccttg cgcgccttgc caccaggacc 300
 aggaggccct cctactacta ccttctggcg ctacacgcct cggataicat catccagggtg 360
 gtcatcgtgt tcgcgggctt cctcctgcag ggagcagtcg tggcccgcga ggtgccccag 420
 gctgtggctg gcacggccaa catcctggag ttgtctgcca accacgcctc agtcctggatc 480
 gccatcctgc tcacggttga ccgtacact gccctgtgce accccctgca ccatcggggc 540

422/518

```

gcctcgtccc caggccggac cgcggggcc attgctgctg tcctgagtgc tgccctgttg 600
accggcatcc ctttctactg gtggctggac atgtggagag acaccgactc acccagaaca 660
ctggacgagg tcctcaagtg ggctcactgt ctactgtct atttcatccc ttgtggcgtg 720
ttcctggica ccaactcggc catcatccac cggctacgga ggaggggccc gagtgggctg 780
cagccccggg tgggcaagag cacagccatc ctcttggga tcaccacact gtccaccctc 840
ctgtgggcgc cccgggtctt cgtcatgctc taccacatgt acgtggcccc tgtccaccgg 900
gactggaggg tcacctggc cttggatgtg gccaatatgg tggccatgct ccacacggca 960
gccaaattcg gcctctactg ctttgtcagc aagactttcc gggccactgt ccgacaggtc 1020
atccacgatg cctacctgcc ctgcactttg gcacacagc cagagggcac ggcggcgaag 1080
cctgtgatgg agcctccggg actccccaca ggggcagaag tggctagcaa aggagaagaa 1140
ctcttcactg gagttgtccc aattcttgtt gaattagatg gtgatgttaa cggccacaag 1200
ttctctgtca gtggagaggg tgaaggatg gcaacatacg gaaaacttac cctgaagttc 1260
atctgcacta ctggcaaact gcctgttcca tggccaacac tagtactac tctgtgctat 1320
gggtgttcaat gcttttcaag atacccggat catatgaaac ggcatgactt tttcaagagt 1380
gccatgcccg aaggttatgt acaggaaagg accatcttct tcaaagatga cggcaactac 1440
aagacacgtg ctgaagtcaa gtttgaaggt gatacccttg ttaatagaat cgagttaaaa 1500
ggatattgact tcaaggaaga tggcaacatt ctgggacaca aattggaata caactataac 1560
tcacacaatg tatacatcat ggcagacaaa caaaagaatg gaatcaaagt gaacttcaag 1620
accgcccaca acattgaaga tggaagcgtt caactagcag accattatca acaaaatact 1680
ccaattggcg atggccctgt ccttttacca gacaaccatt acctgtccac acaatcigcc 1740
ctttcgaaag atcccaacga aaagagagac cacatgggcc ttcttgagtt tgtaacagct 1800
gctgggatta cacatggcat ggaatgaactg tacaactga 1839

```

<210> 169

<211> 1836

<212> DNA

<213> Human

<400> 169

423/518

atggacaccc tggaggaggt gacttgggcc aatgggagca cagcgctacc cccacccctg	60
gcaccaaaca tcagtgtgcc tcatcgctgc ctgctgctgc tctacgaaga cattggcacc	120
tccagggctc ggtactggga cctcttgctg ctcatcccca atgtgctctt cctcatcttc	180
ctgctctgga agcttccatc tgcctgggcg aagatccgca tcacctccag ccccatTTTT	240
atcaccttct acatcctggt gtttgtggtg gcgctgggtg gcattgcccg ggccgtggta	300
tccatgacgg tgagcacctc gaacgctgca actgttgctg ataagatcct gtgggagatc	360
accgccttct tctgctggc catcgagctg agtgtgatca tcctgggcct ggcctttggc	420
cacctggaga gtaagtcag catcaagcgg gtgctggcca tcaccacagt gctgtccctg	480
gcctactctg tcaccaggg gacctggag atcctgtacc ctgatgcca tctctcagct	540
gaggacttta atatctatgg ccatgggggc cgccagttct ggctggctcag ctctgtcttc	600
ttcttcttgg tctactctct ggtggctatc ctcccaaga ccccgctgaa ggagcgcac	660
tccctgcctt ctcgaggag ctctacgtg taigcgggca tcctggcact gctcaacct	720
ctgcaggggc tggggagltg gctgctgtgc ttcgacatca tcgaggggt ctgctgtgta	780
gatgccaaa ccttctgtga cttcagcttc ttgcctccgc tcactctagt ggctttcttc	840
cggggcttct tcggctcgga gccaagatc ctcttctcct acaaatgcca agtggacgag	900
acagaggagc cagatgtaca cctaccccag ccctacgctg tggcccggcg ggagggcctg	960
gaggctgcag gggctgctgg ggcctcagct gccagctact cgagcacgca gttcgactct	1020
gccggcgggg tggcctacct ggatgacatc gcttccatgc cctgccacac tggcagcatc	1080
aacagcacag acagcgagcg ctggaaggcc atcaatgccg ctagcaaagg agaagaactc	1140
ttcactggag ttgtcccaat tcttgttgaa ttagatgggt atgttaacgg ccacaagttc	1200
tctgtcagtg gagagggtga aggtgatgca acatacggaa aacttacct gaagttcatc	1260
tgcactactg gcaaactgcc tgttccatgg ccaacactag tcactactct gtgctatggt	1320
gttcaatgct tttaagata cccggatcat atgaaacggc atgacttttt caagagtgcc	1380
atgccgaag gttatgtaca ggaaaggacc atctttctca aagatgacgg caactacaag	1440
acacgtgctg aagtcaagtt tgaaggatg acccttggtta atagaatcga gttaaaaggt	1500
attgacttca aggaagatgg caacattctg ggacacaaat tggaatacaa ctataactca	1560
cacaatgtat acatcatggc agacaaacaa aagaatggaa tcaaagttaa cttcaagacc	1620
cgccacaaca ttgaagatgg aagcgttcaa ctacgagacc attatcaaca aaatactcca	1680
attggcgaig gccctgtcct ttaccagac aaccattacc tgtccacaca atctgccctt	1740

424/518

tcgaaagatc ccaacgaaaa gagagaccac atggctcttc ttgagtttgt aacagctgct 1800
 gggattacac atggcatgga tgaactgtac aactga 1836

<210> 170

<211> 2016

<212> DNA

<213> Human

<400> 170

atgtgttttt ctcccattct ggaaatcaac atgcagctcg aatctaacaat tacagtgcga 60
 gatgacattg atgacatcaa caccaatatg taccaaccac tatcatatcc gtttaagcttt 120
 caagtgcttc tcaccggatt tcttatgtta gaaatttgtt tgggacttgg cagcaacctc 180
 actgtattgg tactttactg catgaaatcc aacttaatca actctgtcag taacattatt 240
 acaatgaatc ttcatgtact tgatgtaata atttgtgtgg gatgtattcc tctaactata 300
 gttatccttc tgccttcact ggagagtaac actgctctca ttgctgttt ccatgaggct 360
 tgtgtatctt ttgcaagtgt ctcaacagca atcaacgttt ttgctatcac ttiggacaga 420
 tatgacatct ctgtaaaacc tgcaaacga attctgacaa tgggcagagc tgtaatgtta 480
 atgatatcca ttggattttt ttcttttttc tctttctga ttctttttat tgaggtaaat 540
 tttttcagtc ttcaaagtg aaataacctg gaaaacaaga cacttttatg tgtcagta 600
 aatgaatact acactgaact gggaatgtat taccacctgt tagtacagat cccaatatc 660
 tttttcactg ttgtagtaat gttaatcaca tacaccaaaa tacttcaggc tcttaatat 720
 cgaataggca caagattttc aacagggcag aagaagaaaag caagaaagaa aaagacaatt 780
 tctctaacca cacaacatga ggctacagac atgtcacaaa gcagtggigg gagaaatgta 840
 gtctttgggtg taagaacttc agtttctgta ataattgccc tccggcgagc tgtgaaacga 900
 caccgtgaac gacgagaaag acaaaagaga gtcttcagga tgtctttatt gattatttct 960
 acatttcttc tctgtcggac accaatttct gttttaaata ccaccatttt atgttttaggc 1020
 ccaagtgacc ttttagtaaa attaagattg tgttttttag tcatggctta tggacaact 1080
 atatttcacc ctctattata tgcattcact agacaaaaat ttcaaaaggt cttgaaaagt 1140
 aaaatgaaaa agcgagtgtt ttctatagta gaagctgac ccctgcctaa taatgctgta 1200

425/518

atacacaact cttggataga tcctaaaaga aacaaaaaaa ttacctttga agatagttaa 1260
 ataagagaaa aatgttttagt gcctcaggtt gtcacagacg ctagcaaagg agaagaactc 1320
 ttcactggag ttgtcccaat tcttgttgaa ttagatgggt atgttaacgg ccacaagttc 1380
 tctgtcagtg gagaggggtga aggtgatgca acatacggaa aacttaccct gaagttcatc 1440
 tgcactactg gcaaactgcc tgttccatgg ccaacactag tctactactct gtgctatggt 1500
 gttcaatgct tttaagata cccggatcat atgaaacggc atgacttttt caagagtgcc 1560
 atgccgaag gttatgtaca ggaaaggacc atcttcttca aagatgacgg caactacaag 1620
 acacgtgctg aagtcaagtt tgaaggatg atcccttgta atagaatcga gttaaaaggt 1680
 attgacttca aggaagatgg caacattctg ggacacaaat tggaatacaa ctataactca 1740
 cacaatgtat acatcatggc agacaacaaa aagaatggaa tcaaagttaa cttcaagacc 1800
 cgccacaaca ttgaagatgg aagcgttcaa ctagcagacc attatcaaca aaatactcca 1860
 attggcgatg gccctgtcct ttaccagac aaccattacc tgtccacaca atctgccctt 1920
 tcgaaagatc ccaacgaaaa gagagaccac atggtccttc ttgagtttgt aacagctgct 1980
 gggattacac atggcatgga tgaactgtac aactga 2016

<210> 171

<211> 1800

<212> DNA

<213> Human

<400> 171

atgaatgaat ccaggatggac tgaatggagg atcctgaaca tgagcagtgg cattgtgaat 60
 gtgtccgagc gtcactcctg cccacttgga ttggccact acagtgtggt ggatgtctgc 120
 atcttcgaga cagtggttat tgtgttgctg acatttctga tcatgtctgg gaatctaaca 180
 gttatctttg tctttcattg tgtccactg ttacatcatt atactaccag ctatttcatt 240
 cagacgatgg catatgtcga tcttttcgtt ggagttagct gcttggttcc tactctgtca 300
 cttctccact actccacagg tgtccacgag tcatgtactt gccaggtttt tggatataac 360
 atctcagttc taaaaagtgt ttctatggca tgtcttgctt gcacagtggt ggaatgttat 420
 cttgcaataa ccaagcctct ttctacaat caactgggtca ccccttgctg cttgagaatt 480

426/518

tgcaattattt tgatctggat ctactcctgc ctaattttct tgccttcctt ttttggctgg 540
gggaaacctg gttaccatgg tgacattttt gaatgggtgtg ccacgtcttg gctcaccagt 600
gcctatttta ctggctttat tgtttgttta ctttatgctc ctgctgcctt tgttgtctgc 660
ttcacttact tccacatttt caaaatttgc cgtcagcaca ccaaagagat aaatgaccga 720
agagcccgat tccctagtca tgaggttagat tcttccagag agactggaca cagccctgac 780
cgctcgctacg ccatggtttt gtttaggata accagtgat tttataigct gtggctcccc 840
tatataattt actttcttct agaaagctcc cgggtcttgg acaatccaac tctgtccttc 900
ttaacaacct ggcttgcaat aagtaatagt ttttgtaact gtgtaataa cagcctctcc 960
aacagcgitt tccggctagg cctccgaaga ctgctgaga caatgtgcac atcctglatg 1020
tgtgtgaagg atcaggaagc acaagaacct aaacctagga aacgggctaa ttcttgctcc 1080
attgctagca aaggagaaga actcttact ggagtgtcc caattcttgt tgaattagat 1140
ggtgatgta acggccacaa gttctctgtc agtggagagg gtgaaggiga tgcaacatac 1200
ggaaaactta cctgaagtt catctgcact actggcaaac tgcctgttcc atggccaaca 1260
ctagtacta ctctgtgcta tgggtttcaa tgcctttcaa gataccgga tcatatgaa 1320
cggcatgact ttttcaagag tgccatgccc gaaggttatg tacaggaaag gaccatcttc 1380
ttcaaagatg acggcaacta caagacacgt gctgaagtca agtttgaagg tgataccctt 1440
gttaatatga tgcagttaa aggtattgac ttcaaggaag atggcaacat tctgggacac 1500
aaattggaat acaactataa ctacacaaat gtatacatca tggcagacaa acaaaagaat 1560
ggaatcaaag tgaacttcaa gaccgccac aacattgaag atggaagcgt tcaactagca 1620
gaccattatc aacaaaatac tccaattggc gatggccctg tccttttacc agacaacat 1680
tacctgtcca cacaatctgc ctttctgaaa gatccaacg aaaagagaga ccacatggtc 1740
cttcttgagt ttgtaacagc tgcctggatt acacatggca tggatgaact gtacaactga 1800

<210> 172

<211> 1728

<212> DNA

<213> Human

<400> 172

427/518

atgaactcgt gggacgcggg cctggcgggg ctactggagg gcacgatggg cgtctcgcgt	60
ctgtccaacg cgctgggtgt gctctgccgt ctgcacagcg cggacatccg ccgccaggcg	120
ccggcgctct tcacctgaa cctcacgtgc gggaacttgc tggcaccgt ggtcaaatg	180
ccgctcacgc tggccggcgt cgtggcgcag cggcagccgg cgggcgaccg cctgtgccgc	240
ciggctgcct tcttcgacac ctctctggct gccaaactcca tgcctagcat ggccgcgtc	300
agcatcgacc gctgggtggc cgtggcttc ccgctagct accgggcca gatgcgcctc	360
cgcgacgcgg cgctcatgtt ggcttacag tggctgcacg cgctacatt ccagccgcc	420
gcgctcgccc tctctggct cggcttcac cagctgtacg cctcgtgcac gctgtgcagc	480
cggcggccgg acgagcgctt gcgcttcgcc gcttctact gcgcttcca cgctctcagc	540
ttccigtctt ccttcgtgt gctctgtgc acgtacctca aggtgtcaa ggtggccgc	600
ttccattgca agcgcatga cgtatcacc atgcagacgc tcgtgtgtgt ggtggacctg	660
cacccagtg tgcgggaacg ctgtcggag gagcagaagc ggaggcgaca gcgagccacc	720
aagaagatca gcacctcat agggaccttc cttgtgtgt tcgcgcccta tgtatcacc	780
aggctagtgg agctctctc cacggtgccc atcgctccc actgggggt gctgtccaag	840
tgcttggcgt acagcaaggc cgcacccgac cccttgtgt actcctact gcgacaccag	900
taccgcaaaa gctgcaagga gattctgaac aggtctctgc acagacgtc catccactcc	960
tctggctca caggcgactc tcacagccag aacattctgc cgggtgtga ggctagcaaa	1020
ggagaagaac tcttactgg agttgtcca attctgttg aattagatgg tgatgtaac	1080
ggccacaagt tctctgtcag tggagagggt gaaggatg caacatacgg aaaacttacc	1140
ctgaagtcca tctgcactac tggcaaactg cctgttccat ggccaacact agtactact	1200
ctgtgctatg gtgttcaatg cttttcaaga taccggatc atatgaaacg gcatgacttt	1260
ttcaagagt ccatgccga aggttatgta caggaaagga ccatcttcti caaagatgac	1320
ggcaactaca agacacgtgc tgaagtcaag ttggaaggat atacccttgt taatagaatc	1380
gagttaaaag gtattgactt caaggaagat ggcaacattc tgggacacaa attggaatac	1440
aactataact cacacaatgt atacatcatg gcagacaaac aaaagaatgg aatcaaagt	1500
aacttcaaga cccgccacaa catgaagat ggaagcgttc aactagcaga ccattatcaa	1560
caaaatactc caattggcga tggccctgtc cttttaccag acaaccatta cctgtccaca	1620
caatctgccc tttcgaaaga tcccaacgaa aagagagacc acatggctct tcttgagttt	1680
gtaacagctg ctgggattac acatggcatg gatgaactgt acaactga	1728

428/518

<210> 173

<211> 2184

<212> DNA

<213> Human

<400> 173

```

atgaaccctc cttcggggcc aagagtcctg cccagcccaa cccaagagcc cagctgcatg   60
gccaccccag caccaccag ctggctggac agctcccaga gcagcatctc cagcctgggc   120
cggttccat ccatcagtc cacagcacct gggacttggg ctgctgctg ggtccccctc   180
cccacgggtg atgttccgga ccatgcccac tataccttgg gcacagtgat cttgctggtg   240
ggactcacgg ggatgctggg caacctgacg gtcattata ccttctgag agctgtgctt   300
cgtggagica ctgtgatgat gcagagcaga agcctccgga cactgcca catgttcatt   360
atcaacctcg cgtcagcga cttctcatg tccttcccc aggccctgt cttcttacc   420
agtagcctct ataagcagt gctctttggg gagacaggct gcgagttcta tgcttctgt   480
ggagctctct ttggcatttc ctccatgat accctgacgg ccatcgccct ggaccgctac   540
ctggtaatca cagccccgt ggccaccttt ggtgtggcgt ccaagaggcg tgcggcattt   600
gtcctgtctg gcgtttggct ctatgccctg gcctggagtc tgccaccctt cttcggtcgg   660
agcgcttacg tgcccagagg gttgtgaca tctgtctct gggactacat gagcttcacg   720
ccggccgtgc gtgcctacac catgcttctc tgcgtcttc tgttcttct cctctgctt   780
atcatcatct actgtacat cttcatctc agggccatcc gggagacagg acgggctctc   840
cagaccttcg gggcctgcaa gggcaatggc gagtccctgt ggcagcggca gcggctgcag   900
agcgagtgca agatggccaa gatcatgctg ctggctatcc tcctcttctg gctctcctgg   960
gtccctatt ccgtgtggc cctggtgcc tttgtgggt acgcacacgt cctgacacce   1020
tacatgagct cgttgccagc cgtcatgcc aaggcctctg caatccaca ccccatcatt   1080
tacgcatca cccaccccaa gtacagggtg gccattgcc agcacctgcc ctgctgggg   1140
gtgctgctgg gtgtatcac ccggcacagt cggccctacc ccagctaccg ctccaccac   1200
cgctccacgc tgatcagcca cactccaac ctgagctgga tctccatac gagcgccag   1260
gagtccctgg gctcggagag tgaggctggc tggacacaca tggaggcagc agctgtgtgg   1320

```

429/518

ggagctgccc agcaagcaaa tgggcggtcc ctctacggtc agggctctgga ggacttgga 1380
 gccaaaggcac cccccagacc ccaggacac gaagcagaga ctccaggga gaccaagggg 1440
 ctgatcccca gccaggaccc caggatggct agcaaaggag aagaactctt cactggagti 1500
 gtcccaattc ttgttgaatt agatgggat gttacggcc acaagtctc tgtcagtga 1560
 gaggtgaag gtagtcaac atacggaaa cttacctga agttcatctg cactactggc 1620
 aaactgcctg ttccatggcc aacactagtc actactctgt gctatgggtg tcaatgcttt 1680
 tcaagatacc cggatcatat gaaacggcat gactttttca agagtggcat gccgaagg 1740
 tatgtacagg aaaggacat cttcttcaa gatgacggca actacaagac acgtgctgaa 1800
 gtcaagtttg aaggatgac cttgttaat agaatcgagt taaaaggat tgacttcaag 1860
 gaagatggca acattctggg acacaaattg gaatacaact ataactaca caatgtatac 1920
 atcatggcag acaaacaaaa gaatggaatc aaagtgaact tcaagaccg ccacaacatt 1980
 gaagatggaa gcgttcaact agcagacat tatcaacaaa atactccaat tggcgtggc 2040
 cctgtccttt taccagaaa ccattacctg tccacacaat ctgcccttc gaaagatccc 2100
 aacgaaaaga gagaccat ggctctctt gagtttgtaa cagctgctgg gattacacat 2160
 ggcatggatg aactgtacaa ctga 2184

<210> 174

<211> 1851

<212> DNA

<213> Human

<400> 174

atggctctggg ggaaaatttg ctggttcagc cagagggtg gatggacagt gtttgctgag 60
 tcacagatat ctctctcatg tagcctttgt ctccacagtg gtgaccagga ggcacagaac 120
 ccaaacctgg tatctcagct ctgtggcgtc ttcttcaaa atgagacgaa tgaaccata 180
 catatgcaga tgagcatggc agtgggacag caggccctgc cctigaatat cattgcccc 240
 aaggctgtgc tggctccct ctgtgggtc ttattgaatg gcactgtctt ctggctgctt 300
 tgcgtgggg ccacgaatcc ctacatggtg tacatctcc acctggtcgc tgctgacgtg 360
 atctatcttt gctgctcggc agtgggttc ttacagggtg ctctgctaac ttatcatgga 420

430/518

```

gtcgtgtttt ttatccctga tttcctggcc atattgtctc ccttctcctt tgagggtgtgt 480
ctctgtctcc tggiggccat cagcacagag cgggtgtgtgt gtgtcctctt ccccatctgg 540
tacagatgcc accgccc aaa atacacatct aatgttgtct gcaccctcat ctggggcctg 600
cctttttgca tcaacatagt aaaatcacct ttcctaactt actggaaaca tgtaaaggca 660
tggtcatal ttctaaagct ttctgggctc ttccatgcta tccittcact tggatgtgt 720
gtgtcgagtc tgactctact cattagattc ctgtgtgtgt cccagcagca aaaggccacc 780
agggtctatg cggigggtgca gatctcgcc cccatgttcc tactctgggc cctaccctg 840
agcgtggcac cctcataac agatttcaa atgtttgtca ccacctcta ttttaatttc 900
ttgttctca ttataaacag cagcgccaac cctatcattt atttctttgt ggggagcctc 960
agaaagaaaa ggtgaagga atctctcaga gtgattctcc aacgggcgtt agcagataag 1020
ccagagggtg ggaggaacaa aaaggcagct ggcatcgacc caatggagca accacactct 1080
actcagcatg tggagaacct tcttcccagg gagcacaggg tcgatgtgga aacagctagc 1140
aaaggagaag aactcttcac tggagttgtc ccaattcttg ttgaattaga tggatgtgt 1200
aacggccaca agttctctgt cagtggagag ggtgaagggt atgcaacata cggaaaactt 1260
acctgaagt tcacttcac tactggcaaa ctgcctgttc catggccaac actagtcact 1320
actctgtgt atggtgttca atgcttttca agatacccg atcatatgaa acggcatgac 1380
tttttcaaga gtgcatgcc cgaaggttat gtacaggaaa ggaccatctt ctcaaagat 1440
gacggcaact acaagacacg tgetgaagtc aagtttgaag gtgataacct tgttaataga 1500
atcgagttaa aaggtattga ctcaaggaa gatggcaaca ttctgggaca caaattggaa 1560
tacaactata actcacaaa tgtatacatc atggcagaca aacaaaagaa tggaatcaaa 1620
gtgaacttca agaccgcca caacattgaa gatggaagcg ttcaactagc agaccattat 1680
caacaaaata ctccaattgg cgatggccct gtctttttac cagacaacca ttacctgtcc 1740
acacaatctg ccttttcgaa agatcccaac gaaaagagag accacatggt ccttcttgag 1800
tttgaacag ctgctgggat tacacatggc atggatgaac tgtacaactg a 1851

```

<210> 175

<211> 1827

<212> DNA

<213> Human

431/518

<400> 175

```

atggcgaact atagccatgc agctgacaac attttgcaaa atctctcgcc tetaacagcc   60
tttctgaaac tgacttcctt gggtttcata ataggagica gcgtgggtggg caacctcctg  120
atctccatit tgctagttaa agataagacc ttgcatagag caccttacta cttcctgttg  180
gatctttgct gttcagatat cctcagatct gcaatttggt tccatttgtt gttcaactct  240
gtcaaaaatg gctctacctg gacttatggg actctgactt gcaaagtgat tgcctttctg  300
ggggttttgt cctgtttcca cactgccttc atgctcttct gcatcagtgt caccagatac  360
ttagctatcg cccatcacccg cttctataca aagaggctga ctttttgac gtgtctggct  420
gtgatctgta tgggtgtggc tctgtctgtg gccatggcat ttccccggg tttagacgtg  480
ggcacttact cattcattag ggaggaagat caatgcacct tccaacaccg ctctttcagg  540
gctaattgatt ccttaggatt tatgtgtctt ctgtctctca tcttcttagc cacacagctt  600
gtctacctca agctgatatt tttcgtccac gatcgaagaa aatgaagcc agtcagitt  660
gtagcagcag tcagccagaa ctggactttt catggctctg gagccagtgg ccaggcagct  720
gccaattggc tagcaggatt tggaaggggt cccacaccac ccaccttgc tggcatcagg  780
caaatgcaa acaccacagg cagaagaagg ctatttggtc tagacgagtt caaatggag  840
aaaagaatca gcagaatgtt ctatataatg acttttctgt ttctaacctt gtggggcccc  900
tacctgggtg cctgttattg gagagttttt gcaagagggc ctgtagtacc agggggattt  960
ctaacagctg ctgtctggat gagttttgcc caagcaggaa tcaatccttt tgtctgcatt 1020
ttctcaaaaca gggagctgag gcgctgtttc agcacaacce ttctttactg cagaaaatcc 1080
aggttaccaa gggaacctta ctgtgttata tctagaaaag gagaagaact cttcactgga 1140
gttgtcccaa ttcttgttga attagatggt gatgttaacg gccacaagtt ctctgtcagt 1200
ggagaggggt aaggtgatgc aacatacgga aaacttaccc tgaagttcat ctgcactact 1260
ggcaaactgc ctgttccatg gccaacacta gtcactactc tgtgctatgg tgttcaatgc 1320
ttttcaagat acccgatca tatgaaacgg catgactttt tcaagagtc catgcccgaa 1380
ggttatgtac aggaaaggac catcttcttc aaagatgacg gcaactacaa gacacgtgct 1440
gaagtcaagt ttgaaggta tacccttgtt aatagaatcg agttaaaagg tattgacttc 1500
aaggaagatg gcaacattct gggacacaaa ttggaataca actataactc acacaatgta 1560
tacatcatgg cagacaaaca aaagaatgga atcaaagtga acttcaagac ccgccacaac 1620

```

432/518

attgaagatg gaagcgttca actagcagac cattatcaac aaaatactcc aattggcgat 1680
 ggccctgtcc ttttaccaga caaccattac ctgtccacac aatctgccct ttcgaaagat 1740
 cccaacgaaa agagagacca catggtcctt cttgagttag taacagctgc tgggattaca 1800
 catggcatgg atgaactgta caactga 1827

<210> 176

<211> 1719

<212> DNA

<213> Human

<400> 176

atgaatgaag accigaaggt caatttaagc gggctgcctc gggattatit agatgccgct 60
 gctgcggaga acatctcggc tgctgtctcc tcccgggttc ctgccgtaga gccagagcct 120
 gagctcgtag tcaacccttg ggacattgtc ttgtgtacct cgggaaccct catctcctgt 180
 gaaaatgcca ttgtggctct tatcatcttc cacaacccca gccctgcgagc acccatgttc 240
 ctgctaatag gcagcctggc tcttcagac ctgtctggccg gcattggact catcaccaat 300
 ttgttttttg cctacctgtc tcagtcagaa gccaccaagc tggtcacgat cggcctcatt 360
 gtgcctcttt tctctgcctc tgtctgcagc ttgtctggcta tcaactgtga ccgctacctc 420
 tcaactgtact acgctctgac gtaccattcg gagaggacgg tcacgtttac ctatgtcatg 480
 ctctgtcatgc tctgggggac ctccatctgc ctggggctgc tgcccgtcat gggctggaac 540
 tgccctccgag acgagtcac ctgcagcgtg gtcagaccgc tcaccaagaa caacgcggcc 600
 atcctctcgg tgtccttctt ctcatgttt gcgctcatgc ttcagctcta catccagatc 660
 tgtaagattg tgaigaggca cgcccatcag atagccctgc agcaccactt cctggccacg 720
 tcgcaactatg tgaccacccg gaaaggggtc tccaccctgg ctatcatcct ggggacgttt 780
 gctgcttgct ggalgccttt caccctctat tcttgatag cggattacac ctacccctcc 840
 atctatacct acgccaccct cctgcccgcc acctacaatt ccatcatcaa ccctgtcata 900
 tatgttttca gaaaccaaga gatccagaaa gcgctctgtc tcatttgctg cggctgcata 960
 ccgtccagtc tcgcccagag agcgcgctcg cccagtgatg tggctagcaa aggagaagaa 1020
 ctcttacttg gagttgtccc aattcttggt gaattagatg gtgatgttaa cggccacaag 1080

433/518

ttctctgtca gaggagaggg tgaaggatg gcaacatacg gaaaacttac cctgaagttc 1140
 atctgcacta ctggcaaact gccgtttcca tggccaacac tagtactac tctgtgctat 1200
 ggtgttcaat gcitttcaag ataccggat catatgaaac ggcatgactt ttccaagagt 1260
 gccatgcccg aaggttatgt acaggaaagg accatcttct tcaaagatga cggcaactac 1320
 aagacacgtg ctgaagticaa gtttgaaggt gatacccttg ttaatagaat cgagttaaaa 1380
 ggtattgact tcaaggaaga tggcaacatt ctgggacaca aattggaata caactataac 1440
 tcacacaatg tatacatcat ggcagacaaa caaagaatg gaatcaaagt gaacttcaag 1500
 acccgccaca acattgaaga tgggaagcgtt caactagcag accattatca acaaaatact 1560
 ccaattggcg atggccctgt cctttacca gacaaccatt accgtccac acaatctgcc 1620
 ctttcgaaag atcccaacga aaagagagac cacatggctc ttcttgagtt tgtaacagct 1680
 gctgggatta cacatggcat ggatgaactg tacaactga 1719

<210> 177

<211> 1842

<212> DNA

<213> Human

<400> 177

atggatgtga ctcccaagc ccggggcgtg ggcctggaga tgiacctagg caccgcgcag 60
 cctgcggccc ccaacaccac ctccccgag ctcaacctgt cccaccgct cctgggcacc 120
 gccctggcca atgggacagg tgagctctcg gagcaccagc agtacgtgat cggcctgttc 180
 ctctcgtgcc tctacacat ctctctctc cccatcggct ttgtgggcaa catcctgac 240
 ctggtggtga acatcagctt ccgcgagaag atgaccatcc ccgacctga cttcatcaac 300
 ctggcggttg cggacctcat cctggtggcc gactccctca ttgaggigt caacctgcac 360
 gagcggtact acgacatcgc cgtcctgtgc accttcatgt cgctcttct gcaggtaac 420
 atgtacagca gcgtcttctt cctcacctgg atgagcttcg accgctacat cggcctggcc 480
 agggccatgc gctgcagcct gtccgcacc aagcaccacg cccggctgag ctgtggcctc 540
 atctggatgg catccgtgtc agccacgtg gtgcccttca ccgccgtgca cctgcagcac 600
 accgacgagg cctgcttctg ttcccggtat gtccgggagg tgcagtggct cgaggtcacg 660

434/518

```

ctgggcttca tcgtgccctt cgccatcatc ggccctgtgt actccctcat tgtccgggtg 720
ctggtcaggg cgcaccggca ccgtgggctg cggccccggc ggcagaaggc gctccgcatg 780
atcctcgcgg tgggtctggt cttcttcgtc tgcctggctgc cggagaacgt cttcatcagc 840
gtgcacctcc tgcagcggac gcagcciggg gccgctccct gcaagcagtc tttccgcat 900
gcccccccc tcacgggcca cattgtcaac ctgcgccct tctccaacag ctgcctaaac 960
ccccctcatc acagctttct cggggagacc ttcagggaca agctgaggct gtacattgag 1020
cagaaaacaa atttgccggc cctgaaccgc ttctgtcagc ctgccctga ggcctcatt 1080
ccagacagca ctgagcagtc ggatgtgagg ttcagcagtg ccgtggctag caaaggagaa 1140
gaactcttca ctggagtgt cccaattctt gttgaattag atggatgtgt taacggccac 1200
aagtctcttg tcagtggaga gggtaagggt gatgcaacat acggaaaact taccctgaag 1260
ttcatctgca ctactggcaa actgcctgtt ccatggccaa cactagtcac tactctgtgc 1320
tatgggtgtc aatgcttttc aagataccgc gatcatatga aacggcatga ctttttcaag 1380
agtgccatgc ccgaagggtt tgtacaggaa aggaccatct tcttcaaaga tgacggcaac 1440
tacaagacac gtgtgaagt caagtttgaa ggtgataccc ttgttaatag aatcgagtta 1500
aaaggtattg acctcaagga agatggcaac attctgggac acaaattgga atacaactat 1560
aactcacaca atgtatacat catggcagac aaacaaaaga atggaatcaa agtgaacttc 1620
aagaccggcc acaacattga agatggaagc gttcaactag cagaccatta tcaacaaaat 1680
actccaattg gcgatggccc tgtcctttta ccagacaacc attacctgtc cacacaatct 1740
gccctttcga aagatcccaa cgaagagaga gaccacatgg tccttcttga gtttgaaca 1800
gctgtggga ttacacatgg catggatgaa ctgtacaact ga 1842

```

<210> 178

<211> 1725

<212> DNA

<213> Human

<400> 178

```

atgaacaaca atacaacatg tattcaacca tctatgatct cttccatggc tttaaccaatc 60
atttacaacc tcctttgtat tgttgggtgtt ttggaaaca ctctctctca atggatattt 120

```

435/518

ttaacaaaaa taggtaaaaa aacatcaacg cacatctacc tgtcacacct tgtgactgca	180
aacttacttg tgtgcagtcg catgcccttc atgagtatct atttcctgaa aggtttccaa	240
tggaataatc aatctgctca atgcagagtg gtcaatttcc tggaactct atccatgcat	300
gcaagtatgt ttgtcagctc cttaatttta agttggattg ccataagccg ctatgctacc	360
ttaatgcaaa aggattcctc gcaagagact acttcatgct atgagaaaat attttatggc	420
catttactga aaaaatttcg ccagcccaac ttgtctagaa aactatgcat ttacatatgg	480
ggagttgtac tgggcataat cattccagtt accgtatact actcagtcac agaggctaca	540
gaaggagaag agagcctatg ctacaatcgg cagatggaac taggagccat gatctctcag	600
attgcaggtc tcatiggaac cacatttatt ggattttcct ttttagtagt actaacatca	660
tactactctt ttgtaagcca tctgagaaaa ataagaacct gtacgtccat tatggagaaa	720
gatttgactt acagttctgt gaaaagacat cttttggta tccagattct actaatagtt	780
tgcttccttc cttatagtat ttttaaacc ctttttatg ttctacacca aagagataac	840
tgtcagcaat tgaattattt aatagaaaca aaaaacattc tcacctgtct tgcttcggcc	900
agaagtagca cagaccccat tatatttctt ttattagaca aaacattcaa gaagacacta	960
tataatctct ttacaaagtc taattcagca catatgcaat catatgggtc tagcaaagga	1020
gaagaactct tcaactggag tgtcccaatt ctgtttgaat tagatgggta tgttaacggc	1080
cacaagttct ctgtcagtcg agagggtgaa ggtgatgcaa catacggaaa acttaccttg	1140
aagttcatct gcactactgg caaactgcct gtccatggc caacactagt cactactctg	1200
tgctatggtg ttcaatgctt ttcaagatac ccggatcata tgaaacggca tgacttttcc	1260
aagagtgcc aagccgaagg ttatgtacag gaaaggacca tcttcttcaa agatgacggc	1320
aactacaaga cacgtgctga agtcaagttt gaaggatgata cctttgttaa tagaatcgag	1380
ttaaaaggta ttgacttcaa ggaagatggc aacattctgg gacacaaatt ggaatacaac	1440
tataactcac acaatgtata catcatggca gacaaacaaa agaattggaat caaagtgaac	1500
ttcaagaccc gccacaacat tgaagatgga agcgttcaac tagcagacca ttatcaacaa	1560
aatactccaa ttggcgatgg cctgtcctt ttaccagaca accattacct gtccacacaa	1620
tctgcccttt cgaaagatcc caacgaaaag agagaccaca tggtccttct tgagtttgta	1680
acagctgctg ggattacaca tggcatggat gaactgtaca actga	1725

436/518

<211> 3186

<212> DNA

<213> Human

<400> 179

```

atgggaggcc gcgtctttct cgtctttctc gcattctgtg tctggctgac tctgccggga    60
gctgaaaccc aggactccag gggctgtgcc cggtggtgcc ctcaggactc ctcgtgtgtc    120
aatgccaccg cctgtcgctg caatccaggg ttcagctctt tttctgagat catcaccacc    180
cccatggaga cttgtgacga catcaacgag tgtgcaacac tgtcgaaagt gtcatgcgga    240
aaattctcgg actgctggaa cacagagggg agctacgact gcgtgtgcag cccaggatat    300
gagcctgttt ctggggcaaa aacattcaag aatgagagcg agaacacgtg tcaagalgtg    360
gacgaatgtc agcagaaccc aaggctctgt aaaagctacg gcacctgcgt caacaccctt    420
ggcagctata cctgccagtg cctgcctggc ttcaagttca tacctgagga tccgaaggtc    480
tgcacagatg tgaatgaatg cacctccgga caaaacccat gccacagctc caccactgc    540
ctcaacaacg tgggcagcta tcagtgccgc tggcgcccg gctggcaacc gattccgggg    600
tccccaatg gcccaaacia taccgtctgt gaagatgtgg acgagtgcag ctccgggcag    660
catcagtgtg acagctccac cgtctgcttc aacaccgtgg gttcatacag ctgccgtgc    720
cgcccaggct ggaagcccag acacggaatc ccgaataacc aaaaggacac tgtctgtgaa    780
gatatgactt tctccacctg gaccccgccc cctggagtc acagccagac gctttccga    840
ttcttcgaca aagtcagga cctgggcaga gactacaagc caggcttggc caataacacc    900
atccagagca tcttacaggc gctggatgag ctgctggagg tccctgggga cctggagacc    960
ctgccccgct tacagcagca ctgtgtggcc agtcacctgc tggatggcct agaggatgtc   1020
ctcagaggcc tgagcaagaa ctttccaat gggctgttga acttcagtta tcttcaggc   1080
acagaattgt ccttgagggt gcagaagcaa gtagacagga gtgtcacctt gagacagaat   1140
caggcagtga tgcagctcga ctggaatcag gcacagaaat ctggtgaccc aggcccttct   1200
gtggtgggcc ttgtctccat tccagggatg ggcaagtgc tggctgaggc ccctctggtc   1260
ctggaacctg agaagcagat gcttctgcat gagacacacc agggcttgcg gcaggacggc   1320
tcccccatcc tgcctcaga tgtgatctct gcctttctga gcaacaacga caccacaaac   1380
ctcagctccc cagttacctt caccctctcc caccgttcag tgatcccgag acagaagggt   1440

```

437/518

ctctgtgtct tctgggagca tggccagaat ggatgtggc actgggccac cacaggctgc 1500
 agcacaatag gcaccagaga caccagcacc atctgccgtt gcaccacct gagcagcttt 1560
 gccgtcctca tggccacta cgaatgtcag gaggaggatc ccgtgctgac tgtcatcacc 1620
 tacatggggc tgagcgtctc tctgctgtgc ctctctctgg cggccctcac ttttctctg 1680
 tgtaaagcca tccagaacac cagcactca ctgcatctgc agctctcgct ctgcctcttc 1740
 ctggcccacc tctcttctct cgtggcaatt gatcaaaccg gacacaaggt gctgtgtctc 1800
 atcatgccg gtaccttgca ctatctctac ctggccacct tgacctggat gctgtgtggag 1860
 gccctgtacc tcttctctac tgcacggaac ctgacggctg tcaactactc aagcatcaac 1920
 agattcatga agaagctcat gtccctgtg ggctacggag tcccagctgt gacagtggcc 1980
 atttctgcag cctccaggcc tcacctttat ggaacacctt cccgctgctg gctccaacca 2040
 gaaaagggat ttatatgggg cttccttgga cctgtctgcg ccattctctc tgtgaattta 2100
 gttctcttct tggtagctct ctggattttg aaaaacagac tctctctcct caatagttaa 2160
 gtgtccaccc tccggaacac aaggatgctg gcatttaaag cgacagctca gctgttcttc 2220
 ctgggctgca cgtgggtgct gggcatcttg cagggtgggtc cggctgcccg ggtcatggcc 2280
 tactcttca ccatcatcaa cagcctgcag ggtgtcttca tcttcttggt gtactgcctc 2340
 ctccagccagc aggtccggga gcaatatggg aaatgggtcca aagggatcag gaaattgaaa 2400
 actgagtctg agatgcacac actctccagc agtgctaagg ctgacacctc caaaccagc 2460
 acggttaacg ctagcaaagg agaagaactc ttcactggag ttgtcccaat tcttgttgaa 2520
 ttagatgggt atgttaacgg ccacaagttc tctgtcagt gagagggtga aggtgatgca 2580
 acatacgga aacttacct gaagttctc tgcactactg gcaaactgcc tgttccatgg 2640
 ccaacactag tctactctct gtgctatggt gtccaatgct ttccaagata cccggatcat 2700
 atgaaacggc atgacttttt caagagtgcc atgccgaag gttatgtaca ggaaaggacc 2760
 atcttcttca aagatgacgg caactacaag acacgtgctg aagtcaagtt tgaaggatg 2820
 acccttgtaa atagaatcga gttaaaaggt atgacttca aggaagatgg caacattctg 2880
 ggacacaaat tggaatacaa ctataactca cacaatgtat acatcatggc agacaaacaa 2940
 aagaatggaa tcaaagttaa cttaagacc cgccacaaca ttgaagatgg aagcgttcaa 3000
 ctagcagacc attatcaaca aaatactcca attggcgatg gccctgtcct ttaccagac 3060
 aaccattacc tgtccacaca atctgccctt tcgaaagatc ccaacgaaaa gagagaccac 3120
 atggctcttc ttgagtttgt aacagctgct gggattacac atggcatgga tgaactgtac 3180

438/518

aactga

3186

<210> 180

<211> 2262

<212> DNA

<213> Human

<400> 180

atgggacata acgggagctg gatctctcca aatgccagcg agccgcacaa cgcgtccggc	60
gccgaggctg cgggtgtgaa ccgcagcgcg ctcggggagt tcggcgaggc gcagctgtac	120
cgccagttca ccaccaccgt gcaggtcgtc atcttcatag gctcgtgct cggaacttc	180
atgggtttat ggtcaacttg ccgcacaacc gtgttcaaat ctgtcaccaa caggttcatt	240
aaaaacctgg cctgctcggg gatttgtgcc agcctggtct gtgtgccctt cgacatcctc	300
ctcagcacca gtcttactg ttgctggtag atctacacca tgccttctg caaggtcgtc	360
aaatTTTTgc acaaagtatt ctgctctgtg accatcctca gcttccctgc tattgctttg	420
gacaggtact actcagtcct ctatccactg gagaggaaaa tatctgatgc caagtcctgt	480
gaactgggtg tgtacatctg ggcccatgca gtggtagcca gtgtccctgt gtttgagta	540
accaatgtgg ctgacatcta tgcacgtcc acctgcacgg aagctggag caactccttg	600
ggccacctgg tgtacgttct ggtgtataac atcaccacgg tcatttgtcc tgtggtggtg	660
gtgttctct tcttgatact gatccgacgg gccctgagtg ccagccagaa gaagaaggtc	720
atcatagcag cgctccggac cccacagAAC accatctcta ttccctatgc ctcccagcgg	780
gaggccgagc tgcacgccac cctgctctcc atggigatgg tcttcatctt gtgtagcgtg	840
ccctatgccA ccttggtcgt ctaccagact gtgtcaatg tccctgacac ttccgtcttc	900
ttgctgtcA ctgctgtttg gtgccccaa gtctccctgc tggcaaacc tgttctcttt	960
cttactgtga acaaatctgt ccgcaagtgc ttgataggga ccttggtgca actacaccac	1020
cggtacagtc gccgtaatgt ggtcagtaca gggagtggca tggctgaggc cagcctggaa	1080
cccagcatac gctcgggtag ccagctcctg gagatgttcc acattgggca gcagcagatc	1140
tttaagccca cagaggatga ggaagagagt gaggccaagt acattggctc agctgacttc	1200
caggccaagg agatatttag cacctgcctg gagggagagc aggggccaca gtttgcgccc	1260

439/518

```

fctgccccac cctgagcac agtggactct gtatcccagg tggcaccggc agccccctgtg 1320
gaacctgaaa cattccctga taagtattcc ctgcagtttg gctttgggcc ttttgagttg 1380
cctcctcagt ggcctcaga gacccgaaac agcaagaagc ggctgcttcc ccccttgggc 1440
aacaccccag aagagctgat ccagacaaag gtgccaagg taggcagggt ggagcggaag 1500
atgagcagaa acaataaagt gagcattttt ccaaagggtg attccgctag caaaggagaa 1560
gaactcttca ctggagttgt cccaattctt gttgaattag atggtagtgt taacggccac 1620
aagttctctg tcagtggaga gggigaaggt gatgaacat acgaaaaact taccctgaag 1680
ttcatctgca ctactggcaa actgacctgt ccatggccaa cactagtcac tactctgtgc 1740
tatggigtgc aatgcttttc aagatacccg gatcatatga aacggcatga ctttttcaag 1800
agtgccatgc ccgaaggtaa tgtacaggaa aggaccatct tcttcaaaga tgacggcaac 1860
tacaagacac gtgctgaagt caagtttgaa ggtgatcccc ttgttaatag aatcgagtta 1920
aaaggtattg acttcaagga agatggcaac attctgggac acaaattgga atacaactat 1980
aactcacaca atgtatacat catggcagac aaacaaaaga atggaatcaa agtgaacttc 2040
aagacccgcc acaacattga agatggaagc gttcaactag cagaccatta tcaacaaaat 2100
actccaattg gcgatggccc tgtcctttta ccagacaacc attacctgtc cacacaatct 2160
gccctttcga aagatcccaa cgaaaagaga gaccacatgg tcttcttga gtttgtaaca 2220
gtctctggga ttacacatgg catggatgaa ctgtacaact ga 2262

```

<210> 181

<211> 1803

<212> DNA

<213> Human

<400> 181

```

atggatctgc accctcttga ctacgccgag ccagggaact tctcggacat cagctggcca 60
tgcaacagca gcgactgcat cgtggtggac acggtgatgt gtccaacat gccaacaaa 120
agcgtcctgc tctacagct ctcttctatt tacattttca tcttcgtcat cggcatgatt 180
gccaaactccg tggtagcttg ggtgaataac caggccaaga ccacaggcta tgacacgcac 240
tgctacatct tgaacctggc cattgccgac ctgtgggttg tcttaccat cccagctctg 300

```

440/518

gtggtcagtc tcgtgcagca caaccagtgg cccatgggcg agctcacgtg caaagtcaca 360
 caccatcatc tctccatcaa cctcttcggc agcattttct tcctcacgtg catgagcgtg 420
 gaccgctacc tctccatcac ctacttcacc aacaccccca gcagcaggaa gaagatggta 480
 cgccgigtgc tctgcatcct ggtgtggctg ctggccttct gcgtgtctct gcctgacacc 540
 tactacctga agaccgtcac gtctgcgtcc aacaatgaga cctactgccg gtccttctac 600
 cccgagcaca gcatcaagga gtggctgacg ggcatggagc tggctctccg tgtcttgggc 660
 ttigccgttc ccttctccat tatcgctgtc ttctacttcc tgctggccag agccatctcg 720
 gcgtccagtg accaggagaa gcacagcagc cggaagaica tcttctccta cgtgggtggc 780
 ttcccttgtc gtggctgccc ctaccacgtg gcggtgctgc tggacatctt ctccatcctg 840
 cactacatcc ctttcacctg ccggtggag cagccctct tcacggccct gcatgtcaca 900
 cagtgcctgt cgctggtgca ctgctgcgtc aacctgtcc tctacagctt catcaatcgc 960
 aactacaggt acgagctgat gaaggccttc atcttcaagt actcggccaa aacagggtc 1020
 accaagctca tcgatgcctc cagagtctca gagacggagt actctgcctt ggagcagagc 1080
 accaaagcta gcaaaggaga agaactcttc actggagtig tcccaattct tgttgaatta 1140
 gatggigatg ttaacggcca caagtctct gtcagtggag agggatgaagg tgatgaaca 1200
 tacggaaaac ttacctgaa gttcatctgc actactggca aactgcctgt tccatggcca 1260
 acactagtca ctactctgtg ctatgggtgt caatgctttt caagatacc ggatcataatg 1320
 aaacggcatg actttttcaa gatlccatg ccgaagggtt atgtacagga aaggaccatc 1380
 ttcttcaaag atgacggcaa ctacaagaca cgtgtgaag tcaagtttga aggtgatacc 1440
 ctigttaata gaatcgagtt aaaaggtatt gacttcaagg aagatggcaa cattctggga 1500
 cacaaattgg aatacaacta taactcacac aatgtataca tcatggcaga caaacaaaag 1560
 aatggaatca aagtgaactt caagaccgc cacaacattg aagatggaag cgttcaacta 1620
 gcagaccatt atcaacaaaa tactccaatt ggcatggcc ctgtcctttt accagacaac 1680
 cattacctgt ccacacaatc tgccctttcg aaagatccca acgaaaagag agaccacatg 1740
 gtccttcttg agtttgtaac agctgctggg attacacatg gcatggatga actgtacaac 1800
 tga 1803

<210> 182

<211> 2019

441/518

<212> DNA

<213> Human

<400> 182

```
atggaggatc tcttagccc ctcaattctg cgcggcggc ccaacatttc cgtgcccata 60
ttgctgggct ggggtctcaa cctgaccttg gggcaaggag cccctgcctc tggaccgccc 120
agccgccgcg tccgcctggg gtccctgggg gtcattcttg tggtagcggt ggcaggcaac 180
accacagtgc tgtgccgctt gtgcggcggc ggcggggcct gggcggggcc caagcgtcgc 240
aagatggact tcctgctggg gcagctggcc ctggcgagacc tgtacgcgtg cgggggcacg 300
gcgctgtcac agctggcctg ggaactgctg ggcgagcccc gcgcggccac gggggacctg 360
gcgtgccgct tcctgcagct gctacaggca tccgggcggg gcgcctcggc ccacctcgtg 420
gtgtcatcgc cctcgcagcg ccggcgcgcg gtgcgtcttc cgcacggccg gccgctgccc 480
gcgcgtgccc tcgccgccct gggctggctg ctggcactgc tgcctggcgt gccccgggcc 540
ttcgtggctg gcggggactc cccctcgccg ctgccggcgc cgcggccgcc aacgtccctg 600
cagccaggcg cggccccggc cggccgcgcc tggccggggc agcgtcgtg ccacgggata 660
ttcgcgcccc tgccgcgtg gcacctgcag gtctacgcgt tctacaggc cgtcggggc 720
ttcgtcgcgc ctgttacggg cctgggcgtc gcttgcggcc acctactctc cgtctgggtg 780
cggcaccggc cgcaggcccc cgcggctgca gcgccctggg cggcgagccc aggtcgagcc 840
cctgcgcccc gcgcgtgcc ccgcgccaag gtgcagagcc tgaagatgag cctgctgctg 900
gcgctgctgt tcgtgggctg cgagctgccc tactttgccg cccggctggc ggccgcgtgg 960
tcgtccgggc ccgcgggaga ctgggagggg gagggcctgt cggcggcgtg gcgcgtgggt 1020
gcgatggcca acagcgtctt caatcccttc gtctacctt tcttcaggc gggcgactgc 1080
cggctccggc gacagctcgc gaagcggctg ggctctctgt gctgcgcgcc gcagggaggg 1140
gcggaggacg aggagggggc ccggggccac caggcgctct accgccaacg ctggccccac 1200
ccatattatc accatgctcg gcgggaaccg ctggacgagg gcggcttgcg cccacccccct 1260
ccgcgcccc aacccctgcc ttgctcctgc gaaagtgctt tcgctagcaa aggagaagaa 1320
ctcttactg gagttgtccc aattcttggt gaattagatg gtgatgttaa cggccacaag 1380
ttctctgtca gtggagaggg tgaaggatg gcaacatacg gaaaacttac cctgaagttc 1440
atctgcacta ctggcaaact gcctgttcca tggccaacac tagtcactac tctgtgctat 1500
```


442/518

ggtgttcaat gcttttcaag ataccggat cataatgaaac ggcatgactt tttcaagagt 1560
 gccatgcccg aaggttatgt acaggaaagg accatcttct tcaaagatga cggcaactac 1620
 aagacacgtg ctgaagtcaa gtttgaaggt gatacccttg ttaatagaat cgagtiaaaa 1680
 ggtattgact tcaaggaaga tggcaacatt ctgggacaca aattggaata caactataac 1740
 tcacacaatg tatacatcat ggcagacaaa caaaagaatg gaatcaaagt gaacttcaag 1800
 acccgccaca acattgaaga tggaagcgtt caactagcag accattatca acaaaatact 1860
 ccaattggcg atggccctgt ccttttacca gacaaccatt acctgtccac acaatctgcc 1920
 ctttcgaaag atcccaacga aaagagagac cacatggtcc ttcttgagtt tgtaacagct 1980
 gctgggatta cacatggcat ggaatgaactg tacaactga 2019

<210> 183

<211> 1629

<212> DNA

<213> Human

<400> 183

atgctgagca ctgggggtgt gagcttcttc tccctcaagt cggactcggc gcccccttg 60
 atgggtgctg ctgtgctgtg gtgtccatg gcacagacgc tgcctgtgcc ctcttcctc 120
 tggctctgag agcgtaccg cggcgacgtg cgcacagtgt gggagcaatg cgtggccatc 180
 atgtctgagg aggatggaga tgacgatggg ggcgtgacg actatgcaga gggccgagtt 240
 tgcaaagtgc gctttgatgc taacggagcc acaggaccag ggagccggga ccccgccag 300
 gigaagctgc tgcttgaag gcacatgctc ttcctcctc ttgagagagt ccaactacta 360
 caggctcccc tatcccggtg tctgtccat gatgagacaa acatctctc taccctcgg 420
 gaaccaggct ccttcctgca caagtgtca tctctgatg acatccgggt cctcccagcc 480
 cagagccggg ccctcggggg tcctcctgag tacctgggac aaagacacag gttggaggac 540
 gaggaggacg aggaagaggc tgaagggtgg gggctggcca gccttcgcca attcttgag 600
 agtgggggtc tggggtcagg tgggggaccc ccacgggtc ctggctctt cggggaggag 660
 atcaccacct tcatgatga gacacctg ccttctccga ctgcctcacc agggcactct 720
 cctcgtcggc cccggccact gggcctctca cccgcccagc tctcccttgg gtccctgag 780

443/518

```

agcagagccg tiggacttcc ttitgggacta agcgcagggg gacgctgctc cctgacgggg 840
ggtgaagaaa gigcaagggc tiggggagga tcctggggcc caggcaaccc catcttccc 900
cagctgacct tggctagcaa aggagaagaa ctcttcactg gagttgtccc aattcttgtt 960
gaattagatg gtgatgttaa cggccacaag ttctctgtca gtggagaggg tgaaggigat 1020
gcaacatacg gaaaacttac cctgaagttc atctgcacta ctggcaaact gcctgttcca 1080
tggccaacac tagtcactac tctgtgctat ggigtccaat gcttttcaag ataccggat 1140
cataatgaaac ggcatgactt ttcaagagt gccatgccc aaggttatgt acaggaaagg 1200
accatcttct tcaaagatga cggcaactac aagacacgtg ctgaagtcaa gttigaaggt 1260
gatacccttg ttaatagaat cgagttaaaa ggtattgact tcaaggaaga tggcaacatt 1320
ctgggacaca aattggaata caactataac tcacacaatg tatacatcat ggcagacaaa 1380
caaaagaatg gaatcaaagt gaacttcaag acccgccaca acattgaaga tggaagcgtt 1440
caactagcag accattatca acaaaatact ccaattggcg atggccctgt ccttttacca 1500
gacaaccatt acctgtccac acaatctgcc ctttcgaaag atcccaacga aaagagagac 1560
cacatggtec ttcttgagtt tgtaacagct gctgggatta cacatggcat ggatgaactg 1620
tacaactga 1629

```

<210> 184

<211> 1716

<212> DNA

<213> Human

<400> 184

```

atgcctgcta attacacgtg taccaggcca gatggagaca atacagattt tcgatacttt 60
atattatgcag tgacatacac tgcattctt gtgccaggtc tcatagggaa tatattagcc 120
ctgtgggtat tctatggta tatgaaagaa acaaaacgag ctgtgatatt tatgataaac 180
ttagccattg ctgacttact acaagttctt tccttgccac tgaggatctt ctactacttg 240
aatcatgact ggccatttgg gcctggctc tgcatgttct gtttctacct gaagtatgtc 300
aacatgtatg caagcatcta ctcttggtc tgcatcagtg tgcgacgatt ttggtttctc 360
atgtaccctt ttcgttcca tgactgcaa cagaaatatg acctgtacat cagcatigtct 420

```

444/518

```

ggctggctga tcattcgctt tgccctgtgta ctctttccac tcctcagaac cagtgaatgat 480
acctctggca ataggaccac atgctttgtg gatcttccta ccaggaatgt caacctggcc 540
cagtcctgtt ttatgatgac cattggcgag ttgattgggt ttgtaactcc gcttctgatt 600
gtcctatatt gtacctggaa gacggtttta tcactgcaag ataaatatcc catggcccaa 660
gatcttggag agaaacagaa agccctgaag atgattctaa cctgtgcagg ggtattccta 720
atttgctttg caccttatca tticagtttt ccttttagatt tcttggtgaa gtccaatgaa 780
attaaaagct gcctagccag aagggtgatt ctaatatctt attctgtggc atttgtcttt 840
gctagtctga attcatgtct tgaccagtc atatactact tttccactaa tgagttccga 900
agacggcttt caagacaaga ttgcatgac agcatccaac tccatgcaaa atccittgtg 960
agtaaccata cagcttccac catgacacct gaattatgcg ctacgaaagg agaagaactc 1020
ttcactggag ttgtcccaat tcttgttgaa ttgatgggtg atgtaacgg ccacaagttc 1080
tcigtcagtg gagagggtga aggtgatgca acatacggaa aacttacct gaagttcatc 1140
tgcactactg gcaaactgcc tgttccatgg ccaacactag tcaactactt gtgctatggt 1200
gttcaatgct tttcaagata cccggatcat atgaaacggc atgacttttt caagaglgcc 1260
atgcccgaag gttatgtaca ggaaaggacc atcttcttca aagatgacgg caactacaag 1320
acacgtgctg aagtcaagtt tgaaggatg acccttggtt atagaatcga gttaaaaggt 1380
attgacttca aggaagatgg caacattctg ggacacaaat tggaatacaa ctataactca 1440
cacaatgtat acatcatggc agacaaacaa aagaatggaa tcaaagtga cttcaagacc 1500
cgccacaaca ttgaagatgg aagcgttcaa ctagcagacc attatcaaca aaatactcca 1560
attggcgatg gccctgtcct ttaccagac aaccattacc tgtccacaca atctgccctt 1620
tcgaaagatc ccaacgaaaa gagagaccac atggtccttc ttgagtttgt aacagctgct 1680
gggattacac atggcatgga tgaactgtac aactga 1716

```

<210> 185

<211> 1734

<212> DNA

<213> Human

<220>

445/518

<221>

<222> 330

<223> n stands for any base

<400> 185

aigaatggcc ttgaagtggc tccccaggt ctgatcacca acttctccct ggccacggca	60
gagcaatgtg gccaggagac gccactggag aacatgtctg tcgcctccit ctaccttctg	120
gattttatcc tggcttiagt tggcaatacc ctggctctgt ggcttttcat ccgagaccac	180
aagtcggga ccccgccaa cgtgttctg atgcatctgg ccgtggccga ctgtctgtgc	240
gtgtgtgtcc tgcccaccg cctggtctac cacttctctg ggaaccactg gccatttggg	300
gaaatcgcat gccgtctcac cggttccn ttctacctca acatgtacgc cagcatctac	360
ttctcacct gcatcagcg cgaccgttc ctggccattg tgcaccgggt caagtcctc	420
aagctccgca ggccctcta cgcacacctg gcctgtgcct tcctgtgggt ggtgtgggt	480
gtggccatgg ccccgctgt ggtgagcca cagaccgtgc agaccaacca cacggtgtgc	540
tgcctgcagc tgtaccggga gaaggctcc caccatgccc tgggtgtccct ggcatggcc	600
ttcaccttcc cgttcatcac cacggtcacc tgctacctgc tgatcatccg cagcctgcgg	660
cagggcctgc gtgtggagaa gcgcctcaag accaaggcag tgcgcatgat cgccatagt	720
ctggccatct tcctggtctg ctctgtgcc taccagtca accgtccgt ctacgtgtg	780
cactaccgca gccatggggc ctctgtgcc acccagcgca tcctggccct ggcaaaccgc	840
atcacctcct gcctaccag cctcaacggg gcactcgacc ccatcatgta ttcttctgt	900
gctgagaagt tccgccacgc cctgtgcaac ttgtctgtg gcaaaaggct caaggggccg	960
ccccccagct tcgaaggga aaccaacgag agctcgctga gtgccaagtc agagctggct	1020
agcaaaggag aagaactctt cacitggagt gtcccaattc ttgttgaatt agatggtgat	1080
gttaacggcc acaagtctc tgcagtga gaggtgaag gtgatgcaac atacggaaaa	1140
cttaccctga agttcatctg cactactggc aaactgcctg ttccatggcc aacactagtc	1200
actactctgt gctatggtgt tcaatgctt tcaagatacc cggatcatat gaaacggcat	1260
gactttttca agagtccat gccgaagggt tatgtacagg aaaggacat ctcttcaaa	1320
gatgacggca actacaagac acgtgtgaa gtcaagttg aaggtgatac cttgttaat	1380
agaatcgagt taaaaggat tgacttcaag gaagatggca acattctggg acacaaattg	1440

446/518

gaatacaact ataactcaca caatgtatac atcatggcag acaaacaaaa gaatggaatc 1500
 aaagtgaact tcaagacccg ccacaacatt gaagatggaa gcgttcaact agcagaccat 1560
 tatcaacaaa atactccaat tggcgatggc cctgtccttt taccagacaa ccattacctg 1620
 tccacacaat ctgccctttc gaaagatccc aacgaaaaga gagaccacat ggtccttctt 1680
 gagtttgtaa cagctgctgg gattacacat ggcatggatg aactgtacaa ctga 1734

<210> 186

<211> 1644

<212> DNA

<213> Human

<400> 186

atgaatggca cctacaacac ctgtggctcc agcgacctca cctggcccc agcgatcaag 60
 ctgggccttct agcctactt gggcgctctg ctggtgctag gcctgctgct caacagcctg 120
 gcgctctggg tgttctgctg ccgcatgcag cagtggacgg agaccgcat ctacatgacc 180
 aacctggcgg tggccgacct ctgcctgctg tgcaccttgc ccttcgtgct gcactccctg 240
 cgagacacct cagacacgcc gctgtgccag ctctcccagg gcattctacct gaccaacagg 300
 tacatgagca tcagcctggt cacggccatc gccgtggacc gctatgtggc cgtgcggcac 360
 ccgctgcgtg cccgcgggct gcggtcccc aggcaggctg cggccgtgtg cgcggtcctc 420
 tgggtgctgg tcatcggtc cctgggtggct cgctggctcc tggggattca ggaggcggc 480
 ttctgcttca ggagcaccg gcacaatttc aactccatgg cgttcccgt gctgggattc 540
 tacctgcccc tggccgtggt ggtcttctgc tccctgaagg tggtgactgc cctggcccag 600
 aggccacca cgcagctggg gcaggcagag gccaccgca aggctgccc catggtctgg 660
 gccaacctcc tggigtctgt ggtctgcttc ctgccccgc acgtggggct gacagtgcgc 720
 ctgcagtggt gctggaacgc ctgtgccctc ctggagacga tccgtcgcgc cctgtacata 780
 accagcaagc tctcagatgc caactgctgc ctggacgcca tctgctacta ctacatggcc 840
 aaggagtcc aggaggcgtc tgcactggcc gtggctcccc gtgctaaggc ccacaaaagc 900
 caggactctc tgtgcgtgac cctcgccgt agcaaaggag aagaactctt cactggagtt 960
 gtcccaattc ttgttgaatt agatggtgat gttacggcc acaagttctc tgtcagtgga 1020

447/518

gagggatgaag gtagtgaac atacggaaaa cttaccctga agttcaictg cactactggc 1080
 aaactgccig ttccatggcc aacactagtc actactctgt gctatgggtg tcaatgcttt 1140
 tcaagatacc cggatcata gaaacggcat gactttttca agagtggcat gccgaaggt 1200
 tatgtacagg aaaggacat cttcttcaaa gatgacggca actacaagac acgtgctgaa 1260
 gtcaagtttg aaggatgata ccttgtaaat agaactgagt taaaaggat tgacttcaag 1320
 gaagatggca acattctggg acacaaattg gaatacaact ataactcaca caatgtatac 1380
 atcatggcag acaaacaaaa gaatggaatc aaagtgaact tcaagaccg ccacaacatt 1440
 gaagatggaa gcgttcaact agcagacat tatcaacaaa atactccaat tggcgatggc 1500
 ccgtgctttt taccagacaa ccattacctg tccaacaaat ctgcccttc gaaagatccc 1560
 aacgaaaaga gagaccacat ggtccttctt gagttgiaa cagctgctgg gattacacat 1620
 ggcatggatg aactgtacaa ctga 1644

<210> 187

<211> 2040

<212> DNA

<213> Human

<400> 187

atggccatcc acaaagcctt ggtgatgtgc ctgggactgc ctctcttctt gttcccaggg 60
 gcctgggccc agggccatgt cccaccggc tgcagccaag gcctcaaccc cctgtactac 120
 aacctgtgtg accgctctgg ggcgtggggc atcgtcctgg aggccgtggc tggggcgggc 180
 attgtacca cgtttgtgt caccatcatc ctggatggca gcctccctt tgtgcaggac 240
 accaagaaac ggagcctgt ggggaccag gtattcttcc ttctggggac cctgggcctc 300
 ttctgcctcg tgtttgcctg tgtggtgaag cccgacttct ccacctgtgc ctctcggcgc 360
 ttctcttttg gggttctgtt cgccatctgc ttctctgtc tggcggtca cgtctttgcc 420
 ctcaacttcc tggcccgaa gaaccacggg ccccggggct gggatgatt cactgtggct 480
 ctgtgtctga ccttggtaga ggtcatcatc aatacagagt ggctgatcat caccctggtt 540
 cggggcagtg gcgaggcgg cctcagggc aacagcagc caggctgggc cgtggcctcc 600
 cctgtgcca tcgccaacat ggactttgtc atggcactca tctacgtcat gctgtgtctg 660

448/518

```

ctgggtgcct tcctgggggc ciggcccgcc ctgtgtggcc gctacaagcg ctggcgtaag 720
catggggict ttgtgtccf caccacagcc acctccgttg ccatatgggt ggtgtggatc 780
gtcatgtata cttacggcaa caagcagcac aacagtccca cctgggatga cccacgctg 840
gccatgccc tgcgcgcaa tgccctggcc ttctctctt tctacgtcat ccccgaggtc 900
tcccaggta ccaagtcag cccagagcaa agctaccagg gggacatga cccacccgg 960
ggcgtgggct atgagacat cctgaaagag cagaagggtc agagcatgtt cgtggagaac 1020
aaggcctttt ccatggatga gccggttgca gctaagaggc cgggtgcacc atacagcggg 1080
tacaatgggc agctgtgac cagtgtgtac cagccactg agatggcctt gatgcacaaa 1140
gttccgtccg aaggagctta cgacatcatc ctcccacggg ccaccgcaa cagccagggt 1200
atgggcagtg ccaactcgac cctgcgggct gaagacatgt actcgccca gagccaccag 1260
gcggccacac cgccgaaaga cggcaagaac tctcaggtct ttagaaacc ctacgtgtgg 1320
gacgctagca aaggagaaga actcttact ggagttgtcc caattctgt tgaattagat 1380
ggtgatgtta acggccacaa gtctctgtc agtggagagg gtgaaggta tgcaacatac 1440
ggaaaactta cctgaagtt catctgcact actggcaaac tgctgttcc atggccaaca 1500
ctagtacta ctctgtgcta tgggtttcaa tgcttttcaa gatacccgga tcatatgaaa 1560
cggcatgact ttttcaagag tgccatgccc gaaggttatg tacaggaaag gaccatcttc 1620
ttcaaagatg acggcaacta caagacacgt gctgaagtca agtttgaagg tgataccctt 1680
gttaatagaa tcgagttaaa aggtattgac ttcaaggaag atggcaacat tctgggacac 1740
aaattggaat acaactataa ctacacaaat gtatacatca tggcagacaa acaaaagaat 1800
ggaatcaaag tgaacttcaa gaccgcccac aacattgaag atggaagcgt tcaactagca 1860
gaccattatc aacaaaatac tccaattggc gatggccctg tccttttacc agacaacat 1920
tacctgtcca cacaatctgc ctttcgaaa gatcccaacg aaaagagaga ccacatggtc 1980
cttcttgagt ttgtaacagc tgctgggatt acacatggca tggatgaact gtacaactga 2040

```

<210> 188

<211> 1878

<212> DNA

<213> Human

449/518

<400> 188

atgaatcggc accatctgca ggatcacttt ciggaaatag acaagaagaa ctgctgtgtg	60
ticcagagatg acttcattgc caaggtgttg ccgccgggtg tggggctgga gtttatcttt	120
gggcttcttg gcaatggcct tgccctgttg attttctgtt tccacctcaa gtccctggaaa	180
tccagccgga ttttctgtt caaccttgga gtagctgact ttctactgat catctgcctg	240
ccgttcgtga tggactacta tgtgcggcgt tcagactgga agtttgggga catcccttgc	300
cggctgggtg tcttcattgt tgcattgaac cgccagggca gcatcatctt cctcacgggtg	360
gtggcggtag acaggtatct ccgggtggtc catccccacc acgccctgaa caagatctcc	420
aattggacag cagccatcat ctcttgccct ctgiggggca tcactgttgg cctaacagtc	480
cacctctga agaagaagtt gctgatccag aatggccctg caaatgtgtg catcagcttc	540
agcatctgcc ataccttccg gtggcacgaa gctatgttcc tcttgaggtt cctcctgccc	600
ctgggcatca tctgttctg ctgagccaga attatctgga gcctgcggca gagacaaatg	660
gaccggcatg ccaagatcaa gagagccatc acctcatca tgggtgtggc catcgtcttt	720
gtcatctgtt tcttcccag cgtggtgtg cggatccgca tcttctggct cctgcacact	780
tggggcagc agaattgtga agtgtaccgc tgggtggacc tggcgttctt taccactctc	840
agcttcacct acatgaacag catgctggac ccctgggtg actacttctc cagcccatcc	900
tttccaact tcttctccac ttgtatcaac cgctgcctcc agaggaagat gacaggtgag	960
ccagataata accgcagcac gagcgtcgag ctacagggg accccaacaa aaccagaggc	1020
gctccagagg cgtaaatggc caactccgtt gagccatgga gcccctctta tctgggcccc	1080
acctcaata accattccaa gaaggacat tgtaccaag aaccagcatc tctggagaaa	1140
cagttgggtt gttgcatcga ggctagcaaa ggagaagaac tcttacttgg agttgtccca	1200
attcttgttg aattagatgg tgatgttaac ggccacaagt tctctgtcag tggagagggt	1260
gaaggtgatg caacatacgg aaaacttacc ctgaagttca tctgcactac tggcaaactg	1320
cctgttccat ggccaacact agtcactact ctgtgctatg gtgttcaatg cttttcaaga	1380
taccggatc atatgaaacg gcatgacttt ttcaagagt ccatgcccga aggttatgta	1440
caggaaagga ccatcttctt caaagatgac ggcaactaca agacacgtgc tgaagticaag	1500
tttgaagggtg ataccttgt taatagaatc gagttaaaag gtattgactt caaggaagat	1560
ggcaacattc tgggacacaa attggaatac aactataact cacacaatgt atacatcatg	1620
gcagacaaac aaaagaatgg aatcaaagt aacttcaaga cccgccacaa catgaagat	1680

450/518

ggaagcgttc aactagcaga ccattatcaa caaaatactc caattggcga tggccctgtc 1740
 cttttaccag acaaccatta cctgtccaca caatctgccc tticgaaaga tcccaacgaa 1800
 aagagagacc acatggctct tcttgagttt gtaacagctg ctgggattac acatggcatg 1860
 gatgaactgt acaactga 1878

<210> 189

<211> 2337

<212> DNA

<213> Human

<400> 189

atgaactcaa caggccacct tcaggatgcc cccaatgcc cctcgctcca tgtgcctcac 60
 tcacaggaag gaaacagcac ctctctccag gagggcttc aggatctcat ccacacagcc 120
 accttggatg ccgtacttt tctactggcg gtcattctt gccitgggtc ctatggcaac 180
 ttcatgtct tctgtcctt ctctgatcca gccctcagga aattcagaac caactttgat 240
 ttcatgatcc tgaacctgtc ctctgtgac ctcttcattt gtggagtac agcccccatg 300
 ttacccttg tgttattctt cagctcagcc agtagtatcc cggatgcttt ctgcttcact 360
 ttccatctca ccagttcagg ctctcatc acgtctctga agacagtggc agtgatcgcc 420
 ctgcaccggc tccgatggt gtgggggaaa cagcctaacc gcacggcctc ctttccctgc 480
 accgtactcc tcacctgct tctctgggcc accagtttca ccttggccac ctggcttacc 540
 ttgaaaacca gcaagtccca cctctgtctt cccatgtcca gctgattgc tggaaaaggg 600
 aaagccattt tgtctctcia tgtggtcgac ttaccttct gtgttgctgt ggtctctgtc 660
 tcttacatca tgattgtca gacctgcgg aagaacgctc aagtcagaaa gtgccccct 720
 gtaatcacag tcgatgttc cagaccacag cctttcatgg ggttcctgt gcaggaggt 780
 ggagatccca tccagtgtc catgccggct ctgtatagga accagaatta caacaactg 840
 cagcacgttc agaccgtgg atataccaag agtcccaacc aactggcac cctgcagca 900
 agccgactcc agctcgtatc agccatcaac ctctccactg ccaaggattc caaagccgtg 960
 gtcacctgtg tgatcattgt gctgtcagtc ctgggtgtgt gcttccact ggggatttcc 1020
 ttggtacagg tggttctctc cagcaatggg agcttcattc ttaccagtt tgaattgttt 1080

451/518

```

ggatttactc ttatatTTTT caagtcagga ttaaaccctt ttatatattc tcggaacagt 1140
gcagggtga gaaggaaagt gctctggtgc ctccaataca taggcctggg tttttctgc 1200
tgcaaacaaa agactcgact tcgagccatg ggaaaaggga acctcgaagt caacagaaac 1260
aaatcctccc atcatgaaac aaactctgcc tacatgttat ctccaaagcc acagaagaaa 1320
tttgtggacc aggcttgtgg cccaagtcac tcaaaagaaa gtatggtgag tccaagatc 1380
tctgttgac atcaacactg tggtcagagc agctcgacc ccatcaaac tcggattgaa 1440
ccitactaca gcatctataa cagcagccct tcccaggagg agagcagccc atgtaactta 1500
cagccagtaa actcttttgg atttgccaat tcatatatg ccatgcatta tcacaccact 1560
aatgacttag tgcaggaata tgacagcact tcagccaagc agattccagt cccctccgtt 1620
gctagcaaag gagaagaact cttcactgga gttgtccaa ttcttgtga attagatggt 1680
gatgtaacg gccacaagt ctctgtcagt ggagagggtg aaggatgac aacatacgga 1740
aaacttacc tgaagtcac ctgcactact ggcaaacgc cgttccatg gccaacacta 1800
gtcactactc tgtgctatgg tgttcaatgc ttttcaagat acccgatca tatgaaacgg 1860
catgactttt tcaagagtc catgcccga gggtatgtac aggaaaggac catcttctc 1920
aaagatgacg gcaactacaa gacacgtgct gaagtcaagt ttgaaggta tacccttgtt 1980
aatagaatcg agttaaagg tattgacttc aaggaagatg gcaacattct gggacacaaa 2040
ttggaataca actataactc acacaatgia tacatcatgg cagacaaaca aaagaatgga 2100
atcaaagtg acttcaagac ccgccacaac attgaagatg gaagcgttca actagcagac 2160
cattatcaac aaaatactcc aattggcgat ggccctgtcc ttttaccaga caaccattac 2220
ctgtccacac aatctgccct ttcgaaagat cccaacgaaa agagagacca catggtcctt 2280
cttgagtttg taacagctgc tgggattaca catggcatgg atgaactgta caactga 2337

```

<210> 190

<211> 1755

<212> DNA

<213> Human

<400> 190

```

atgtacaacg ggtcgtgctg ccgcatcgag ggggacacca tctcccaggt gatgccgccg 60

```

452/518

ctgctcattg tggcctttgt gctgggcgca ctaggcaatg gggtcgccct gtgtggtttc 120
 tgcttcaca tgaagacctg gaagcccagc actgtttacc ttttcaattt ggccgtggct 180
 gatttcctec ttatgatctg cctgcccttt cggacagact attacctcag acgtagacac 240
 tgggcttttg gggacattcc ctgccgagtg gggctcttca cgttggccat gaacagggcc 300
 gggagcctcg tgttccttac ggtgggtggct gcggacaggt atttcaaagt ggtccacccc 360
 caccacgcgg tgaacactat ctccaccggg gggcggctg gcacgtctg caccctgtgg 420
 gccctggica tcctgggaac agtgtatctt ttgctggaga accatctctg cgtgcaagag 480
 acggccgtct cctgtgagag ctctatcatg gactcggcca atggctggca tgacatcatg 540
 ttccagctgg agttctttat gccctcggc atcatcttat ttgtctctt caagattgtt 600
 tggagcctga ggccggaggca gcagctggcc agacaggctc ggaatgaaga ggcgacccgg 660
 ttcatcatgg tggtaggaat tgtgttcac acatgctacc tgcccagcgt gtctgctaga 720
 ctctatttcc tctggacggt gccctcgagt gcctgcgac cctctgtcca tggggccctg 780
 cacataacce tcagcttcac ctacatgaac agcatgctgg atccccctgt gtattatttt 840
 tcaagccctt cttttccaa attctacaac aagctcaaaa tctgcagtct gaaacccaag 900
 cagccaggac actcaaaaac acaaaggccg gaagagatgc caatttcgaa cctcggtcgc 960
 aggagttaga tcagtgtggc aaatagtctt caaagccagt ctgatgggca atgggatccc 1020
 cacattgttg agtggcacgc tagcaaagga gaagaactct tcactggagt tgtcccaatt 1080
 cttgttgaat tagatggtga tgttaacggc cacaagttct ctgtcagtgg agagggtgaa 1140
 ggtgatgcaa catacggaaa acttaccctg aagttcatct gcactactgg caaactgcct 1200
 gtccatggc caacactagt cactactctg tgctatggtg ttcaatgctt ttcaagatac 1260
 ccgcatcata tgaacggca tgactttttc aagagtggca tgcccgaagg ttatgtacag 1320
 gaaaggacca tcttcttcaa agatgacggc aactacaaga cacgtgctga agtcaagttt 1380
 gaaggtgata cccttggtta tagaatcgag ttaaaaggta ttgacttcaa ggaagatggc 1440
 aacattctgg gacacaaatt ggaatacaac tataactcac acaatgtata catcatggca 1500
 gacaaacaaa agaattggaat caaagtgaac ttcaagaccc gccacaacat tgaagatgga 1560
 agcgttcaac tagcagacca ttatcaacaa aatactccaa ttggcgatgg ccctgtcctt 1620
 ttaccagaca accattacct gtccacacaa tctgcccttt cgaaagatcc caacgaaaag 1680
 agagaccaca tggctcttct tgagtttgta acagctgctg ggattacaca tggcatggat 1740
 gaactgtaca actga 1755

453/518

<210> 191

<211> 1758

<212> DNA

<213> Human

<400> 191

```

atgggggatg agctggcacc ttgccctgtg ggcactacag ctggccggc cctgatccag   60
ctcatcagca agacaccctg catgccccaa gcagccagca acatttcctt gggcctgggg   120
gaccicaggg tggccagctc catgctgtac tggcttttcc ttccctcaag cctgctggct   180
gcagccacac tggctgtcag cccctgtctg ctggtagcca tctgcggaa ccaacggctg   240
cgacaggagc cccactacct gctcccggt aacatcctgc tctcagacct ggcctacatt   300
ctcctccaca tgctcatctc ctccagcagc ctgggtggct gggagctggg ccgcatggcc   360
tgtggcattc tcactgatgc tgtcttcgcc gccagacca gcaccatcct gtccttcacc   420
gccattgtgc tgcacacctt cctggcagtc atccatccac tgcgtacct ctccttcatg   480
tcccatgggg ctgccctggaa ggcagtggcc ctcatctggc tggtagcctg ctgcttcccc   540
acattcctta tttggctcag caagtggcag gatgccagc tggaggagca aggagcttca   600
tacatcctac caccaagcat gggcacccag ccgggatgtg gcctcctggt cattgttacc   660
tacacctcca ttctgtggt tctgttcctc tgcacagctc tcattgcaa ctgtttctgg   720
aggatctatg cagaggccaa gacttcaggc atctgggggc agggctattc ccgggccagg   780
ggcacccctg tgatccactc agtgctgac acattgtacg tgagcacagg ggtggtgttc   840
tccctggaca tgggtgtgac caggtaccac cacattgact ctgggactca cacatggctc   900
ctggcagcta acagtgaggt actcatgatg ctccccctg ccatgtccc atacctgtac   960
ctgtccgct accggcagct gttgggcag gtccggggcc acctccatc caggaggcac  1020
caggccatct ttaccatttc cgctagcaaa ggagaagaac tcttactgg agttgtccca  1080
attcttgttg aattagatgg tgatgttaac ggccacaagt tctctgtcag tggagagggt  1140
gaaggtgatg caacatacgg aaaacttacc ctgaagtcca tctgcactac tggcaaactg  1200
cctgttccat ggccaacact agtcactact ctgtgctatg gtgttcaatg cttttcaaga  1260
taccgggatc atatgaaacg gcatgacttt ttcaagagtg ccatgccga aggttatgta  1320

```

454/518

caggaaagga ccattcttctt caaagatgac ggcaactaca agacacgtgc tgaagtcag 1380
 ttgaagggtg atacccttgt taatagaatc gagttaaaag gtattgactt caaggaagat 1440
 ggcaacattc tgggacacaa atiggaatac aactataact cacacaatgt atacatcatg 1500
 gcagacaaac aaaagaatgg aatcaaagtg aacttcaaga cccgccacaa cattgaagat 1560
 ggaagcgttc aactagcaga ccattatcaa caaaatactc caattggcga tggccctgtc 1620
 cttttaccag acaaccatta cctgtccaca caatctgccc tticgaaaga tcccaacgaa 1680
 aagagagacc acatggctct tcttgagttt gtaacagctg ctgggattac acatggcatg 1740
 gatgaactgt acaactga 1758

<210> 192

<211> 1836

<212> DNA

<213> Human

<400> 192

atgagaatgg aggatgaaga ttacaacact tccatcagtt acggatgatga ataccctgat 60
 tattttagact ccatttgtgt tttggaggac ttatccccct tggaagccag ggtgaccagg 120
 atcttctctg tgggtgtcta cagcatcgtc tgcttctctg ggattctggg caatggctctg 180
 gtgatcatca ttgccacctt caagatgaag aagacagtga acatggctctg gttcctcaac 240
 ctggcagtgg cagatttctt gttcaacgtc ttcttcccaa tccatatcac ctatgccgcc 300
 atggactacc actgggtttt cgggacagcc atgtgcaaga tcagcaactt ctttctcatc 360
 cacaacatgt tcaccagcgt cttctgtctg accatcatca gctctgaccg ctgcatctct 420
 gtgtctctcc ctgtctggtc ccagaaccac cgcagcgttc gcctggctta catggcctgc 480
 atggatcatct gggctctggc tttcttcttg agttcccat ctctctctt ccgggacaca 540
 gccaacctgc atgggaaaat atcttcttc aacaacttca gcctgtccac acctgggtct 600
 tcctctgggc cactcactc ccaaattggac cctgtgggt atagccggca catggtgggt 660
 actgtacccc gtttctctg tggcttctg gtccagtc tcatcatcac agcttgctac 720
 ctcccatcgt tgtgcaaac gcagcgaac cgcctggcca agaccaagaa gcccttcaag 780
 attattgtga ccacatcat taccttctc ctctgtgtgt gccctacca cacactcaac 840

455/518

```

ctcctagagc tccaccacac tgccatgcct ggctctgtct tcagcctggg ttigcccctg 900
gccactgccc ttgccattgc caacagctgc atgaacccca ttctgtatgt tttcatgggt 960
caggacttca agaagttcaa ggtggccctc ttctctcgcc tggtaaatgc tctaagtga 1020
gatacaggcc actcttccta cccagccat agaagcitta ccaagatgc atcaatgaat 1080
gagaggactt ctatgaatga gagggagacc ggcatgcttg ctagcaaagg agaagaactc 1140
ttcactggag ttgtcccaat tcttgttgaa ttatagtggt atgttaacgg ccacaagttc 1200
tctgtcagtg gagaggtga agtgatgca acatagcaa aacttacct gaagttcatc 1260
tgcactactg gcaaactgcc tgttccatgg ccaacactag tcactactct gtgctatggt 1320
gttcaatgct tttaagata cccggatcat atgaacggc atgactttt caagagtgcc 1380
atgccgaag gttatgtaca ggaaaggacc atctcttca aagatgacgg caactacaag 1440
acacgtgctg aagtaagtt tgaagtgat acccttgta atagaatga gttaaaaggt 1500
attgacttca aggaagatgg caacattctg ggacacaaat tggaaataca ctataactca 1560
cacaatgat acatcatggc agacaaacaa aagaatggaa tcaaagtga cttcaagacc 1620
cgccacaaca ttgaagatgg aagcgttcaa ctagcagacc attatcaaca aaatactcca 1680
attggcgaig gccctgtcct ttaccagac aaccattacc tgtccacaca atctgccctt 1740
tcgaaagatc ccaacgaaaa gagagaccac atggtccttc ttgagtttgt aacagctgct 1800
gggattacac atggcatgga tgaactgtac aactga 1836

```

<210> 193

<211> 1776

<212> DNA

<213> Rat

<400> 193

```

atggaagtct caagggaat gctatttga gaactggaca actactccta tgccttagaa 60
tattactccc aggaacctga cgcagaggag aatgigtacc cggaatcgt tcaactggatc 120
tccctgtctt tatatgccct tgcgtttgtt ctgggaattc caggaatgc catcgtcatt 180
tggttcatgg gatcaagtg gaagaagacg gtcaccactc ttgggtttct caatctggcc 240
attgcagact tcgtctttgt tctcttcttg cctctgtata ttccctatgt ggcactgagt 300

```

456/518

```

ttccactggc cctttggccg atggctctgc aagcittaatt ccttcattgc ccaactgaac 360
atgttttcca gtgtattctt cttagacagt attagcctgg accgctacat tcaattgatc 420
caccctggct tgtctcatcc gcaccggacc ctgaagaact cactgcttgt tgttctattt 480
gtctggctgt tggcttctct gctcggaggt cctaccctgt acttccggga caccgtggag 540
gtcaacaacc gcattatttg ttataacaac ttccaggagt atgagctcac ccgatgaga 600
caccacgttc tgacctgggt gaagttcctt ttgggtacc tcttgccctt gctgacaatg 660
agctcctgct acctgtgcct catcttcaag acgaagaagc aaaacattct gatattcagt 720
aagcatctct ggatgatcct gtctgtggtc atgccttca tggtttgctg gactcctttt 780
cacctgttca gcatttggga actcagcatt catcacaaca gctctttcca gaacgtgctg 840
cagggcggaa tccctctctc tacttgcttg gccttcttca acagctgctt gaaccccatc 900
ctttacgttc taataagcaa gaagtttcaa gctcgattca gggcctctgt tgccgaggta 960
ctaaagcgtt cactgtggga ggccagttgc tctggtacag tgagtgaaca actcaggagt 1020
gctgaaacca agagcctgtc tctcctagaa actgcccaag ctacgaaagg agaagaactc 1080
ttcactggag ttgtcccaat tcttgttgaa ttgatgggtg atgttaacgg ccacaagttc 1140
tctgtcagtg gagagggtga aggtgatgca acatacggaa aacttaccct gaagttcatc 1200
tgcactactg gcaaactgcc tgttccatgg ccaacactag tcaactactt gtgctatggt 1260
gttcaatgct tttaagata cccggatcat atgaaacggc atgacttttt caagagtgcc 1320
atgcccgaag gttatgtaca ggaaaggacc atcttcttca aagatgacgg caactacaag 1380
acacgtgctg aagtcaagtt tgaaggatg acccttggtt atagaatcga gttaaaaggt 1440
attgacttca aggaagatgg caacattctg ggacacaaat tggaatacaa ctataactca 1500
cacaatgtat acatcatggc agacaaacaa aagaatggaa tcaaagtga cttaagacc 1560
cgccacaaca ttgaagatgg aagcgttcaa ctacgagacc attatcaaca aaatactcca 1620
attggcgatg gccctgtcct ttaccagac aaccattacc tgtccacaca atctgccctt 1680
tcgaaagatc ccaacgaaaa gagagaccac atggctcttc ttgagtttgt aacagctgct 1740
gggattacac atggcatgga tgaactgtac aactga 1776

```

<210> 194

<211> 1707

<212> DNA

457/518

<213> Human

<400> 194

```

atgatgtggg gtgcaggcag ccctctggcc tggctctcag ctggctcagg caacgtgaat   60
gtaagcagcg tgggcccagc agagggggccc acaggctccag cgcaccact gccctcgcc   120
aaggccitggg atgtggtgct ctgcatctca ggcacccitgg tgtccctgca gaatcgct   180
gtggtggcca tcatctggg cactcctgcc ttccgtgccc ccatgttcc   240
agcctggccg tggcagacct gctggcaggc ctgggcctgg tcctgcactt tgctgctgc   300
ttctgcatcg gctcagcga gatgagcctg gtgctggttg gcgtgctggc aatggcctt   360
accgccagca tcggcagct actggccatc actgtcgacc gctacctt   420
gccctcacct actattcaga gacaacagtg acacggacct atgtgatgct ggccttagtg   480
tggggaggtg ccctgggcct ggggctgctg cctgtgctgg cctggaactg cctggatggc   540
ctgaccacat gtggcgtggt ttatccactc tccaagaacc atctggtagt tctggccatt   600
gccttcttca tgggtgttgg catcatgctg cagctctacg cccaaatctg cgcctcgtc   660
tgccgccatg ccagcagat tgcccttcag cggcacctgc tgcctgcctc ccactatgtg   720
gccacccgca agggcattgc cacacitggc gtggtgcttg gagcctttgc cgcctgctgg   780
ttgcccttca ctgtctactg cctgctgggt gatgccact ctccacctct ctacacctat   840
cttaccttgc tccctgccac ctacaactcc atgatcaacc ctatcatcta cgccttcgc   900
aaccaggatg tgcagaaagt gctgtgggct gctgctgct gctgttctc ttccaagatc   960
cccttccgat ccgctcccc cagtgatgtc gctagcaaag gagaagaact ctacttgga   1020
gttgtccaa ttcttgttga attagatggt gatgttaacg gccacaagtt ctctgtcagt   1080
ggagagggtg aaggigatgc aacatacga aaacttacc tgaagtcat ctgcactact   1140
ggcaaaactgc ctgttccatg gccaaacta gtcactactc tgtgctatgg tgttcaatgc   1200
ttttcaagat acccgatca tatgaaacgg catgactttt tcaagagtgc catgcccga   1260
ggttatgtac aggaaaggac catcttctt aaagatgacg gcaactaaa gacacgtgct   1320
gaagtcaagt ttgaaggiga tacccttgtt aatagaatcg agttaaagg tattgactt   1380
aaggaagatg gcaacattct gggacacaaa ttggaatata actataactc acacaatgta   1440
tacatcatgg cagacaaaca aaagaatgga atcaaagtga acttcaagac ccgccacaac   1500
attgaagatg gaagcgttca actagcagac cattatcaac aaaatctcc aattggcgt   1560

```


458/518

ggccctgtcc ttttaccaga caaccattac ctgtccacac aatctgccct ttcgaaagat 1620
 cccaacgaaa agagagacca catggtcctt cttgagtttg taacagctgc tgggattaca 1680
 catggcatgg atgaactgta caactga 1707

<210> 195

<211> 1803

<212> DNA

<213> Human

<400> 195

atgaacgcga ggcgccctc gctcaacgac tcccaggtagg tggtagtggc ggccgaagga 60
 gcggcggcgg cggccacagc agcagggggg ccggacacgg gcgaatgggg accccctgct 120
 gcggcggctc taggagccgg cggcggagct aatgggtctc tggagctgic ctgcagctg 180
 tcggctgggc caccgggact cctgctgcc a gcgtgaatc cgtgggacgt gctcctgtgc 240
 gtgtcgggga cagtatcgc tggagaaaac gcgctggtagg tggcgctcat cgcgtccact 300
 ccggcgctac gcacgcccac gtctgtgctg gtaggcagcc tggccaccgc tgacctgttg 360
 gcgggcgttg gccatcctt gcactttgtg ttccagtact tggtagccctc ggagactgtg 420
 agtctgtca cggtagggctt cctctgggcc tcttcgccg cctctgtcag cagcctgtctg 480
 gccattacgg tggaccgcta cctgtccctg tataacgcgc tcacctatta ctgcgccgg 540
 acccgtgttg gcgtgcacct cctgtctgcc gccacttggc cgtgtccct aggcctgggg 600
 ctgctgcccg tctgggctg gaactgcctg gcagagcgcg ccgcctgcag cgtgggtgcgc 660
 ccgctggcgc gcagccacgt ggctctgctc tccgccgct tcttcattgt cttcggcatc 720
 atgctgcacc tgtacgtgcg catctgccag gtggcttggc gccacgcgca ccagatcgcg 780
 ctgcagcagc actgcctggc gccaccccat ctgcctgcca ccagaaaggg tgtgggtaca 840
 ctggctgttg tctgggcac tttcggcgcc agctggctgc ccttcgccat ctattgcgtg 900
 gtgggcagcc atgaggaccc ggcggtctac acttacgcca ccctgtgcc cgccacctac 960
 aactccatga tcaatcccat catctatgcc ttccgcaacc aggagatcca gcgcgccctg 1020
 tggtcctctg tctgtggctg ttccagtc aaagtccct ttcgttccag gtctccagc 1080
 gaggtcgcta gaaaaggaga agaactctt actggagttag tccaattct tgttgaatta 1140

459/518

gatggatg ttaacggcca caagtctct gtcagtggag aggtgaagg tgaigcaaca 1200
 tacggaaaac ttacctgaa gtcatctgc actactggca aactgccgtg tccatggcca 1260
 acactagica ctactctgtg ctatgggtgt caatgctttt caagataccc ggaicatatg 1320
 aaacggcatg actttttcaa gaggccatg cccgaagggt atgtacagga aaggaccatc 1380
 ttcttcaaag atgacggcaa ctacaagaca cgtgctgaag tcaagttiga aggtgatacc 1440
 cttgttaata gaatcgagtt aaaaggtatt gacttcaagg aagatggcaa cattciggga 1500
 cacaattgg aatacaacta taactcacac aatgtataca tcatggcaga caaacaaaag 1560
 aatggaatca aagtgaactt caagaccgc cacaacattg aagatggaag cgttcaacta 1620
 gcagaccatt atcaacaaaa tactccaatt ggcatggcc ctgtcctttt accagacaac 1680
 cattacctgt ccacacaatc tggccttcg aaagatccca acgaaaagag agaccacatg 1740
 gtcttcttg agtttgaac agctgctggg attacacatg gcatggatga actgtacaac 1800
 tga 1803

<210> 196

<211> 1788

<212> DNA

<213> Human

<400> 196

atggctacaa cagtcctga tggttgccgc aatggcctga aatccaagta ctacagactt 60
 tgtgataagg ctgaagcttg gggcatcgtc ctgaaacgg tggccacagc tggggttg 120
 acctcgggtg ccttcatgct cactctcccg atcctcgtct gcaagggtga ggactccaac 180
 aggcgaaaaa tgcigcctac tcagtttctc ttctcctgg gtgtgttggg catctttggc 240
 ctacacctcg ccttcatcat cggactggac gggagcacag ggcccacag cttcttctc 300
 ttgggatcc tctttccat ctgcttctcc tgctgctgg ctcatgctgt cagctgacc 360
 aagctcgtcc gggggaggaa gcccctttcc ctgttggga ttctgggtct ggccgtgggc 420
 ttcagcctag tccagatgt tatcgctatt gaatatattg tctgacct gaataggacc 480
 aacgtcaatg tctttctga gctttccgct cctcgtcgca atgaagactt tgcctcctg 540
 ctacactacg tctcttctt gatggcgctg accttctca tgcctcctt caccitctgt 600

460/518

gggttccttca cgggctggaa gagacatggg gcccacatct acctcacgat gctcctctcc 660
 attgccatct ggggtggcctg gatcaccctg ctcattgttc ctgactttga ccgcaggtgg 720
 gatgacacca tcttcagctc cgccttggct gccaatggct ggggtttcct gttaggttat 780
 gttagtcctg agttttggct gctcacaag caacgaaacc ccatggatta tctgttgag 840
 gatgctttct gtaaacctca actcgtgaag aagagctatg gtgtggagaa cagagcctac 900
 tctcaagagg aaatcactca aggttttgaa gagacagggg acacgctcta tgcctcctat 960
 tccacacatt ttcagctgca gaaccagcct ccccaaaagg aattctccat cccacgggcc 1020
 cacgcttggc cgagccctta caaggactat gaagtaaaga aagagggcag cgctagcaaa 1080
 ggagaagaac tcttcactgg agttgtccca attcttgtt aattagatgg tgatgttaac 1140
 ggccacaagt tctctgtcag tggagagggt gaaggtgatg caacatacgg aaaacttacc 1200
 ctgaagtcca tctgcactac tggcaactg cctgttccat ggccaacact agtcactact 1260
 ctgtgctatg gtgttcaatg cttttcaaga taccggatc atatgaaacg gcatgacttt 1320
 ttcaagagt ccatgcccga aggttatgta caggaaagga ccatcttctt caaagatgac 1380
 ggcaactaca agacacgtgc tgaagtcaag ttgaagggtg atacccttgt taatagaatc 1440
 gagttaaaag gtattgactt caaggaagat ggcaacattc tgggacacaa attggaatac 1500
 aactataact cacacaatgt atacatcatg gcagacaaac aaaagaatgg aatcaaagtg 1560
 aacttcaaga cccgccacaa cattgaagat ggaagcggtc aactagcaga ccattatcaa 1620
 caaaatactc caattggcga tggccctgtc cttttaccag acaaccatta cctgtccaca 1680
 caatctgccc ttctgaaaga tccaacgaa aagagagacc acatggctct tcttgagttt 1740
 gtaacagctg ctgggattac acatggcatg gatgaactgt acaactga 1788

<210> 197

<211> 1974

<212> DNA

<213> Human

<400> 197

atgctggcag ctgcctttgc agactctaac tccagcagca tgaatgtgtc ctttgcctac 60
 ctccactttg ccggagggtg cctgcctctt gattcccagg actggagAAC catcatcccg 120

461/518

gctctcttgg tggctgtctg cctgggtggc ttcgtgggaa acctgtgtgt gattggcatt 180
 ctccttcaca atgcttggaa aggaaagcca tccatgatcc actccctgat tctgaatctc 240
 agcctggctg atctctccct cctgctgitt tctgcaccta tccgagctac ggcgtactcc 300
 aaaagtgitt gggatctagg ctggtttgtc tgcaagtcct ctagctgggt tatccacaca 360
 tgcatggcag ccaagagcct gacaatcgtt glgggtggcca aagtatgctt catgtatgca 420
 agigaccag ccaagcaagt gagtatccac aactacacca tctggctagt gctgggtggc 480
 atctggactg tggctagcct gttacccctg ccggaatggt tctttagcac catcaggcat 540
 catgaagggt tggaaatgtg cctcgtggat gtaccagctg tggctgaaga gtttatgtcg 600
 atgtttggta agctctaccc actcctggca ttggcccttc cattattttt tgccagcttt 660
 tatttcigga gagcttatga ccaatgtaaa aaacgaggaa ctaagactca aaatcttaga 720
 aaccagatac gctcaaagca agtcacagtg atgctgciga gcattgccat catctctgct 780
 ctcttgtggc tccccgaatg ggtagcttgg ctgtgggtat ggcatctgaa ggctgcaggc 840
 ccggcccccac cacaaggitt catagccctg tctcaagtct tgatgttttc catctcttca 900
 gcaaactctc tcatttttct tgtgatgtcg gaagagtcca gggaaggctt gaaagggtga 960
 tggaaatgga tgataaccaa aaaacctcca actgtctcag agtctcagga aacaccagct 1020
 ggcaactcag agggctcttc tgacaagggt ccatctccag aatccccagc atccatacca 1080
 gaaaaagaga aaccagctc tccctcctct ggcaaaggga aaactgagaa ggcagagatt 1140
 cccatccttc ctgacgtaga gcagttttgg catgagaggg acacagtcct tctgttacag 1200
 gacaatgacc ctatcccttg ggaacatgaa gatcaagaga cagggggaagg tgttaaaact 1260
 agcaaaggag aagaactctt cactggagtt gtcccaattc ttgttgaatt agatgggtgat 1320
 gttaacggcc acaagttctc tgtcagtga gaggggtgaag gtgatgcaac atacggaaaa 1380
 cttaacctga agtcatctg cactactggc aaactgccctg ttccatggcc aacactagtc 1440
 actactctgt gctatgggtg tcaatgcttt tcaagatacc cggatcatat gaaacggcat 1500
 gactttttca agagtgccat gcccgaagg tttgtacagg aaaggacat cttcttcaaa 1560
 gatgacggca actacaagac acgtgctgaa gtcaagtttg aagggtgata ccttgttaat 1620
 agaatcgagt taaaagggtat tgacttcaag gaagatggca acattctggg acacaaattg 1680
 gaatacaact ataactcaca caatgtatac atcatggcag acaaacaaaa gaatggaatc 1740
 aaagtgaact tcaagaccg ccacaacatt gaagaiggaa gcgttcaact agcagacat 1800
 tataacaaa atactccaat tggcgatggc cctgtccttt taccagacaa ccattacctg 1860

462/518

tccacacaat ctgccctttc gaaagatccc aacgaaaaga gagaccacat ggtcctttct 1920
 gagtttgtaa cagctgctgg gattacacat ggcatggatg aactgtacaa ctga 1974

<210> 198

<211> 1974

<212> DNA

<213> Human

<400> 198

atgctggcag ctgcccttgc agactctaac tccagcagca tgaatgtgtc ctttgctcac 60
 ctccactttg cgggagggtta cctgccctct gattcccagg actggagaac catcatcccg 120
 gctctcttgg tggctgtctg cctgggtgggc ttctgtggaa acctgtgtgt gattggcatc 180
 ctccctcaca atgcttggaa aggaaagcca tccatgatcc actccctgat tctgaatctc 240
 agcctggctg atctctccct cctgctgttt tctgcaccta tccgagctac ggcgtactcc 300
 aaaagtgttt gggatctagg ctggtttgtc tgcaagtcct ctgactgggt tateccacaca 360
 tgcattggcag ccaagagcct gacaatcgtt gtgggtggcca aagtatgctt catgtatgca 420
 agtgaccag ccaagcaagt gagtatccac aactacacca tctggctcagt gctgggtggcc 480
 atctggactg tggctagcct gttaccctg cgggaatggt tcttttagcac catcaggcat 540
 catgaagggtg tggaaatgtg cctcgtggat gtaccagctg tggctgaaga gtttatgtcg 600
 atgtttggta agctctaccc actcctggca ttggcccttc cattatcttt tggcagcttt 660
 taittctgga gagcttatga ccaatgtaaa aaacgaggaa ctaagactca aaatcttaga 720
 aaccagatac gctcaaagca agtcacagtg atgctgctga gcattgccat catctctgct 780
 gtcttgtggc tccccgaatg ggtagcttgg ctgtgggtat ggcatctgaa ggcctgcaggc 840
 ccggccccac cacaagggtt catagccctg tctcaagtct tgatgttttc catctcttca 900
 gcaaattctc tcatttttct tgtgatgtcg gaagagtcca gggaaggctt gaaagggtga 960
 tggaaatgga tgataaccaa aaaacctcca actgtctcag agtctcagga aacaccagct 1020
 ggcaactcag agggctcttc tgacaagggt ccatctccag aatccccagc atccatacca 1080
 gaaaaagaga aaccagctc tccctcctct ggcaaaggga aaactgagaa ggcagagatt 1140
 cccatccttc ctgacgtaga gcagttttgg catgagaggg acacagtcctt ttctgtacag 1200

463/518

gacaatgacc ctatccccctg ggaacatgaa gatcaagaga caggggaagg tgttaaaact 1260
 agcaaaggag aagaactctt cactggagtt gtcccaattc ttgttgaatt agatggatg 1320
 gttacggcc acaagttctc tgtcagtga gaggtgaag gtgatgcaac atacggaaaa 1380
 cttacctga agttcatctg cactactggc aaactgcctg tccatggcc aacactagtc 1440
 actactctgt gctatgggtg tcaatgcttt tcaagatacc cggatcataa gaaacggcat 1500
 gactttttca agagtggcat gccgaaggt tatgtacagg aaaggacat cttcttcaaa 1560
 gatgacggca actacaagac acgtgctgaa gtcaagtttg aaggatgata ccttggtta 1620
 agaatcgagt taaaaggtat tgacttcaag gaagatggca acattctggg acacaaattg 1680
 gaatacaact ataactcaca caatgtatac atcatggcag acaaacaaaa gaatggaatc 1740
 aaagtgaact tcaagacccg ccacaacatt gaagatggaa gcgttcaact agcagacat 1800
 tatcaacaaa atactccaat tggcgatggc cctgtccctt taccagacaa ccattacctg 1860
 tccacacaat cgtcccttcc gaaagatccc aacgaaaaga gagaccacat ggtccttctt 1920
 gagtttgtaa cagctgctgg gattacacat ggcatggatg aactgtacaa ctga 1974

<210> 199

<211> 3699

<212> DNA

<213> Human

<400> 199

atggtctgtt cggctgcccc actgctgctc ctggccacaa ctcttcccc tctgggggtca 60
 ccagttgccc aagcatccca acctggacag agtcaggctg gaggggaatc tggatctggg 120
 cagctcctgg accaagagaa tggagcaggg gaatcagcgc tggctctccgt ctatgtacat 180
 ctggactttc cagataagac ctggccccct gaactctcca ggacactgac tctccctgct 240
 gccicagctt cctcttcccc aaggcctctt ctactggcc tcagactcac aacagagtgt 300
 aatgtcaacc acaaggggaa ttctatttgt gcttgcctct ctggctacca gtggaacacc 360
 agcatctgcc tccattaccc tcttgtcaa agcctccaca accaccagcc ttgtggctgc 420
 ctgtcttcca gccatccga acccggttac tggcagttgc tggcaccigt ccccgggatc 480
 ctcaacctga actcccagct gcagatgcct ggtgacacgc tgagccigac tctccatctg 540

464/518

agccaggagg ccaccaacct gagctgggtc ctgaggcacc caggagagccc cagtcccatc 600
 ctctgcagc caggacaca ggtgtctgtg acttccagcc acggccaggc tgccctcagc 660
 gtctccaaca tgtcccatca ctgggcaggt gagiacaatga gctgcttcga ggcccagggc 720
 ttcaagtgga acctgtatga ggtggtagg gtgcccttga aggcgacaga tgtggctcga 780
 ctccatacc agctgtccat ctctgtgcc acctccctg gcttccagct gagctgtgc 840
 atccccagca caaacctggc ctacaccgc gcctggagcc ctggagagg cagcaaagct 900
 tcttcttca acgagtcagg ctctcagtgc ttgtgtctgg ctgttcagcg ctgccgatg 960
 gctgacacca cgtacacttg tgacctgcag agcctgggcc tggctccact cagggtcccc 1020
 atctccatca ccatcatcca ggatggagac atcacctgcc ctgaggacgc ctgggtgctc 1080
 acctggaatg tcaccaaggc tggccacgtg gcacaggccc catgtcctga gagcaagagg 1140
 ggcatagtga ggaggctctg tggggctgac ggagctctgg ggccgggtcca cagcagctgc 1200
 acagatgcga ggctcctggc ctgtttcact agaaccaagc tctgtcaggc aggccagggc 1260
 agtctgtctg aggaggtgcc acagatcctg gcacagctgc cagggcaggc ggacagaggca 1320
 agttcacct cagacttact gacctgtctg agcaccatga aatacgtggc caaggtggtg 1380
 gcagaggcca gaatacagct tgaccgcaga gccctgaaga atctcctgat tgccacagac 1440
 aaggtcctag atatggacac caggtctctg tggacctgg cccaagccc gaagccctgg 1500
 gcaggctcga ctctcctgtt ggctgtggag accttggcat gcagcctgtg cccacaggac 1560
 tacccttctg ctttcagctt acctaatgtg ctgtgcaga gccagctgtt tggaccacg 1620
 ttctctgtg actacagcat ctcttccct actcgcccc cactgcaggc tcagattccc 1680
 aggcactcac tggccccatt ggtccgtaat ggaactgaaa taagtattac tagcctggtg 1740
 ctgcgaaaac tggaccacct tctgccctca aactatggac aagggtggg ggattccctc 1800
 tatgccactc ctggcctggt ccttgtcatt tccatcatgg caggtagccg ggcttcagc 1860
 caggagagg tcatcatgga ctgtgggaac acagatggtt cccctcactg tgtcttctgg 1920
 gatcacagtc tcttccaggg cagggggggt tggccaaaag aagggtgcca ggcacaggtg 1980
 gccagtgcca gcccactgc tcagtgcctc tgccagcacc tcactgcctt ctccgtcctc 2040
 atgtccccc acactgttcc ggaagaacc gctctggcgc tgctgactca agtgggcttg 2100
 ggagcttcca tactggcgct gcttgtgtgc ctgggtgtgt actggctggt gtggagagtc 2160
 gtgggtcgga acaagatctc ctatttccgc cagccgccc tgctcaacat ggtgttctgc 2220
 ttgtggccg cagacacttg ctctctgggc gcccattcc tctctccagg gcccgaagc 2280

465/518

```

ccgctctgcc ttgctgccgc ctccctctgt catttctct acctgccac cttttctgg 2340
atgctggcgc aggccctggg gtggccac cagctgctt ttgtcttca ccagctggca 2400
aagcaccgag ttctccccc catggctc ctgggctacc tgtgccact ggggttggca 2460
gggtgcacc tgggctcta cctacctaa gggcaatacc tgaggagg ggaatgctgg 2520
ttggatggga agggagggg gtatacacc ttctggggc cagtctggc calcataggc 2580
gtgaatgggc tggtagc catggccat ctgaagtgc tgagacctc gctgtcagag 2640
ggacccccag cagagaagcg ccaagctct ctgggggtga tcaaagccct gctcattct 2700
acacccatct ttggcctcac ctggggctg ggcctggcca ctctgttaga ggaagtctcc 2760
acggctccctc attacatctt caccattctc aacacccctc agggcgctct catctattg 2820
tttgggtgcc tcatggacag gaagatacaa gaagcttgc gcaaagcct ctgccgcgc 2880
caagccccca gctccacat ctccctggcc acaaatgaag gctgcatctt ggaacacagc 2940
aaaggaggaa gcgacactgc caggaagaca gatgcttcag aggttagcaa aggagaagaa 3000
ctcttcactg gagttgtccc aattcttgt gaattagatg gtgatgttaa cggccacaag 3060
ttctctgtca gtggagagg tgaaggtag gcaacatag gaaaacttac cctgaagtc 3120
atctgcacta ctggcaaaact gctgttcca tggccaacac tagtactac tctgtgctat 3180
gggtttcaat gcttttcaag ataccggat catatgaaac ggcattgact tttcaagagt 3240
gccatgcccg aaggttatgt acaggaaagg accatcttct tcaaagatga cggcaactac 3300
aagacacgtg ctgaagtcaa gtttgaaggt gatacccttg ttaatagaat cgagttaaaa 3360
ggatttgact tcaaggaaga tggcaacatt ctgggacaca aattggaata caactataac 3420
tcacacaatg tatacatcat ggcagacaaa caaagaatg gaatcaaagt gaacttcaag 3480
acccgccaca acattgaaga tggaagcgtt caactagcag accattatca aaaaatact 3540
ccaattggcg atggccctgt ccttttacca gacaaccatt acctgtccac acaatctgcc 3600
ctttcgaaag atcccaacga aaagagagac cacatggctc ttcttgagtt tgaacagct 3660
gctgggatta cacatggcat ggatgaactg tacaactga 3699

```

<210> 200

<211> 2796

<212> DNA

<213> Human

466/518

<400> 200

```

atgactcccc agtcgtctgt gcagacgaca ctgttccctgc tgagtctgtct ctccctggtc      60
caaggtagccc acggcagggg ccacagggaa gactttcgtct tctgcagcca gcggaaccag    120
acacacagga gcagcctcca ctacaaaccc acaccagacc tgcgcctctc catcgagaac    180
tccgaagagg ccttcacagt ccatgcccct ttccctgcag cccaccctgc ttcccgatcc    240
ttccctgacc ccagggggcct ctaccacttc tgcctctact ggaaccgaca tgctgggaga    300
ttacatcttc tctatggcaa gcgtgacttc ttgctgagtg acaaagcctc tagcctcctc    360
tgcttccagc accaggagga gagcctggct cagggccccc cgctgttagc cacttctgtc    420
acctcctggg ggagccctca gaacatcagc ctgcccagtg ccgccagctt caccttctcc    480
ttccacagtc ctccccacac ggccgctcac aatgcctcgg tggacatgtg cgagctcaaa    540
agggacctcc agctgctcag ccagttcctg aagcatcccc agaaggcctc aaggaggccc    600
tcggctgccc ccgccagcca gcagttgcag agcctggagt cgaaactgac ctctgtgaga    660
ttcatggggg acatgggtgtc cttcgaggag gaccggatca acgccacggt gtggaagctc    720
cagcccacag ccggcctcca ggacctgcac atccactccc ggcaggagga ggagcagagc    780
gagatcatgg agtactcggg gctgtctgct cgaacactct tccagaggac gaaaggccgg    840
agcggggagg ctgagaagag actcctcctg gtggacttca gcagccaagc cctgttccag    900
gacaagaatt ccagccaagt cctgggtgag aaggctcttg ggattgtggt acagaacacc    960
aaagtagcca acctcacgga gcccgtagtg ctacatttcc agcaccagct acagccgaag   1020
aatgtgactc tgcaatgtgt gtcttggtt gaagaccca cattgagcag cccggggcat   1080
tgagcagtg ctgggtgtga gaccgtcagg agagaaaccc aaacatcctg cttctgcaac   1140
cacttgacct accttgagcgt gctgatggtc tctcggtagg aggtggacgc cgtgcacaag   1200
cactacctga gcctcctctc ctacgtgggc tgtgtcgtct ctgccctggc ctgccttgtc   1260
accattgccg cctacctctg ctccaggggtg cccctgccgt gcaggaggaa acctcgggac   1320
tacaccatca aggtgcacat gaacctgctg ctggccgtct tctgtctgga cagcagcttc   1380
ctgctcagcg agccggtagg cctgacaggc tctgaggctg gctgccgagc cagtgccatc   1440
ttcctgcact tctccctgtc cactgcctt tcttgatgg gcctcgagggt gtacaacctc   1500
taccgactcg tggtaggagt cttggcacc tatgtccctg gctacctact caagctgagc   1560
gccatgggct ggggcttccc catctttctg gtgacgctgg tggccctggt ggatgtggac   1620

```

467/518

```

aactaigggc ccatcatctt ggctgtgcat aggaticcag agggcgatcat ctacccttcc 1680
atgtgtcggg tccgggacac cctgggcagc tacatcacca acctgggcct cttcagcctg 1740
gtgtttctgt tcaacatggc catgctagcc accatgggtg tgcagatcct ggggctgcgc 1800
ccccacacc caaaagtggc acatgtgtg acactgtgtg gcctcagcct ggtccttggc 1860
ctgcccctgg ccttgatctt cttctccitt gcttctggca ccttcagct tgtcgtccic 1920
taccttttca gcatcatcac ctcttccaa ggcttccca tcttcatctg gtactgttcc 1980
atgcggctgc agggccgggg tggccctcc cctctgaaga gcaactcaga cagcgccagg 2040
ctccccatca gctcgggcag caccctgtcc agccgatct ctagcaaagg agaagaactc 2100
ttcactggag ttgtcccaat tcttgttgaa ttagatgggt atgttaacgg ccacaagttc 2160
tctgtcagtg gagagggtga aggtgatgca acatacggaa aacttaccct gaagtctatc 2220
tgcactactg gcaaactgcc tgttccatgg ccaacactag tcactactct gtgctatggt 2280
gttcaatgct tttcaagata cccggatcat atgaaacggc atgacttttt caagagtgcc 2340
atgccgaag gttatgtaca ggaaaggacc atcttcttca aagatgacgg caactacaag 2400
acacgtgtgt aagtcaagtt tgaaggatg acccttggtt atagaatcga gttaaaaggt 2460
attgacttca aggaagatgg caacattctg ggacacaaat tggaatacaa ctataactca 2520
cacaatgtat acatcatggc agacaaacaa aagaatggaa tcaaagtga cttcaagacc 2580
cgccacaaca ttgaagatgg aagcgttcaa ctacgagacc attatcaaca aaatactcca 2640
attggcgatg gccctgtcct ttaccagac aaccattacc tgtccacaca atctgccctt 2700
tcgaaagatc ccaacgaaaa gagagaccac atggtccttc ttgagtttgt aacagctgtc 2760
gggattacac atggcatgga tgaactgtac aactga 2796

```

<210> 201

<211> 4755

<212> DNA

<213> Human

<400> 201

```

atgaaatccc caaggagaac cactttgtgc ctcatgttta ttgtgattta ttcttccaaa 60
gctgcactga actggaatta cgagtctact attcatcctt tgagtcctta tgaacatgaa 120

```

468/518

ccagctggtg aagaggcact gaggcaaaaa cgagccgttg ccacaaaaag tcctacggct	180
gaagaatata ctgttaatat tgagatcagt ttigaaaatg catccttccg ggatcctatc	240
aaagcctact tgaacagcct cagtittcca attcatggga ataacaciga ccaaattacc	300
gacattttga gcataaatgt gacaacagtc tgcagacctg ctggaaatga aatctgggtg	360
tccitgcgaga caggttatgg gtggcctcgg gaaagggtgc ttcacaatct catttgtcaa	420
gagcgtgacg tcttctccc agggcaccat tgcagttgcc ttaaagaact gcctcccaat	480
ggaccttttt gccitgctta ggaagatgtt accctgaaca tgagagtcag actaaatgta	540
ggctttcaag aagacctcat gaacacttcc tccgccctct ataggctcta caagaccgac	600
ttggaaacag cgttccggaa gggttacgga atttaccag gcttcaaggc cgtgactgtg	660
acagggttca agtcitggaag tgtgtgtgtg acataitgag tcaagactac accaccatca	720
cttgagttaa tacataaagc caatgaacaa gtgtacaga gccitcaatca gacctacaaa	780
atggactaca acitctttca agcagttact atcaatgaaa gcaatttctt tgtcacacca	840
gaaatcatct ttgaaggga cacagtcagt ctgggtgtgtg aaaaggaagt tttgtcctcc	900
aatgtgtctt ggcgtatga agaacagcag ttggaaatcc agaacagcag cagattctcg	960
atttacaccg cacttttcaa caacatgact tcgggtgtcc agctcaccat ccacaacatc	1020
actccaggtg atgcaggtga atatgtttgc aaactgatat tagacatttt tgaatatgag	1080
tgcaagaaga aaatagatgt tatgcccatc caaattttgg caaatgaaga aatgaagggtg	1140
atgtgcgaca acaatcctgt atctttgaac tgctgcagtc agggtaatgt taattggagc	1200
aaagtagaat ggaagcagga aggaaaaata aatattccag gaacccctga gacagacata	1260
gattctagct gcagcagata caccctcaag gctgatggaa cccagtgtcc aagcgggtcg	1320
tcitggaacaa cagtcatcta cacttgtgag ttcatcagtg cctatggagc cagaggcagt	1380
gcaaacataa aagtacatt catctctgtg gccaatctaa caataacccc ggaccaatt	1440
tcitgtttctg agggacaaaa cttttctata aaatgcatca gtgatgtgag taactatgat	1500
gaggtttatt ggaacacttc tgctggaatt aaaatatacc aaagatttta taccagagg	1560
aggtatcttg atggagcaga atcagtactg acagtcaaga cctcgaccag ggagtggat	1620
ggaacctatc actgcataat tagatataag aattcataca gtattgcaac caaagacgtc	1680
attgttcacc cgtgcctct aaagctgaac atcatggttg atcctttgga agctactgtt	1740
tcatgcagtg gtcccatca catcaagtgc tgcataagagg aggatggaga ctacaaagtt	1800
actttccata tgggttcctc atcccttccg gctgcaaaaag aagttaacaa aaaacaagtg	1860

469/518

tgctacaaac acaatttcaa tgcaagctca gtttcctggg gticaaaaac tgttgatgtg 1920
 tgttgtcact ttaccaatgc tgctaataat tcagtttggg gcccatctat gaagctgaat 1980
 ctggttcctg gggaaaacat cacatgccag gatcccgtaa taggtgtcgg agagccgggg 2040
 aaagtcattc agaagctatg ccggttttca aacgttccca gcagccctga gattccatt 2100
 ggccgggacca tcatttaca atgtgtaggc tcccagtggg aggagaagag aaatgactgc 2160
 atctctgccc caataaacag tctgtccag atggctaagg ctttgatcaa gagccccctt 2220
 caggatgaga tgctccctac atacctgaag gatctttcta ttagcataga caaagcggaa 2280
 catgaaatca gctcttctcc tgggagtctg ggagccatta ttaacatcct tgatctgctc 2340
 tcaacagttc caaccaagt aaattcagaa atgatgacgc acgtgctctc tacggttaat 2400
 gtcatccttg gcaagccgt cttgaacacc tggaagggtt tacaacagca atggaccaat 2460
 cagagttcac agctactaca ttcagtggaa agattttccc aagcattaca gtcaggagat 2520
 agccctcctt tgtccttctc ccaaactaat gtgcagatga gcagcacggg aatcaagtc 2580
 agccaccag aaacctatca acagagggtt gttttcccat acttgacct ctggggcaat 2640
 gtggtcattg acaagagcta tctagaaaac ttgcagtcgg attcgtctat tgtcaccatg 2700
 gctttcccaa ctctccaagc catccttgct caggatatcc aggaaaataa ctttgagag 2760
 agcttagtga tgacaaccac tgcagccac aatacgacta tgccattcag gatttcaatg 2820
 acttttaaga acaatagccc ttcaggcggc gaaacgaagt gtgtcttctg gaacttcagg 2880
 cttgccaaca acacaggggg gttggacagc agtgggtgct atgttgaaga aggtgatggg 2940
 gacaatgtca cctgtatctg tgaccacctt acatcattct ccattctcat gtccctgac 3000
 tcccagatc ctagtctctt cctgggaata ctcttgata ttatttctta tgttgggtg 3060
 ggcttttcca tcttgagctt ggcagcctgt ctagtgtgg aagctgtgtg gtggaaatcg 3120
 gtgaccaaga atcgacttc ttatatgcgc cacacctgca tagtgaatat cgtgcctcc 3180
 cttctggtcg ccaacacctg gticattgtg gtctgtcca tccaggacaa tgcctacata 3240
 ctctgcaaga cagcctgtgt ggctgccacc ttcttcatcc acttcttcta cctcagcgtc 3300
 ttcttctgga tgcagacact gggcctcatg ctgttctatc gcctggtttt cattctgcat 3360
 gaaacaagca ggctcactca gaaagccatt gccttctgtc ttggctatgg ctgccactt 3420
 gccatctcgg tcatcacgtt gggagccacc cagccccggg aagctctatac gaggaagaat 3480
 gtctgttggc tcaactggga ggacaccaag gccctgtctg ctttcgcat cccagcactg 3540
 atcattgttg tggatgaacat aacctcact attgtgttca tcaccaagat cctgaggcct 3600

470/518

tccattggag acaagccatg caagcaggag aagagcagcc tgtttcagat cagcaagagc 3660
 atiggggtcc tcacaccact ctigggcctc acttggggtt ttggtctcac cactgtgttc 3720
 ccagggacca accttgtgtt ccataatcata ttggccatcc tcaatgtctt ccagggatta 3780
 ttcatitttac tctttggatg cctctgggat ctgaaggtag aggaagcttt gctgaataag 3840
 ttttcattgt cgagatggtc ttacacagcac tcaaagtcaa catccctggg ttcattccaca 3900
 cctgtgtttt ctatgagttc tccaatatca aggagattta acaatttgtt tggtaaaaca 3960
 ggaacgtata atgtttccac ccagaagca accagctcat ccctggaaaa ctcatccagt 4020
 gcttcttctg tgctcaacgc tagcaaagga gaagaactct tcaactggagt tgcaccaatt 4080
 cttgttgaat tagatggtag tgtaaacggc cacaagtctt ctgtcagtag agagggtgaa 4140
 ggtgatgcaa catacggaaa acttaccctg aagttcatct gcactactgg caaactgcct 4200
 gtccatggc caacactagt cactactctg tgctatggtag ttcaatgctt ttcaagatac 4260
 ccggatcata tgaaacggca tgactttttc aagagtgccca tgcccgaagg ttatgtacag 4320
 gaaaggacca tcttcttcaa agatgacggc aactacaaga cacgtgctga agtcaagttt 4380
 gaaggtagata cctttgttaa tagaatcgag ttaaaaggta ttgacttcaa ggaagatggc 4440
 aacattctgg gacacaaatt ggaatacaac tataactcac acaatgtata catcatggca 4500
 gacaaacaaa agaattggaat caaagtgaac ttcaagacc gccacaacat tgaagatgga 4560
 agcgttcaac tagcagacca ttatcaacaa aatactccaa ttggcgatgg cctgtctt 4620
 ttaccagaca accattacct gtccacacaa tctgcccttt cgaaagatcc caacgaaaag 4680
 agagaccaca tggctcttct tgagtttgta acagctgctg ggattacaca tggcatggat 4740
 gaactgtaca actga 4755

<210> 202

<211> 1938

<212> DNA

<213> Human

<400> 202

atgagcctca actcctccct cagctgcagg aaggagctga gtaatctcac tgaggaggag 60
 ggtggcgaag ggggcgtcat catcaccag ttcatcgcca tcattgcat caccattttt 120

471/518

gtctgccitgg gaaacctggt catcgtggtc acctgtiaca agaagtccta cctccctcacc 180
 ctcagcaaca agttcgtctt cagccctgact ctgtccaact tccgtctgtc cgtgttgggtg 240
 ctgcccttttg tggtagcagag ctccatccgc agggaatgga tctttgggtg agtgttgggtg 300
 aactttctctg ccttcctcta cctgtgatc agctctgcca gcatgctaac cctcggggtc 360
 attgccatcg accgtacta tgcgttcctg taccctatgg tgtaccccat gaagatcaca 420
 gggaaccggg ctgtgatggc acttgtctac atctggcttc actcgtctat cggctggctg 480
 ccacccctgt ttggttgggtc atccgtggag tttagcaggt tcaaattgat gtgtgtggct 540
 gcttggcacc gggagccttg ctacacggcc ttctggcaga tctgggtgtc cctcttcccc 600
 tttctggica tgcgtgtgtg ctatggcttt atcttccgcg tggccagggt caaggcacgc 660
 aaggtgcact gtggcacagt cgtcatcgtg gaggaggatg ctacagggac cgggaggaag 720
 aactccagca cctccacctc ctcttcaggc agcaggagga atgcctttca ggggtgtgtc 780
 tactcggcca accagtgcga agccctcctc accatccttg tggctctcgg tgccttcctg 840
 gtcacctggg gccctacat ggttgtctc gccctcagg cctctcggg gaaaagctcc 900
 gtctccccga gccctggagac ttgggccaca tggctgtcct ttgccagcgc tgcctgccac 960
 cccctgatct atggactctg gaacaagaca gtctgcaaag aactactggg catgtgtctt 1020
 ggggaccggt attatcggga accatttgtg caacgacaga ggacttccag gctcttcagc 1080
 atttccaaca ggatcacaga cctgggcctg tccccacacc tcactgcgt catggcaggt 1140
 ggacagcccc tggggcacag cagcagcacg ggggacacig gcttcagctg ctcccaggac 1200
 tcaggtaacc tgcgtgtctt agctagcaaa ggagaagaac tcttacttg agttgtccca 1260
 attcttgttg aattagatgg tgatgttaac ggccacaagt tctctgtcag tggagagggt 1320
 gaaggtgatg caacatacgg aaaacttacc ctgaagtca tctgactac tggcaaaactg 1380
 cctgttccat ggccaacact agtactact ctgtgctatg gtgttcaatg cttttcaaga 1440
 taccggatc atatgaaacg gcatgacttt ttcaagagt ccatgcccga aggttatgta 1500
 caggaaagga ccatcttctt caaagatgac ggcaactaca agacacgtgc tgaagtcaag 1560
 ttggaagggt atacccttgt taatagaatc gagttaaaag gtattgactt caaggaagat 1620
 ggcaacattc tgggacacaa attggaatac aactataact cacacaatgt atacatcatg 1680
 gcagacaaac aaaagaatgg aatcaaagt aacttcaaga cccgccaca cattgaagat 1740
 ggaagcgttc aactagcaga ccattatcaa caaaatact caattggcga tggccctgtc 1800
 cttttaccag acaaccatta cctgtccaca caatctgccc ttctgaaaga tcccaacgaa 1860

472/518

aagagagacc acatggtcct tcttgagttt gtaacagctg ctgggattac acatggcatg 1920
 gatgaactgt acaactga 1938

<210> 203

<211> 1914

<212> DNA

<213> Human

<400> 203

atggctcaaa gggccttccc gaatccttat gctgattata acaaatccct ggccgaaggc 60
 tactttgatg ctgccgggag gctgactcct gagttctcac aacgcttgac caataagatt 120
 cgggagcttc ttacagcaat ggagagaggc ctgaaatcag cagaccctcg ggaatggcacc 180
 ggttacactg gctgggcagg tattgctgtg ctttacttac atctttatga tgtatttggg 240
 gaccctgcct acctacagtt agcacatggc tatgtaaagc aaagtctgaa ctgcttaacc 300
 aagcgctcca tcaccttccct ttgtggggat gcaggccccc tggcagtggc cgctgtgcta 360
 tatcacaaga tgaacaatga gaagcaggca gaagattgca tcacacggct aattcaccta 420
 aataagattg atcctcatgc tccaaatgaa atgctctatg ggccaatagg ctacatctat 480
 gctcttcttt ttgtcaataa gaactttgga gggaaaaga ttcttcaaag ccatattcag 540
 cagatttgtg aaacaatttt aacctctgga gaaaacctag ctaggaagag aaacttcacg 600
 gcaaagtctc cactgatgta tgaatggtag caggaatatt atgtaggggc tgctcatggc 660
 ctggctggaa ttattacta cctgatgcag ccagaccttc aagttagcca aggaagtta 720
 catagtttgg tcaagcccag ttagacttac gctgccagc tgaaattccc ttctggcaat 780
 taccctccat gtagagtga taatcgagat ctgcttgccc attggtgcca tggcgccct 840
 ggggtaatct acatgctcat ccaggcctat aaggtattca gagaggaaaa gtatctctgt 900
 gatgcctatc agtgtgctga tgtgatctgg caatatgggt tgcgaagaa gggatatggg 960
 ctgtgccacg gttctgcagg gaatgcctat gccttctga cactctacaa cctcacacag 1020
 gacatgaagt acctgtatag ggctgtgaag ttgtctgaat ggtgcttaga gtatggagaa 1080
 catggatgca gaacaccaga caccctttc tctctctttg aaggaatggc tggaacaata 1140
 tatttcttgg ctgacctgct agtccccaca aaagccaggt tccctgcatt tgaactcgct 1200

473/518

agcaaaggag aagaactctt cacitggagt gicccaattc ttgttgaatt agatggtgat 1260
 gttacggcc acaagttctc tgtcagtga gaggtgaag gtgatgcaac atacggaaaa 1320
 ctaccctga agtcatctg cactactggc aaatgcctg ttccatggcc aacactagtc 1380
 actactctgt gctatggtgt tcaatgcttt tcaagatacc cggatcatat gaaacggcat 1440
 gactttttca agagtgccat gccgaaggt tatgtacagg aaaggacat ctctttcaaa 1500
 gatgacggca actacaagac acgtgcigaa gtcaagtttg aaggatgatac ccttgttaat 1560
 agaatcgagt taaaagggtat tgacttcaag gaagatggca acattctggg acacaaattg 1620
 gaatacaact ataactcaca caatgtatac atcatggcag acaaacaaaa gaatggaatc 1680
 aaagtgaact tcaagacccg ccacaacatt gaagatggaa gcgttcaact agcagacat 1740
 tatcaacaaa atactccaat tggcgatggc cctgtccttt taccagacaa ccattacctg 1800
 tccacacaat ctgccctttc gaaagatccc aacgaaaaga gagaccacat ggtccttctt 1860
 gagtttgtaa cagctgtgg gattacacat ggcatggatg aactgtacaa ctga 1914

<210> 204

<211> 1842

<212> DNA

<213> Human

<400> 204

atggcgaacg cgagcgagcc gggatggcagc ggcgggcgcg aggcggccgc cctgggcctc 60
 aagctggcca cgctcagcct gctgctgtgc gtgagcctag cgggcaacgt gctgttcgcg 120
 ctgctgatcg tgcgggagcg cagcctgcac cgcgccccgt actacctgct gctcgacctg 180
 tgcctggccg acgggctgcg cgcgctcgcc tgcctcccgg ccgtcatgct ggcgggcgcg 240
 cgtgcggcgg ccgcggcggg ggcgccgccc ggcgcgctgg gctgcaagct gctcgccctc 300
 ctggccgcgc tcttctgctt ccacgcgcc ttcctgctgc tggcggtggg cgtcaccgcg 360
 tacttggcca tcgcgcacca ccgcttctat gcagagcgcc tggccggctg gccgtgcgcc 420
 gccatgctgg tgtgcgccgc ctgggcgtg gcgctggccg cggccttccc gccagtgtg 480
 gacggcggtg gcgacgacga ggacgcgcc tgcgccctgg agcagcggcc cgacggcgcc 540
 cccggcgcgc tgggcttctt gctgctgtg gccgtgggtg tggcgccac gcacctcgtc 600

474/518

tacctccgcc tgctcttctt catccacgac cgccgcaaga tgcggcccg gcgccttggtg 660
 cccgccgtca gccacgactg gaccttccac ggcccgggcg ccaccggcca ggcggccgcc 720
 aactggacgg cgggcttcgg ccgcccggccc acgcccggcg cgcttggtgg catccggccc 780
 gcaggggccgg gccgcggcgc gcgcccctc ctgctgtgg aagaattcaa gacggagaag 840
 aggctgtgca agatgttcta cgccgtcag ctgctcttcc tgctcctctg ggggccctac 900
 gtcgtggcca gctacctgcg ggtcctgggtg cggcccggcg ccgtccccc ggcttacctg 960
 acggcctcgg tgtggctgac ctgcgcgag gccggcatca acccgtcgt gtgcttctc 1020
 ttcaacaggg agctgagga ctgcttcagg gccagttcc ctgctgcca gagccccgg 1080
 accaccagg cgacctatcc ctgcgacctg aaaggcattg gtttagctag caaaggagaa 1140
 gaactcttca ctggagtgt cccaattctt gtgaattag atgggtgatgt taacggccac 1200
 aagttctctg tcagtggaga ggtgaaggt gatgcaacat acggaaaact taccctgaag 1260
 ttcatctgca ctactggcaa actgcctgtt ccatggccaa cactagtcac tactctgtgc 1320
 tatggtgttc aatgcttttc aagatacccg gatcatatga aacggcatga ctttttcaag 1380
 agtgccatgc ccgaaggta tgtacaggaa aggacctct tcttcaaaga tgacggcaac 1440
 tacaagacac gtgctgaagt caagtttgaa ggtgataccc ttgttaatag aatcgagta 1500
 aaaggtattg acttcaagga agatggcaac attctgggac acaaattgga atacaactat 1560
 aactcacaca atgtatacat catggcagac aaacaaaaga atggaatcaa agtgaacttc 1620
 aagaccggcc acaacattga agatggaagc gttaactag cagaccatta tcaacaaaat 1680
 actccaattg gcatggccc tgctctttta ccagacaacc attacctgtc cacacaatct 1740
 gccctttcga aagatcccaa cgaaaagaga gaccacatgg tccttcttga gtttgtaaca 1800
 gctgctggga ttacacatgg catggatgaa cgtacaact ga 1842

<210> 205

<211> 3438

<212> DNA

<213> Human

<400> 205

atggacacct cccggctcgg tgtgctcctg tccttgccctg tgctgctgca gctggcgacc 60

475/518

gggggcagct ctcccaggtc tgggtgtgtg ctgaggggct gcccacaca ctgtcatigc 120
 gagcccgacg gcaggatgtt gctcagggig gactgtctcg acctggggct ctcgagctg 180
 ccttccaacc tcagcgtctt caccctctac ctagacctca gtatgaacaa catcagtcag 240
 ctgctcccgga atccccctgcc cagtctccgc ttcctggagg agttacgtct tgcgggaaac 300
 gctctgacat acgttcccaa gggagcattc actggccttt acagtcttaa agttcttatg 360
 ctgcagaata atcagctaag acacgtaccc acagaagctc tgcagaattt gcgaagcctt 420
 caatccctgc gtciggatgc taaccacatc agctatgtgc cccaagctg tttcagtggc 480
 ctgcattccc tgaggcacct gtggctggat gacaatgcgt taacagaaat ccccgctccag 540
 gcttttagaa gtttatcggc attgcaagcc atgacctigg ccttgaacaa aatacaccac 600
 ataccagact atgcccttgg aaacctctcc agcttggtag ttctacatct ccataacaat 660
 agaatccact ccttgggaaa gaaatgcttt gatgggctcc acagcctaga gactttagat 720
 ttaaattaca ataaccttga tgaattcccc actgcaattt ggacactctc caaccitaaa 780
 gaactaggat ttcatagcaa caatacagg tcgatacttg agaaagcatt tgiaggcaac 840
 ccttctctta ttacaatata tttctatgac aatcccatcc aatttgitgg gagatctgct 900
 tttcaacatt tacctgaact aagaacactg actctgaatg gtgcctcaca aataactgaa 960
 tttccigatt taactggaac tgcaaacctg gagagtctga ctttaactgg agcacagatc 1020
 tcactctctc ctcaaaccgt ctgcaatcag ttacctaatc tccaagtgct agatctgtct 1080
 tacaacctat tagaagattt acccagtttt tcagtctgcc aaaagcttca gaaaattgac 1140
 ctaagacata atgaaatcta cgaaattaaa gttgacactt tccagcagtt gcttagcctc 1200
 cgatcgctga atttggcttg gaacaaaatt gctattatc accccaatgc attttccact 1260
 ttgccatccc taataaagct ggacctatcg tccaacctcc tgtcgtcttt tcctataact 1320
 gggttacatg gtttaactca cttaaaatta acaggaaatc atgccttaca gagcttgata 1380
 tcacttgaaa acittccaga actcaagggt atagaaatgc cttatgctta ccagtgtgt 1440
 gcatttggag tgtgtgagaa tgcciatag atttctaate aatggaataa aggtgacaac 1500
 agcagtatgg acgaccttca taagaaagat gctggaatgt ttcaggctca agatgaacgt 1560
 gaccttgaag atttctgtct tgactttgag gaagacctga aagcccttca ttcagtgcag 1620
 tgttaccctt ccccaggccc cttaaacccc tgtaaacacc tgcctgatgg ctggctgatc 1680
 agaattggag tgggacat agcagttctg gcacttactt gtaatgcttt ggtgacttca 1740
 acagttttca gatccctctt gtacatttcc ccattaaac tgttaattgg ggtcatcgca 1800

476/518

gcagtgaaca tgctcacggg agtctccagt gccgtgctgg ctggtgtgga tgcgttcact 1860
 tttggcagct ttgcacgaca tgggtgctgg tgggagaatg gggttggttg ccatgtcatt 1920
 ggttttttgt ccatttttgc ttcagaatca tctgttttcc tgcttactct ggcagccctg 1980
 gagcgtgggt tctctgtgaa atattctgca aaatttgaaa cgaaagctcc attttctagc 2040
 ctgaaagtaa tcattttgct ctgtgccctg ctggccttga ccatggccgc agttcccctg 2100
 ctgggtggca gcaagtatgg cgctccctt cctgtccctg ctttgccctt tggggagccc 2160
 agcaccatgg gctacatggt cgctctcctc ttgctcaatt ccttttgctt cctcatgatg 2220
 accatigcct acaccaagct ctactgcaat ttggacaagg gagacctgga gaatatitgg 2280
 gactgctcta tggtaaaaca cattgccctg ttgctcttca ccaactgcat cctaaactgc 2340
 cctgtggctt tcttgtcctt ctctcttita ataaacctta cattatcag tcttgaagta 2400
 attaagtita tcttcttggt ggtagtccca ctctctgcat gtctcaatcc ccttctctac 2460
 atcttgttca atctctactt taaggaggat ctggtgagcc tgagaaagca aacctacgtc 2520
 tggacaagat caaaacaccc aagcttgatg tcaattaaact ctgatgatgt cgaaaaacag 2580
 tctgtgact caactcaagc cttggtaacc ttaccagct ccagcatcac ttaagacctg 2640
 cctcccagtt ccgtgccatc accagcttat ccagtgactg agagctgcca tctttcctct 2700
 gtggcatttg tcccatgtct cgctagcaaa ggagaagaac tcttcactgg agttgtccca 2760
 attcttgttg aattagatgg tgatgttaac ggccacaagt tctctgtcag tggagagggt 2820
 gaaggtgatg caacatacgg aaaacttacc ctgaagtica tctgcactac tggcaaaactg 2880
 cctgttccat ggccaacact agtcactact ctgtgctatg gtgttcaatg cttttcaaga 2940
 taccgggatc atatgaaacg gcattgactt ttcaagagt ccatgcccga aggttatgta 3000
 caggaaagga ccatcttctt caaagatgac ggcaactaca agacacgtgc tgaagtcaag 3060
 tttgaaggig atacccttgt taatagaatc gatttaaaag gtattgactt caaggaagat 3120
 ggcaacattc tgggacacaa attggaatac aactataact cacacaatgt atacatcatg 3180
 gcagacaaac aaaagaatgg aatcaaagt aacttcaaga cccgccacaa cattgaagat 3240
 ggaagcgttc aactagcaga ccattatcaa caaaatactc caattggcga tggccctgtc 3300
 cttttaccag acaaccatta cctgtccaca caatctgccc ttctgaaaga tcccaacgaa 3360
 aagagagacc acatggtcct tcttgagttt gtaacagctg ctgggattac acatggcatg 3420
 gatgaactgt acaactga 3438

477/518

<210> 206

<211> 1683

<212> DNA

<213> Human

<400> 206

```

atggattcaa ccatcccagt cttgggtaca gaactgacac caatcaacgg acgtgaggag    60
actccttgct acaagcagac cctgagcttc acggggctga cgtgcatcgt ttcccttgct   120
gcgctgacag gaaacgcggt tgtgctctgg ctccctgggt gccgcatgcg caggaacgct   180
gtctccatct acatcctcaa cctggtcgcg gccgacttcc tcttccctag cggccacatt   240
atatgttcgc cgttacgcct catcaatata cgccatccca tctccaaaat cctcagtcct   300
gtgatgacct ttccctactt tataggccta agcatgctga gcgccatcag caccgagcgc   360
tgcctgtcca tctgtggcc catctgttac cactgccgc gccccagata cctgtcatcg   420
gtcatgtgtg tctgtctctg ggcccgttcc ctgtgcgga gtatcctgga gtggatgttc   480
tgtgacttcc tgtttagtgg tgctgattct gtttgggtg aaacgtcaga ttctattaca   540
atcgcgiggc tggtttttt atgtgtggtt ctctgtgggt ccagcctggt cctgtctgtc   600
aggattctct gtggatcccg gaagatgccg ctgaccaggc tgtacgtgac catcctcctc   660
acagtgtctg tcttctcct ctgtggcctg ccttttgcca ttcagtgggc cctgttttcc   720
aggatccacc tggattggaa agtcttattt tgtcatgtgc atctagtctt cattttcctg   780
tccgtcttta acagcagtgc caaccccatc atttacttct tctgtggctc ctttaggcag   840
cgtcaaaaata ggcagaacct gaagctggtt ctccagaggg ctctgcagga cacgcctgag   900
gtggatgaag gtggagggtg gcttctcag gaaaccctgg agctgtcggg aagcagattg   960
gagcaggcta gcaaaggaga agaactcttc actggagtgt tccaattct tgttgaatta  1020
gatggatgatg ttaacggcca caagttctct gtcagtggag aggttgaagg tgatgcaaca  1080
tacggaaaac ttacctgaa gtcatctgc actactggca aactgcctgt tccatggcca  1140
acactagtca ctactctgtg ctatggtgtt caatgcittt caagataccc ggatcatatg  1200
aaacggcatg actttttcaa gactgccatg cccgaagggt atgtacagga aaggaccatc  1260
ttcttcaaag atgacggcaa ctacaagaca cgtgctgaag tcaagtttga aggtgatacc  1320
cttgtaaata gaatcgagtt aaaaggtatt gacttcaagg aagatggcaa catcttgga  1380

```

478/518

cacaaattgg aatacaacta taactcacac aatgtataca tcatggcaga caaacaaaag 1440
 aatggaatca aagigaactt caagacccgc cacaacattg aagatggaag cgttcaacta 1500
 gcagaccatt atcaacaaaa tactccaatt ggcgatggcc ctgtcctttt accagacaac 1560
 cattacctgt ccacacaatc tgccctttcg aaagatccca acgaaaagag agaccacatg 1620
 gtccttcttg agtttgaac agctgctggg attacacatg gcatggatga actgtacaac 1680
 tga 1683

<210> 207

<211> 1707

<212> DNA

<213> Human

<400> 207

atggatccaa ccaccccggc ctggggaaca gaaagtacaa cagtgaatgg aaatgaccaa 60
 gcccttcttc tgcttttggg caaggagacc ctgatcccg tcttctgat ccttttcatt 120
 gccctggctg ggctggtagg aaacgggttt gtgctctggc tcttgggctt ccgcatgcgc 180
 aggaacgcct tctctgtcta cgtctcagc ctggccgggg ccgacttctt ctctctctgc 240
 ttccagatta taaattgcct ggtgtacctc agtaacttct tctgttccat ctccatcaat 300
 ttccctagct tcttcaccac tgtgatgacc tgtgcctacc ttgcaggcct gagcatgctg 360
 agcacgltca gcaccgagcg ctgcctgtcc gtcctgtggc ccatctggta tgcctgccgc 420
 cgccccagac acctgtcagc ggtcgtgtgt gtcctgtctt gggccctgtc cctactgtct 480
 agcatcttgg aaggaagti ctgtggcttc ttatttagtg atggtgactc tggttggtgt 540
 cagacatttg atttcatcac tgcagcgtgg ctgatttttt tattcatggt tctctgtggg 600
 tccagtctgg cctgtctggt caggatcttc tgtggctcca ggggtctgcc actgaccagg 660
 ctgtacctga ccctctgct cacagtgtct gtgttctctc tctgggcct gcccttggc 720
 attcagtggg tccaatatt atggatctgg aaggattctg atgtcttatt ttgtcatatt 780
 catccagttt cagtgtctt gtcattctt aacagcagtg ccaaccccat catttacttc 840
 ttctgggctt ctittaggaa gcagtggcgg ctgcagcagc cgatctcaa gctggctctc 900
 cagagggctc tgcaggacat tctgaggtg gatcacagtg aaggatgctt ccgtcagggc 960

479/518

accccggaga tgtcgagaag cagtctggcg gctagcaaag gagaagaact cttcactgga 1020
 gttgtcccaa ttcttgttga attagatggt gatgttaacg gccacaagtt ctctgtcagt 1080
 ggagagggcg aagggtgatgc aacatacga aaacttaccc tgaagttcat ctgcactact 1140
 ggcaaactgc ctgttccaig gccaacacta gtcactactc tgtgctatgg tgttcaatgc 1200
 ttttcaagat acccggtatca tatgaaacgg catgactttt tcaagagtc catgcccga 1260
 ggttatgtac aggaaaggac catcttcttc aaagatgacg gcaactacaa gacacgtgct 1320
 gaagtcaagt ttgaaggatg tacccttggt aatagaatcg agttaaaagg tatgtacttc 1380
 aaggaagatg gcaacattct gggacacaaa ttggaatata actataactc acacaatgta 1440
 tacatcatgg cagacaaaca aaagaatgga atcaaagtga acttcaagac ccgccacaac 1500
 attgaagatg gaagcggtca actagcagac cattatcaac aaaatactcc aattggcgat 1560
 ggccctgtcc ttttaccaga caaccattac ctgtccacac aatctgccct ttcgaaagat 1620
 cccaacgaaa agagagacca catggctctt cttagatttg taacagctgc tgggattaca 1680
 catggcatgg atgaactgta caactga 1707

<210> 208

<211> 1653

<212> DNA

<213> Human.

<400> 208

atgatggagc ccagagaagc tggacagcac gtgggggccc ccaacagcgc ccaggaggat 60
 gtggccttca acctcatcat cctgtccctc accgaggggc tggcctcgg tgggctgctg 120
 gggaatgggg cagtctctcg gctgctcagc tccaatgtct acagaaaccc cttcgccatc 180
 tacctcctgg acgtggcctg cgcggatctc atcttccctg gctgccacat ggtggccatc 240
 gtccccgact tgcctgaagg ccggctggac ttcccggtct tctgcagac cagcctggca 300
 acgctgcgct tcttctgcta catcgtgggc ctgagctctc tggcgccgt cagcgtggag 360
 cagtgcctgg ccgccctctt ccagcctgg tactcgtgcc gccgccacg ccacctgacc 420
 acctgtgtgt gcgccctcac ctgggccctc tgcctgctgc tgcacctgct gctcagcagc 480
 gccctgaccc agttcttcgg ggagcccagc cgcacttgt gccggacgct gtggctggtg 540

480/518

gcagcgggtgc tgctggctct gctgtgttgc accatgtgtg gggccagcct tatgtgtctg 600
 ctgcgggttg agcgaggccc ccagcggccc ccacccggg gcttccttg gctcatcctc 660
 ctacccgtcc tctcttctct ctctcgcggc ctgcccttcg gcatctactg gctgtcccgg 720
 aacctgtctt ggtacatccc ccaactactt taccacttca gcttcctcat ggccgcccgtg 780
 cactgcgcgg ccaagcccg t gctctactt tgcctgggca gtgcccagg ccgcaggctg 840
 cccctccggc tggctctcca gcgagcgctg ggagacgagg ctgagctggg ggccgtcagg 900
 gagacctccc gccggggcct ggtggacata gcagccgcta gcaaaggaga agaactcttc 960
 actggagtig tcccaattct tgttgaatta gatggtgatg ttaacggcca caagtctctt 1020
 gtcagtggag aggggtgaagg tgatgaaca tacggaaaac ttaccctgaa gttcatctgc 1080
 actactggca aactgcctgt tccatggcca acactagica ctactctgtg ctatgggtgtt 1140
 caatgctttt caagataccc ggatcatatg aaacggcatg actttttcaa gagtgccatg 1200
 cccgaagggt atgtacagga aaggaccatc ttcttcaaag atgacggcaa ctacaagaca 1260
 cgtgtgaag tcaagttga aggtgatacc ctgtttaata gaatcgagtt aaaaggtatt 1320
 gacttcaagg aagatggcaa cattctggga cacaatttg aatacaacta taactcacac 1380
 aatgtataca tcatggcaga caaacaaaag aatggaatca aagtgaactt caagaccgc 1440
 cacaacattg aagatggaag cgttcaacta gcagaccatt atcaacaaaa tactccaatt 1500
 ggcgatggcc ctgtcctttt accagacaac cattacctgt ccacacaatc tgcccttctg 1560
 aaagatccca acgaaaagag agaccacatg gtccttcttg agtttgaac agctgtctgg 1620
 attacacatg gcatggatga actgtacaac tga 1653

<210> 209

<211> 1686

<212> DNA

<213> Human

<400> 209

atgccactcc ctgtgcccc agcgggggca caaaagactc ctgaggacca tgtctgtctc 60
 catcttgcag gtccctcgcc agcaccctct gagccggcca ggatgtttgg gctgttcggc 120
 ctctggagaa ccttcgacag tgtggtcttc tacctgacgc tgatcgtggg cctcggggga 180

481/518

ccggtaggta acgggctggt gctctggaac ctcggttcc gcatcaagaa gggccccctc 240
 tccatctacc tgcctcacct ggccgccgcc gacttcctgt tctctctcig ccgtgtgggc 300
 ttctccgtgg ctacggctgc cctggggccc caggacacac tctacttcgt gctcaccttc 360
 ctgtgggttc cgggtgggct ctggctgctg gcggccttca gcgtggagcg ctgcctctcc 420
 gacctcttcc ccgcctgcta ccagggtgc cggcccagac acgcctcggc cgtcctctgc 480
 gccctgggtg ggaccccagc cctgccggcc gtgccgtgc ccgccaacgc ctgcggcctg 540
 ctgcgcaaca gcgcgtgccc cctggcttgc ccgcgtacc acgtggccag cgtcacctgg 600
 ttcttggtgc tggcccgct cgccctggacg gctggcgctg tctcttttgt ctgggtgacc 660
 tgcgtctcca ctgcccgcg gccaggtc tacggcatcg tctggggcg gctgctcctg 720
 ctctttcttct gtggcctgcc ctgggtcttc tactggagcc tgcagccct gctgaacttc 780
 ctgctgcccc tgttttcccc gctggccacg ctgctggcct gcgtcaacag cagctccaag 840
 cccctcatct actcggggtt gggccgacag cccgggaagc gggagccgct gaggtcggta 900
 ctgcggaggg cctggggga gggcgccgag ctgggtgccg ggggacagtc cctgcccag 960
 ggtctcctag ctacaaagg agaagaactc ttactggag ttgtcccaat tcttgttgaa 1020
 ttagatgggtg atgttaacgg ccacaagttc tctgtcagtg gagagggta aggtgatgca 1080
 acatacgaa aacttacct gaagttcctc tgcactactg gaaaactgcc tgttccatgg 1140
 ccaacactag tcaactactc gtgctatggt gttcaatgt tttcaagata cccgatcat 1200
 atgaaacggc atgacttttt caagagtgc atgccgaag gttatgtaca gaaaggacc 1260
 atcttcttca aagatgacgg caactacaag acacgtgctg aagtcaagtt tgaaggatg 1320
 acccttgita atagaatcga gttaaaagg attgacttca aggaagatgg caacttctg 1380
 ggacacaaat tggaatacaa ctataactc cacaatgtat acatcatggc agacaaaca 1440
 aagaatggaa tcaaagtga cttcaagacc cgccacaaca ttgaagatgg aagcgttcaa 1500
 ctagcagacc attatcaaca aaatactcca attggcgatg gccctgtcct tttaccagac 1560
 aaccattacc tgtccacaca atctgccctt tcgaaagatc ccaacgaaa gagagaccac 1620
 atggtccttc ttgagtttgt aacagctgct gggattacac atggcatgga tgaactgiac 1680
 aactga 1686

<210> 210

<211> 1776

482/518

<212> DNA

<213> Human

<400> 210

```

atggagcaca cgcacgcca cctcgagcc aacagctgc tgtcttggtg gtcccccggc   60
tcggcctgcg gcttgggttt cgtgcccggt gtctactaca gcctcttgct gtgcctcggt  120
ttaccagcaa atatcttgac agtgcacac cctcccagc tggtaggaag aagacagaag  180
tcctcctaca actatctctt ggcactcgt gctgccgaca tcttggtcct ctttttcata  240
gigtgttggt acttccctgt ggaagatttc atcttgaaca tgcagatgcc tcaggcccc  300
gacaagatca tagaagtgtt ggaattctca tccatccaca cctccatag gattactgta  360
ccgttaacca ttgacaggta tatcgtgtgc tgccaccgc tcaagtacca cagggtctca  420
taccagccc gcaccggaa agtcattgta agtgtttaca tcacctgctt cctgaccagc  480
atcccctatt actggtggcc caacatctgg actgaagact acatcagcac ctctgtgcat  540
cagtcctca tctggatcca ctgcttacc gtctacctgg tgccctgctc catcttcttc  600
atcttgaact caatcattgt gtacaagtc aggaggaaga gcaattttcg tctccgtggc  660
tactccacgg ggaagaccac cgccatcttg ttaccatta cctccatctt tgccacactt  720
tgggcccccc gcacatcat gattctttac cactctatg gggcgcccat ccagaaccgc  780
tggtgtgtgc acatcatgtc cgacattgcc aacatgctag cccttctgaa cacagccatc  840
aacttcttcc tctactgctt catcagcaag cgttccgca ccatggcagc cgccagctc  900
aaggctttct tcaagtgcc gaagcaacct gtacagttct acaccaatca taacttttcc  960
ataacaagta gcccctggat ctgcgggca aactcacact gcacaaagt gctggtgtac 1020
cagtatgaca aaaatggaaa acctataaaa gtatccccgt ctagcaaagg agaagaactc 1080
ttacttgag ttgtccaat tctgttgaa ttagatggtg atgttaacgg ccacaagttc 1140
tctgtcagt gagagggtga aggtgatgca acatacgaa aacttacct gaagttcatc 1200
tgcactactg gcaaactgcc igtccatgg ccaacactag tcactactct gtgctatggt 1260
gttcaatgct ttcaagata cccgatcat atgaaacggc atgacttttt caagagtgcc 1320
atgcccgaag gttatgtaca ggaaaggacc atcttcttca aagatgacgg caactacaag 1380
acacgtgctg aagicaagtt tgaaggtgat acccttgta atagaatga gttaaaaggt 1440
attgacttca aggaagatgg caacattctg ggacacaaat tggaatacaa ctataactca 1500

```

483/518

cacaatgtat acatcatggc agacaaacaa aagaatggaa tcaaagtgaa ctccaagacc 1560
 cgccacaaca ttgaagatgg aagcggtcaa ctagcagacc attatcaaca aaatactcca 1620
 attggcgatg gccctgtcct ttaccagac aaccattacc tgccacaca atctgccctt 1680
 tcgaaagatc ccaacgaaaa gagagaccac atggtccctc ttgagttgt aacagctgct 1740
 gggattacac atggcatgga tgaactgtac aactga 1776

<210> 211

<211> 1791

<212> DNA

<213> Human

<400> 211

atgcectcig tgtctccagc ggggccctcg gccggggcag tcccaatgc caccgcagtg 60
 acaacagtcg ggaccaatgc cagcgggctg gaggtgcccc tgttccacct gtttggccgg 120
 ctggacgagg agctgcatgg caccitccca ggctgtggc tggcgctgat ggcggtgcac 180
 ggagccatct tcctggcagg gctgggtgctc aacgggctgg cgctgtacgt ctctgtctgc 240
 cgcacccggg ccaagacacc ctcatcatc tacacatca acctggtgtg gaccgatcta 300
 ctggtagggc tgtccctgcc cagcgcttc gctgtgtact acggcgccag gggctgccctg 360
 cgctgtgcct tccgcacgt cctcggttac ttcctcaaca tgcactgctc catctcttc 420
 ctacactgca tctgcgtgga cgctacctg gccatcgtgc ggctgaagg ctcccgccgc 480
 tgccgccagc ctgcctgtgc cagggccgtg tgcgccttcg tgtggctggc cgccggtgcc 540
 gtcacctgt cgggtgtggg cgtgacaggc agccggccct gctgccgtgt ctttgcgtg 600
 actgtcctgg agttcctgct gcctctgtg gtcacagcg tgtttaccgg ccgcatcatg 660
 tgtgactgt cgcggccggg tctgctccgc cagggtcgcc agcgcgcgt gcgggccatg 720
 cagctcctgc tcacggtgt catcatctt ctgctgtct tcacgccctt ccacgccgc 780
 caagtggccg tggcgctgtg gccgacatg ccacaccaca cgagcctcgt ggtctaccac 840
 gtggcgtga cctcagcag cctcaacagc tgcattgacc ccatcgtcta ctgttcgtc 900
 accagtggct tccaggccac cgtccgaggc ctcttcggcc agcacggaga gcgtgagccc 960
 agcagcgtg acgtggtcag catgcacagg agctccaagg gctcaggccg tcatcacatc 1020

484/518

cticagtccg gccctcacgc cctcacccag gccctggcta atgggcccga ggctgctagc 1080
 aaaggagaag aactcttcac tggagttgtc ccaattcttg ttgaattaga tggatgatt 1140
 aacggccaca agttctctgt cagtgagag ggtgaagggt atgcaacata cggaaaactt 1200
 accctgaagt tcatctgcac tactggcaaa ctgcctgttc catggccaac actagtcact 1260
 actctgtgct atgggtttca atgcttttca agatacccg atcatatgaa acggcatgac 1320
 tttttcaaga gtgccatgcc cgaaggttat gtacaggaaa ggaccatctt ctccaagat 1380
 gacggcaact acaagacacg tgctgaagtc aagtttgaag gtgataccct tgttaataga 1440
 atcgagttaa aaggtattga ctccaaggaa gatggcaaca ttctgggaca caaattggaa 1500
 tacaactata actcacaca tgtatacatc atggcagaca aacaaaagaa tggaatcaaa 1560
 gtgaacttca agaccgccca caacattgaa gatggaagcg ttcaactagc agaccattat 1620
 caacaaaata ctccaattgg cgatggccct gtccctttac cagacaacca ttacctgtcc 1680
 acacaatctg ccttttcgaa agatcccaac gaaaagagag accacatggt ccttcttgag 1740
 tttgtaacag ctgctgggat tacacatggc atggatgaac tgtacaactg a 1791

<210> 212

<211> 1632

<212> DNA

<213> Human

<400> 212

atgcctggcc acaatacctc caggaattcc tcttgcgac ctatagtgac accccactta 60
 atcagcctct acttcatagt gcttattggc gggctgggtg gtgtcatttc cattctttc 120
 ctctgtgtga aaatgaacac ccggtcagtg accaccatgg cggtcattaa ctgtgtgtg 180
 gtccacagcg tttttctgct gacagtgcc tttcgcttga cctacctcat caagaagact 240
 tggatgtttg ggctgccctt ctgcaaatit gtgagtgcca tgctgcacat ccacatgtac 300
 ctacggttcc tattctatgt ggtgacctg gtcaccagat acctcatctt ctccaagtgc 360
 aaagacaaag tggaattcta cagaaaactg catgctgtgg ctgccagtgc tggcatgtgg 420
 acgtgtgtga ttgtcattgt ggtaccctg gttgtctccc ggtatggaat ccatgaggaa 480
 tacaatgagg agcactgttt taaatttcac aaagagcttg cttacacata tgtgaaaatc 540

485/518

```

atcaactata tgatagtcac tttgtcata gccgttctg tgattctgtt ggtcttccag 600
gtcttcatca ttatgttgat ggtgcagaag ctacgccact ctttactatc ccaccaggag 660
ttctgggctc agctgaaaaa cctatTTTT ataggggtca tccttggttg tttccttccc 720
taccagtctt ttaggatcta ttacttgaat gttgtgacgc attccaatgc ctgtaacagc 780
aaggttgcat ttataacga aatcttcttg agtgaacag caattagctg ctatgatttg 840
cttctctttg tctttggggg aagccattgg titaagcaa agataattgg cttatggaat 900
tgigtgttgt gccgtgctag caaaggagaa gaactcttca ctggagtgtt cccaattctt 960
gttgaattag atggtgatgt taacggccac aagtctctg tcagtggaga gggigaaggt 1020
gatgaacat acggaaaact taccctgaag ttcatctgca ctactggcaa actgcctgtt 1080
ccatggccaa cactagtcac tactctgtgc tatggtgttc aatgcctttc aagatacccg 1140
gatcatatga aacggcatga ctttttcaag agtccaatgc ccgaaggta tgtacaggaa 1200
aggaccatct tcttcaaaga tgacggcaac tacaagacac gtgctgaagt caagtttgaa 1260
ggtgataccc ttgttaatag aatcgagtta aaaggtattg acttcaagga agatggcaac 1320
attctgggac acaaattgga atacaactat aactcacaca atgtatacat catggcagac 1380
aaacaaaaga atggaatcaa agtgaacttc aagaccgcc acaacattga agatggaagc 1440
gttcaactag cagaccatta tcaacaaaat actccaattg gcgatggccc tgtcctttta 1500
ccagacaacc attacctgtc cacacaatct gcccttctga aagatcccaa cgaaaagaga 1560
gaccacaagg tccttcttga gtttgtaaca gctgctggga ttacacatgg catggatgaa 1620
ctgtacaact ga 1632

```

<210> 213

<211> 1734

<212> DNA

<213> Human

<400> 213

```

atgaatgagc cactagacta tttagcaaat gcttctgatt tccccgatta tgcagctgct 60
tttggaaatt gcactgatga aaacatccca ctcaagatgc actacctccc tgttatttat 120
ggcattatct tcctcgtggg atttccaggc aatgcagtag tgatatccac ttacattttc 180

```

486/518

aaaatgagac cttggaagag cagcaccatc attatgctga acctggcctg cacagatctg	240
ctgtatctga ccagcctccc ctccctgatt cactactatg ccagtggcga aaactggatc	300
tttggagatt tcatgtgtaa gtttatccgc ttcagcttcc atttcaacct gtatagcagc	360
atcctcttcc tcacctgttt cagcatcttc cgctactgtg tgatcattca cccaatgagc	420
tgcttttcca ttacaaaaac tcgatgtgca gttgtagcct gtgctgtggt gtggatcatt	480
tcactggtag ctgtcattcc gatgaccttc ttgatcacat caaccaacag gaccaacaga	540
tcagcctgtc tcgacctcac cagttcggat gaactcaata ctattaagtg gtacaacctg	600
atcttgactg caactacttt ctgcctcccc ttggigatag tgacactttg ctataccacg	660
attateccaca ctctgacca tggactgcaa actgacagct gccttaagca gaaagcacga	720
aggctaacca ttctgtact ccttgcattt tacgtatgtt ttttaccctt ccatactttg	780
agggtcattc ggatcgaatc tcgctgtctt tcaatcagtt gtccattga gaatcagatc	840
catgaagctt acatcgtttc tagaccatta gctgctctga acacctttgg taacctgtta	900
ctatatgttg tggtcagcga caactttcag caggctgtct gctcaacagt gagatgcaaa	960
gtaagcggga accttgagca agcaaagaaa attagttact caaacaaccc tgctagcgct	1020
agcaaaggag aagaactctt cactggagtt gtcccaattc ttgttgaatt agatggatgat	1080
gttaacggcc acaagttctc tgtcagtga gagggatgaag gtgatgcaac atacggaaaa	1140
cttaccctga agttcatctg cactactggc aaactgcctg ttccatggcc aacactagtc	1200
actactctgt gctatggtgt tcaatgcttt tcaagatacc cggatcatac gaaacggcat	1260
gactttttca agagtgccat gccgaaggt tatgtacagg aaaggacat cttcttcaaa	1320
gatgacggca actacaagac acgtgctgaa gtcaagtttg aaggatgatac ccttgttaat	1380
agaatcgagt taaaaggat tgaattcaag gaagatggca acattctggg acacaaattg	1440
gaatacaact ataactcaca caatgtatac atcatggcag acaaacaaaa gaatggaatc	1500
aaagtgaact tcaagaccg ccacaacatt gaagatggaa gcgttcaact agcagacat	1560
tatcaacaaa atactccaat tggcgtggc cctgtccttt taccagacaa ccattacctg	1620
tccacacaat ctgccctttc gaaagatccc aacgaaaaga gagaccacat ggtccttctt	1680
gagtttgtaa cagctgctgg gattacacat ggcatggatg aactgtacaa ctga	1734

<210> 214

<211> 1710

487/518

<212> DNA

<213> Human

<400> 214

```

atgatcacc  tgaacaatca agatcaacct gtccctttta acagctcaca tccagatgaa   60
tacaaaattg cagcccttgt cttctatagc tgatctttca taattggatt atttgttaac  120
atcactgcat tatgggtttt cagtgtgacc accaagaaga gaaccacggt aaccaictat  180
atgatgaatg tggcattagt ggacttgata ttataatga ctttaccctt tcgaatgttt  240
tattatgcaa aagatgaatg gccatttggg gacttcttcc gccagattct tggagctctc  300
acagtgtttt acccaagcat tgccttatgg cttcttgccct ttattagtgc tgacagatac  360
atggccattg tacagccgaa gtacgccaaa gaacttaaaa acacgtgcaa agccgtgctg  420
gcgtgtgtgg gactctggat aatgaccttg accacgacca cccctctgct actgctctat  480
aaagaccagc ataaagactc cactcccgcc acctgccica agatttctga catcatctat  540
ctaaaagctg tgaacgtgct gaacctcact cgactgacat ttttttctt gattcctttg  600
ttcatcatga ttgggtgcta cttggtcatt attcataatc tccttcacgg caggacgtct  660
aagctgaaac ccaaagtcac ggagaagtcc ataaggatca tcatcacgct gctgggtcag  720
gtgctcgtct gccttatgcc ctccacatc tgtttcgctt tctgatgct gggaacgggg  780
gagaacagtt acaatccctg gggagccctt accaccttcc tcatgaacct cagcacgtgt  840
ctggatgtga ttctctacta catcgtttca aaacaatttc aggtctgagt cattagtgtc  900
atgctatacc gtaattacct tcgaagcatg cgcagaaaaa gtttccgac tggtagtcta  960
cggctactaa gcaatataaa cagtgaatg ttagctagca aaggagaaga actcttcact 1020
ggagtgttcc caattcttgt tgaattagat ggtgatgtta acggccacaa gtctctgtc 1080
agtggagagg gigaaggatg tgcaacatac ggaaaactta ccctgaagtt catctgcact 1140
actggcaaac tgctgttcc atggccaaca ctagtcacta ctctgtgcta tgggtgttcaa 1200
tgcttttcaa gataccgga tcatatgaaa cgcatgact tttcaagag tgccatgccc 1260
gaaggitatg tacaggaaag gaccatcttc ttcaaagatg acggcaacta caagacacgt 1320
gctgaagtca agtttgaagg tgataccctt gttaatagaa tcgagttaaa aggtattgac 1380
ttcaaggaag atggcaacat tctgggacac aaattggaat acaactataa ctacacaaat 1440
gtatacatca tggcagacaa aaaaaaat ggaatcaaag tgaacttcaa gaccgcccac 1500

```

488/518

aacattgaag atggaagcgt tcaactagca gaccattatc aacaaaatac tccaattggc 1560
 gatggccctg tccttttacc agacaacat tacctgtcca cacaatctgc cttttcgaaa 1620
 gatcccaacg aaaagagaga ccacatggtc cttcttgagt ttgtaacagc tgctgggatt 1680
 acacatggca tggatgaact gtacaactga 1710

<210> 215

<211> 2364

<212> DNA

<213> Human

<400> 215

atggcgacgc ccaggggcct gggggccctg ctctgtctcc tcctgtctcc gacctcaggt 60
 caggaaaagc ccaccgaagg gccaaagaaac acctgcctgg ggagcaacaa catgtacgac 120
 atcttcaact tgaatgacaa ggctttgtgc ttcaccaagt gcaggcagtc gggcagcgac 180
 tcctgcaatg tggaaaactt gcagagatac tggctaaact acgaggecca tctgatgaag 240
 gaaggittga cgcagaaggt gaacacgcct ttctgaagg ctttgggtcca gaacctcagc 300
 accaacactg cagaagactt ctatttctct ctggagccct ctgaggtcc gaggcaggtg 360
 atgaaggacg aggacaagcc ccctgacaga gtgcgacttc ccaagagcct ttttcgatcc 420
 ctgccaggca acaggtctgt ggtccgcttg gccgtacca ttctggacat tgggtccaggg 480
 actctcttca agggcccccg gctcggcctg ggagatggca gcggcgtgtt gaacaatcgc 540
 ctgggtgggtt tgagtgtggg acaaatgcat gtcaccaagc tggctgagcc tctggagatc 600
 gtcttctctc accagcgacc gccccctaac atgacctca cctgtgtatt ctgggatgtg 660
 actaaaggga ccactggaga ctggtcttct gagggctgct ccacggaggt cagacctgag 720
 gggaccgtgt gctgctgtga ccacctgacc tttttcgccc tgctcctgag acccaccttg 780
 gaccagtcca cggatgatat cctcacacgc atctcccagg cgggctgtgg ggtctccatg 840
 atcttcttgg ccttcacat tattctttat gcctttctga ggctttcccg ggagaggttc 900
 aagtcagaag atgccccaaa gatccacgtg gccctgggtg gcagcctgtt cctcctgaat 960
 ctggccttct tggatcaatgt ggggagtgcc tcaaaggggt ctgatgtgc ctgctgggcc 1020
 cggggggctg tcttccacta ctctctgctc tgtgccttca cctggatggg ccttgaagcc 1080

489/518

```

ttccacctct accgtctcgc tgtcagggic ttcaacacct acttcgggca ctacttcctg 1140
aagctgagcc tggtagggctg gggccctgcc gccctgatgg tcatcggcac tgggagtgcc 1200
aacagctacg gcctctacac catccgtgat agggagaacc gcacctctct ggagctatgc 1260
tggttccgtg aagggaacaac catgtacgcc ctctatatca ccgtccacgg ctacttcctc 1320
atcaccttcc tctttggcat ggtggctcctg gccctggtag tctggaagat cttcaccttg 1380
tcccgtagta cagcgggtcaa ggagcggggg aagaaccgga agaaggtagt caccctgctg 1440
ggcctctcga gccctggtagg tgtgacatgg gggtaggcca tcttcacccc gttgggcctc 1500
tccacgtctt acatctttgc acttttcaac tccctgcaag gtgtcttcat ctgctgctgg 1560
ttcaccatcc ttacctccc aagtcagagc accacagtct cctcctctac tgcaagattg 1620
gaccaggccc actccgcac tcaagaagct agcaaaggag aagaactctt cactggagtt 1680
gtcccaattc ttgttgaatt agatggtagt gttacggcc acaagttctc tgtcagtga 1740
gagggtgaag gtgatgcaac atacggaaaa cttacctga agttcatctg cactactggc 1800
aaactgcctg ttcataggcc aacactagtc actactctgt gctatggtag tcaatgcttt 1860
tcaagatacc cggatcatat gaaacggcat gactttttca agagtccat gccgaaggt 1920
taigtacagg aaaggacat cttcttcaaa gatgacggca actacaagac acgtgctgaa 1980
gtcaagtttg aaggtagac ccttgtaat agaatcgagt taaaaggtag tgacttcaag 2040
gaagatggca acattctggg acacaaattg gaatacaact ataactcaca caatgtatac 2100
atcatggcag acaaacaaaa gaatggaatc aaagtgaact tcaagaccg ccacaacatt 2160
gaagatggaa gcgttcaact agcagacat tatcaacaaa atactccaat tggcgaatggc 2220
cctgtccttt taccagacaa ccattacctg tccacacaa ctgccctttc gaaagatccc 2280
aacgaaaaga gagaccacat ggtccttctt gagtttglaa cagctgctgg gattacacat 2340
ggcatggatg aactgtacaa ctga 2364

```

<210> 216

<211> 1827

<212> DNA

<213> Human

<400> 216

490/518

atgggtgaca gaagattcat tgacttccaa ticcaagatt caaattcaag cctcagaccc	60
aggttgggca atgctactgc caataatact tgcattgttg atgattcctt caagtataat	120
ctcaatggtg ctgtctacag tgttgtattc atcttgggtc tgataaccaa cagtgtctct	180
ctgtttgtct tctgtttccg catgaaaatg agaagtgaga ctgtatattt tatcaccaat	240
ctagctgtct ctgatttgct ttttgtctgt aactacctt ttaaaatatt ttacaacttc	300
aaccgccact ggccttttgg tgacaccctc tgcaagatct ctggaactgc attccttacc	360
aacatctatg ggagcatgct ctttctcacc tgtattagtg tggatcgttt cctggccatt	420
gtctatcctt ttcatctcgc tactattagg actaggagga attctgccat tgtgtgtgct	480
ggtgtctgga tcttagtctt cagtggcggt atttcagcct ctttgttttc caccactaat	540
gtcaacaatg caaccaccac ctgctttgaa ggcttctcca aacgtgtctg gaagacttat	600
ttatccaaga tcacaatatt tattgaagtt gttgggttta tcattcctct aatatatgaat	660
gtctcttgct cttctgttgt gctgagaact cttcgcaagc ctgctactct gtctcaaatt	720
gggaccaata agaaaaaagt actgaaaatg atcacagtac atatggcagt ctttgttgta	780
tgctttgtac cctacaactc tgtcctcttc ttgtatgccc tggtcgctc ccaagctatt	840
actaatgct ttttgaaag atttgcaaag atcatgtacc caatcacctt gtgccttgca	900
actctgaact gttgttttga ccttttctc tattacttca ccttgaatc ctttcagaag	960
tccttctaca tcaatgccca catcagaatg gagtcctgt ttaagactga aacacctttg	1020
accacaaagc cttcccttcc agctattcaa gaggaagtga gtgatcaaac aacaaataat	1080
ggtggtgaat taatgctaga atccaccttt gctagcaaag gagaagaact cttcacigga	1140
gttgtcccaa ttcttgttga attagatggt gatgttaacg gccacaagtt ctctgtcagt	1200
ggagagggtg aaggatgatc aacatacgga aaacttacct tgaagttcat ctgcactact	1260
ggcaaactgc ctgttccatg gccaacacta gtcactactc tgtgctatgg tgttcaatgc	1320
ttttcaagat acccgatca tatgaaacgg catgactttt tcaagagtgc catgcccga	1380
ggttatgtac aggaaaggac catcttcttc aaagatgacg gcaactacaa gacacgtgct	1440
gaagtcaagt ttgaagtgta tacccttgtt aatagaatcg agttaaaagg tattgacttc	1500
aaggaagatg gcaacattct gggacacaaa ttggaataca actataactc acacaatgta	1560
tacatcatgg cagacaaaca aaagaatgga atcaaagtga acttcaagac ccgccacaac	1620
attgaagatg gaagcgttca actagcagac cattatcaac aaaatacttc aattggcgat	1680
ggcctgtcc ttttaccaga caaccattac ctgtccacac aatctgcctt ttcgaaagat	1740

491/518

cccaacgaaa agagagacca catggctcct citgagtttg taacagctgc tgggattaca 1800
 catggcatgg atgaactgta caactga 1827

<210> 217

<211> 1734

<212> DNA

<213> Human

<400> 217

atggctaacc ttgacaaata cactgaaaca ttcaagatgg gtagcaacag taccagcact 60
 gctgagattt actgtaatgt cactaatgtg aaatttcaat actccctcta tgcaaccacc 120
 tatactctca taticattcc tggctctctg gctaacagtg cagccttggtg ggttctgtgc 180
 cgcttcatca gcaagaaaaa taaagccatc atttcatga tcaacctctc tgtggctgac 240
 ctgtctcatg tattatcttt acccctccgg atttactatt acatcagcca ccactggcct 300
 ttccagagag ccccttgcct gctctgcctc tacctgaagt atctcaacat gtagccagc 360
 atttgcttcc tgacgtgcat cagcttctca aggtgctttt ttctcctcaa gcccttcagg 420
 gccagagact ggaagcgtag gtacgatgtg ggcatcagtg ctgccatctg gatcgttgtg 480
 gggactgcct gtttgccatt tcccatccig agaagcacag acttaaaaa caacaagtc 540
 tgccttgctg atcttgata caagcaaatg aatgcagttg cgttggtcgg gatgattaca 600
 gtgtctgagc ttgcaggatt tgtgatccca gtgatcatca tcgcatgggtg tacctggaaa 660
 actactatat ccttgagaca gccaccaatg gctttccaag ggatcagtg gaggcagaaa 720
 gcactgcgga tgggtgcat gtgtgctgca gtcttctca tctgcttcac tccctatcat 780
 attaacttta ttttttacac catggtaaag gaaacatca ttagcagttg tcccggtgtc 840
 cgaatcgcac tgtatttcca ccccttttgc ctgtgccttg caagtctctg ctgccttttg 900
 gatccaattc tttattactt tatggcttca gagtttcgtg accaactatc ccgccaatggc 960
 agttctgtga cccgctcccg cctcatgagc aaggagagt gttcatcaat gattggctct 1020
 agcaaaggag aagaactctt cactggagtt gtcccaattc ttgttgaatt agatggtgat 1080
 gttaacggcc acaagttctc tgtcagtga gaggggtgaag gtgatgcaac atacgaaaa 1140
 cttaccctga agttcatctg cactactggc aaactgcctg ttccatggcc aacactagtc 1200

492/518

actactctgt gctatggigt tcaatgcttt tcaagatacc cggatcatat gaaacggcat 1260
 gactttttca agagtgccat gccgaaggt tatgtacagg aaaggacat cttcttcaaa 1320
 gatgacggca actacaagac acgtgctgaa gtcaagtgtg aaggatgatac cttgttaat 1380
 agaatcgagt taaaaggtat tgacttcaag gaagatggca acattctggg acacaaattg 1440
 gaatacaact ataaticaca caatgtatac atcatggcag acaaacaaaa gaatggaatc 1500
 aaagtgaact tcaagacccg ccacaacatt gaagatggaa gcgttcaact agcagacat 1560
 tatcaacaaa atactccaat tggcgtggc cctgtccttt taccagacaa ccattacctg 1620
 tccacacaat ctgccctttc gaaagatccc aacgaaaaga gagaccacat ggtccttctt 1680
 gagtittgtaa cagctgctgg gattacacat ggcatggatg aactgtacaa ctga 1734

<210> 218

<211> 2556

<212> DNA

<213> Human

<400> 218

atgcgagccc cgggcgcgt tctcgccgc atgtcgcggc tactgtttct gctactgctc 60
 aagggtctg cctcttctgc cctcggggc gccctgcgt ccagaaacga aacttgtctg 120
 ggggagagct gtgcacctac agtgatccag cgccgcggca gggacgcctg gggaccggga 180
 aattctgcaa gagacgttct gcgagcccga gcaccaggg aggagcagg ggcagcgttt 240
 ctgcgggac cctcctggga cctgccggcg gcccgggcc gtgaccggc tgcaggcaga 300
 gggcggagg cgtcggcagc cggacccccg ggacctcaa ccaggccacc tggcccctgg 360
 aggtggaaag gtgctcgggg tcaggagcct tctgaaactt tggggagagg gaaccccacg 420
 gccctccagc tcttcttca gatctcagag gaggaagaga aggttcccag aggcgctggc 480
 atttccgggc gtagccagga gcagagtgtg aagacagtcc ccggagccag cgatcttttt 540
 tactggccaa ggagagccgg gaaactccag ggttcccacc acaagcccct gtccaagacg 600
 gccaatggac tggcggggca cgaagggtgg acaattgcac tcccgggccg ggcgctggcc 660
 cagaatggat ccttgggtga aggaatccat gagcctgggg gtccccgccg gggaacacagc 720
 acgaaccggc gtgtgagact gaagaacccc ttctaccgcg tgaccagga gtcctatgga 780

493/518

gcctacgagg tcatgtgtct gtccgtggig atcttcggga ccggcatcat tggcaacctg 840
 gcggtgatgt gcatcgtgtg ccacaactac tacatgcgga gcatctccaa ctccctcttg 900
 gccaacctgg ccttctggga ctttctcctc atcttcttct gccctccgtt ggtcatcttc 960
 cagcagctga ccaagaagtg gctgctggag gacttctcct gcaagatcgt gccctatata 1020
 gaggtcgctt ctctgggagt caccacttct acctatgtgt ctctgtgcat agaccgcttc 1080
 cgtgctgcca ccaacgtaca gatgtactac gaaatgatcg aaaactgttc ctcaacaact 1140
 gccaaacttg ctgttatatg ggtgggagct ctattgttag cacttccaga agttgttctc 1200
 cgccagctga gcaaggagga ttgggggttt agtggccgag ctccggcaga aagggtgcatt 1260
 attaagatct ctccgtgatt accagacacc atctaigtct tagccctcac ctacgacagt 1320
 gcgagactgt ggtggtatct ttgctgttac tttgtttgc ccacgctttt caccatcacc 1380
 tgcctcttag tgaactgcag gaaaaaccgc aaagcagaga aagcctgtac ccgagggaat 1440
 aaacggcaga ttcaactaga gactcagatg aactgtacag tagtggcact gaccatttta 1500
 tatggatttt gcattattcc tgaaaatata tgcaacattg ttactgccta catggctaca 1560
 ggggtttcac agcagacaat ggacctcctt aatatcatca gccagttcct tttgttcttt 1620
 aagtcctgtg tcacccagct cctccttttc tgtctctgca aaccttcag tggggccttc 1680
 atggagtgtt gctgctgttg ctgtgaggaa tgcattcaga agtcttcaac ggtgaccagt 1740
 gatgacaatg acaacgagta caccacggaa ctgcaactct cgcctttcag taccatacgc 1800
 cgtgaaatgt ccacttttgc ttctgtcgga actcattgct ctagcaaagg agaagaactc 1860
 ttactggag ttgtcccaat tcttgttgaa ttagatgggt atgttaacgg ccacaagttc 1920
 tctgtcagtg gagagggtga aggtgatgca acatacggaa aacttacctt gaagttcctc 1980
 tgcactactg gcaaactgcc tgttccatgg ccaacactag tcaactactt gtgctatggt 2040
 gttcaatgct tttaagata cccggatcat atgaaacggc atgacttttt caagagtgcc 2100
 atgccgaag gttatgtaca ggaaaggacc atcttcttca aagatgacgg caactacaag 2160
 acacgtgtg aagtcaagtt tgaaggatg acccttggtt atagaatcga gttaaaaggt 2220
 attgacttca aggaagaagg caacattctg ggacacaaat tggaaataca ctataactca 2280
 cacaatgtat acatcatggc agacaaacaa aagaatggaa tcaaagtga cttcaagacc 2340
 cgccacaaca ttgaagatgg aagcgttcaa ctacgagacc attatcaaca aaatactcca 2400
 attggcgaat gccctgtcct ttaccagac aaccattacc tgtccacaca atcigccctt 2460
 tcgaaagatc ccaacgaaaa gagagaccac atggctcctt ttgagtttgt aacagctgct 2520

494/518

gggattacac atggcatgga tgaactgtac aactga

2556

<210> 219

<211> 2160

<212> DNA

<213> Human

<400> 219

atgcggtggc tgtggccct ggctgtctct cttgctgtga ttttggctgt ggggctaagc	60
agggctctctg ggggtgcccc cctgcacctg ggcaggcaca gagccgagac ccaggagcag	120
cagagccgat ccaagagggg caccgaggat gaggaggcca agggcgtgca gcagtatgtg	180
cctgaggagt gggcggagta cccccggccc attcaccctg ctggcctgca gccaaccaag	240
cccttgggtg ccaccagccc taaccccgac aaggatgggg gcaccccaga cagtgggcag	300
gaactgaggg gcaatctgac aggggcacca gggcagaggc tacagatcca gaacccccctg	360
tatccggtga ccgagagctc ctacagtgcc tatgccatca tgcttctggc gctggigtg	420
tttgcggtgg gcattgtggg caacctgtcg gicatgtgca tcgtgtggca cagctactac	480
ctgaagagcg cctggaactc catccttgcc agcctggccc tctgggattt tctggctctc	540
tttttctgcc tccctattgt catcttcaac gagatcacca agcagaggct actgggtgac	600
gittcttgtc gtgccgtgcc ctatcatggag gtctctctc tgggagtcac gactttcagc	660
ctctgtgccc tgggcattga ccgcttccac gtggccacca gcacccctgcc caaggtagg	720
cccctcgagc ggtgccaatc catcctggcc aagttggctg tcatctgggt gggctccatg	780
acgctggctg tgccctgagct cctgctgtgg cagctggcac aggagcctgc ccccaccatg	840
ggcaccctgg actcatgcat catgaaacct tcagccagcc tgcccagatc cctgtattca	900
ctgggtgatga cctaccagaa cgcccgatg tgggtgtact ttggctgcta cttctgcctg	960
cccatcctct tcacagtcac ctgccagctg gtgacatggc ggggtcgagg ccctccaggg	1020
aggaagtcag agtgcagggc cagcaagcac gagcagtgtg agagccagct caacagcacc	1080
gtgggtggcc tgaccgtggt ctacgccttc tgcacctcc cagagaacgt ctgcaacatc	1140
gtgggtggcct acctctccac cgagctgacc cgccagacct tggacctcct gggcctcatc	1200
aaccagttct ccaccttctt caaggcgccc atcaccacag tgctgtcctt ttgcatctgc	1260

495/518

aggccgctgg gccaggcctt cctggactgc tgctgctgct gctgctgtga ggagtcgggc 1320
 ggggcttcgg aggcctctgc tgccaatggg tcggacaaca agctcaagac cgagggtgcc 1380
 tcttccatct acttccacaa gcccaggag tcacccccac tcctgcccct gggcacacct 1440
 tgcgctagca aaggagaaga actcttcact ggagttgcc caattcttgt tgaattagat 1500
 ggtgatgta acggccacaa gtctctgtc agtggagagg gtgaaggta tgcaacatac 1560
 ggaaaactta ccctgaagtt catctgcact actggcaaac tgcctgttc atggccaaca 1620
 ctagtacta ctctgtgcta tgggtttcaa tgcttttcaa gatacccgga tcatatgaaa 1680
 cggcatgact tttcaagag tgccatgccc gaaggttatg tacaggaaag gaccatcttc 1740
 ttcaaagatg acggcaacta caagacacgt gctgaagtca agtttgaagg tgataccctt 1800
 gttaatagaa tcgagttaaa aggtattgac ttcaaggaag atggcaacat tctgggacac 1860
 aaattggaat acaactataa ctacacaaat gtatacatca tggcagacaa acaaaagaat 1920
 ggaatcaaag tgaacttcaa gaccgcccac aacattgaag atggaagcgt tcaactagca 1980
 gaccattatc aacaaaatac tccaattggc gatggcctg tccttttacc agacaacat 2040
 tacctgtcca cacaatctgc ctttcgaaa gatcccaacg aaaagagaga ccacatggtc 2100
 cttcttgagt ttgtaacagc tgctgggatt acacatggca tggatgaact gtacaactga 2160

<210> 220

<211> 1776

<212> DNA

<213> Human

<400> 220

atggaaacca acttctccat tctctgaat gaaactgagg aggtgctccc tgagcctgct 60
 ggccacaccg ttctgtgat cttctcattg ctagtccacg gaticacctt tgtcttcggg 120
 gtcctgggca atgggcttgt gatctgggtg gctggattcc ggatgacacg cacagtcaac 180
 accatctgtt acctgaacct ggccctagct gacttctctt tcagtcccat cctaccattc 240
 cgaatggctc cagtcgcat gagagaaaaa tggccttttg gctattcct atgtaagtta 300
 gtcatgtta tgatagacat caacctgttt gtcagtgtct acctgatcac catcattgct 360
 ctggaccgct gtatttgtgt cctgcatcca gccggggccc agaaccatcg caccatgagt 420

496/518

```

ctggccaaga gggtagatgac gggactctgg attttcacca tagtccttac cttaccaaatt 480
ttcatcttct ggactacaat aagtactacg aatggggaca catactgtat tttcaacttt 540
gcattctggg gtgacactgc ttagagagg ttgaacgtgt tcattaccat ggccaaggtc 600
tttctgatcc tccacttcat tattggcttc agcgtgccta tgtccatcat cacagtctgc 660
tatgggatca tcgctgcaa aattcacaga aaccacatga ttaaattccag ccgtccctta 720
cgtgtcttcg ctgctgtggt ggcttcttct ttcactctgt ggttccctta tgaactaatt 780
ggcattctaa tggcagctcg gctcaaagag atgttggtta atggcaaata caaatcatt 840
cttgcctga ttaaccaaac aagctccttg gcctttttta acagctgcct caaccaatt 900
ctctacgtct ttatgggtcg taacttcaa gaaagactga ttgctcttt gccactagt 960
ttggagaggg ccctgactga ggtccctgac tcagcccaga ccagcaacac agacaccact 1020
tctgttcac ctctgagga gacggagta caagcaatgg ctagcaaagg agaagaactc 1080
ttcactggag ttgtcccaat tcttgttgaa ttagatggtg atgttaacgg ccacaagttc 1140
tctgtcagtg gagagggtga aggtgatgca acatacgga aacttaccct gaagttcatc 1200
tgcactactg gcaactgcc tgttccatgg ccaacactag tcaactactt gtgctatggt 1260
gttcaatgct tttcaagata cccgatcat atgaaacggc atgacttttt caagagtgcc 1320
atgcccgaag gttatgtaca ggaaaggacc atcttcttca aagatgacgg caactacaag 1380
acacgtgctg aagtcaagtt tgaagggtat acccttgta atagaatcga gttaaaaggt 1440
attgacttca aggaagatgg caacattctg ggacacaaat tggaaataca ctataactca 1500
cacaatgtat acatcatggc agacaaacaa aagaatggaa tcaaagtga cttcaagacc 1560
cgccacaaca ttgaagatgg aagcgttcaa ctgacagacc attatcaaca aaatactcca 1620
attggcgatg gccctgtcct tttaccagac aaccattacc tgtccacaca atctgccctt 1680
tcgaaagatc ccaacgaaaa gagagaccac atggctcttc ttgagtttgt aacagctgct 1740
gggattacac atggcatgga tgaactgtac aactga 1776

```

<210> 221

<211> 1785

<212> DNA

<213> Human

497/518

<400> 221

atgaatgggg tctcggaggg gaccagaggg tgcagtgaca ggcaacctgg ggtcctgaca	60
cgtgatcgct cttgttccag gaagatgaac tcttccggat gcctgtciga ggaggtgggg	120
tccctccgcc cactgactgt ggttatcctg tctgcgtcca ttgtcgtcgg agtgctgggc	180
aatgggctgg tgcgtggat gactgtcttc cgtatggcac gcacggcttc caccgtctgc	240
ttcttccacc tggcccttgc cgatttcatg ctctcactgt ctctgccc atgccaatgtac	300
tatatgtctt ccaggcagtg gctcctcgga gagtgggcct gcaaactcta catcaccttt	360
gtgttctca gctactttgc cagtaactgc ctcttgtct tcatctctgt ggaccgttgc	420
atctctgtcc tctaccccg tggggccctg aaccaccgca ctgtgcagcg ggcgagctgg	480
ctggcccttg ggggtggct cctggccgcc gccttgtgt ctgcgcacct gaaattccgg	540
acaaccagaa aatggaatgg ctgtacgcac tgcacttgg cgttcaactc tgacaatgag	600
acigcccaga ttggattga aggggtcgtg gagggacaca ttataggac catlggccac	660
ttcctgctgg gcttccctgg gcccttagca atcataggca cctgcgcca cctcatccgg	720
gccaaactct tgcgggaggg ctgggtccat gccaacgggc ccaagaggct gctgctggtg	780
ctggtagcgg ctttctttat cttctggctc ccgtttaacg tggtagctgtt ggtccatctg	840
tggcgacggg tgatgctcaa ggaaactac caccgccga tgcgtctcat cctccaggct	900
agctttgcct tgggctgtgt caacagcagc ctcaacccct tcctctacgt cttcgttggc	960
agagatttcc aagaaaagt tttccagtct ttgacttctg ccctggcgag ggcgtttgga	1020
gaggaggagt ttctgtcatc ctgtcccggt ggcaacggcc cccgggaagc tagcaaagga	1080
gaagaactct tcaactggagt tgtcccaatt cttgttgaat tagatgtga tgttaacggc	1140
cacaagtctt ctgtcagtgg agagggtgaa ggtagtgcaa catacggaaa acttaccctg	1200
aagttcatct gcactactgg caaactgcct gtccatggc caacactagt cactactctg	1260
tgctatggtg ttcaatgctt ttcaagatac ccgatacata tgaaacggca tgactttttc	1320
aagagtcca tggccgaagg ttatgtacag gaaaggacca tcttcttcaa agatgacggc	1380
aactacaaga cacgtgctga agtcaagttt gaaggigata ccttgttaa tagaatcgag	1440
ttaaaaggta ttgacttcaa ggaagatggc aacattctgg gacacaaatt ggaatacaac	1500
tataactcac acaatgtata catcatggca gacaaacaaa agaattggaat caaagtgaac	1560
ttcaagaccc gccacaacat tgaagatgga agcgtticaac tagcagacca ttatcaacaa	1620
aataticcaa ttggcgatgg cctgtctctt ttaccagaca accattacct gtccacacaa	1680

498/518

tctgcccttt cgaagatcc caacgaaaag agagaccaca tggctcttct tgagtttgta 1740
 acagctgctg ggattacaca tggcatggat gaactgtaca actga 1785

<210> 222

<211> 4380

<212> DNA

<213> Human

<400> 222

atgatgtttc gctcagatcg aatgtggagc tgccattgga aatggaagcc cagtcctctc 60
 ctgttcttat ttgctttata tatcatgtgt gtctctcact cagtggtggg atgtgccaac 120
 tgccgagtggt ttttgtccaa ccttcttggg acctttactt ctccatgcta ccctaacgac 180
 tacccaaaca gccaggcttg catgtggacg ctccgagccc ccaccggta tatcattcag 240
 ataacattta acgactttga cattgaagaa gctcccaatt gcatttatga ctcatatcc 300
 cttgataatg gagagagcca gactaaattt tgtggagcaa ctgccaaagg cctatcattt 360
 aactcaagtg cgaatgagat gcatgtgtcc ttttcaagtg acttttagcat ccagaagaaa 420
 ggtttcaalg ccagctacat cagagttgcc gtgtccttaa ggaatcaaaa ggtcatttta 480
 cccagacat cagatgctta ccaggatatct gttgcaaaaa gcatctctat tccagagctc 540
 agtgctttca cactctgctt tgaagcaacc aaagttggcc atgaagacag tgattggaca 600
 gccttctcct actcaaatgc atccttcaca caattgtca gttttggaaa ggccaagagt 660
 ggctactttc tatccatttc tgattcaaaa tgtttgttga ataattgcatt acctgtcaaa 720
 gaaaaagaag acatttttgc agaaagcttt gaacagctct gccttgtttg gaataattct 780
 ttgggctcta ttgggtgtaa ttcaaaaaga aactatgaaa cagttccatg tgattctacc 840
 attagtaaag ttattccttg gaatgggaaa ttgttgttgg gctccaatca aaatgaaatt 900
 gtctctctaa aaggggacat ttataacttt cgactttgga attttacat gaatgcaaaa 960
 atcctctcca acctcagctg taatgtgaaa gggaatgtag tcgactggca aaatgacttc 1020
 tggaatatcc caaacctagc tctgaaagct gaaagcaacc taagctgtgg ttcttacctg 1080
 atcccgtcc cagcagcaga actggccagc tgtgcagacc tggggaccct ctgtcaagct 1140
 actgtaaact ctcttagtac tacaccaccc actgtcacca ctaacatgcc tgttactaac 1200

499/518

agaatcgata aacaaaggaa tgatggaatt atciatagaa tatccgtagt gattcagaac 1260
 atccctcgic accctgaggt aaaagtacag agcaaggigg cagaatggct caattcaacc 1320
 ttccaaaatt ggaactacac ggtttatgtc gttaatatca gtttcacct gaggctgga 1380
 gaggacaaga ttaaagtc aaagaagcctt gaggatgagc caaggttggt gccttgggcc 1440
 cttctagttt acaatgctac caacaatact aattitagaag gaaaaatcat tcagcagaag 1500
 ctcttaaaaa ataatgagtc ctgggatgaa ggcttgaggc tacatacagt gaatgtgaga 1560
 caactgggtc attgtcttgc catggaggaa cccaaaggct actactggcc atciatccaa 1620
 ccttctgaat acgttcttcc ttgtccagac aagcctggct tttctgcttc tcggatatgt 1680
 ttttacaatg ctaccaaccc attggttaacc tactggggac ctgttgatat ctccaactgt 1740
 ttaaaagaag caaatgaagt tgctaaccag attttaaatt taactgctga tgggcagaac 1800
 ttaacctcag ccaatattac caacattgtg gaacaggctc aaagaattgt gaataaagaa 1860
 gaaaacattg atataacact tggtcaact ctaatgaata tattttctaa tatcttaagc 1920
 agttcagaca gtgacttgct tgagtcactt tctgaagcct taaaaacaat tgaigaattg 1980
 gccttcaaga tagacctaaa tagcacatca catgtgaata ttacaactcg gaactiggct 2040
 ctacgcgtat catccctgtt accaggagaa aatgcaattt caaatcttag cattggcttt 2100
 ccaagcaata atgaatcgta tttccagatg gattttgaga gtggacaagt ggatccactg 2160
 gcatctgtaa ttttgcctcc aaacttactt gagaatttaa gtccagaaga ttctgtatta 2220
 gttagaagag cacagtttac tttcttcaac aaaactggac tttccagga ttaggaccc 2280
 caaagaaaaa ctttagtgag ttatgtgatg gcgtgcagta ttggaaacat tactatccag 2340
 aatctgaagg atccgttca aataaaaaac aaacatacaa gaactcagga agtgcacat 2400
 cccatctgtg ccttctggga tctgaacaaa aacaaaagt ttggaggatg gaacacgtca 2460
 ggatgtgttg cacacagaga ttcatatgca agtgagacag tctgcctgtg taaccacttc 2520
 acacactttg gagttctgat ggaccttcca agaagtgcct cacagttaga tgcaagaaac 2580
 actaaagtcc tcactttcat cagctatatt ggggtgtgga tatctgctat ttttcagca 2640
 gcaactctcc tgacataatg tgcttttgag aaattgcaa gggattatcc ctccaaaac 2700
 ttgatgaacc tgagcacagc ctgtctgttc ctgaatctcc tcttctctct agatggctgg 2760
 atcacctcct tcaatgtgga tggacttgc attgtgttg cagtcctgtt gcatttcttc 2820
 cttctggcaa cctttacctg gatggggcta gaagcaattc acatgtacat tgctctagtt 2880
 aaaglatitaa acattacat tcgccgatac attctaaaat tctgcatcat tggctggggt 2940

500/518

ttgcctgcct tagtgggtgc agttgttcta gcgagcagaa acaacaatga agtctatgga 3000
aaagaaagtt atgggaaaga aaaaggatga gaattctgtt ggattcaaga tccagtcata 3060
ttttatgtga cctgtgctgg gtattttgga gtcatgtttt ttctgaacat tgccatgttc 3120
attgtggtaa tggigcagat ctgtgggagg aatggcaaga gaagcaaccg gaccctgaga 3180
gaagaagigt taaggaacct gcgcagtgtg gttagcttga cttttctgtt gggcatgaca 3240
tggggttttg cattctttgc ctggggaccc ttaaataacc ctttcattga cctcttctcc 3300
atcttcaatt cattacaagg cttatttata ttcatcttcc actgtgctat gaaggagaat 3360
gttcagaaac agtggcggcg gcatctctgc tgtggtagat ttgggttagc agataactca 3420
gattggagta agacagctac caatatcatc aagaaaagtt ctgataatct aggaaaatct 3480
ttgtcttcaa gctccattgg ttccaactca acctatctta catccaaatc taaatccagc 3540
tctaccacct atttcaaaag gaatagccac acagataatg tctcctatga gcattccttc 3600
aacaaaagtg gatcactcag acagtgttc catggacaag tccttgtcaa aactggccca 3660
tgctctagca aaggagaaga actcttcact ggagttgtcc caattcttgt tgaattagat 3720
ggtagatgta acggccacaa gtctctctgc agtggagagg gtgaaggtga tgcaacatac 3780
ggaaaactta ccctgaagtt catctgcact actggcaaac tgccgtgttc atggccaaca 3840
ctagtcacta ctctgtgcta tggigttaa tgcttttcaa gataccgga tcatatgaaa 3900
cggcatgact ttttcaagag tgccatgccc gaaggttatg tacaggaaag gaccatcttc 3960
ttcaaagatg acggcaacta caagacacgt gctgaagtca agtttgaagg tgataccctt 4020
gttaatagaa tcgagttaaa aggtattgac ttcaaggaag atggcaacat tctgggacac 4080
aaattggaat acaactataa ctacacacat gtatacatca tggcagacaa acaaaagaat 4140
ggaatcaaag tgaacttcaa gacccgccac aacattgaag atggaagcgt tcaactagca 4200
gaccattatc aacaaaatac tccaattggc gatggccctg tccttttacc agacaacat 4260
tacctgtcca cacaatctgc ctttctgaaa gatcccaacg aaaagagaga ccacatggtc 4320
cttcttgagt ttgtaacagc tgcitgggatt acacatggca tggatgaact gtacaactga 4380

<210> 223

<211> 1914

<212> DNA

<213> Human

501/518

<400> 223

atggctcaaa ggcagcctca ctcacctaat cagacittaa tttcaatcac aaatgacaca	60
aatcatcaa gctcigtggt ttctaacgat aacacaaaata aaggatggag cggggacaac	120
tctccaggaa tagaagcatt gtgtgccatc tatattactt atgctgtgat catttcagtg	180
ggcatccttg gaaatgctat tctcatcaaa gtctttttca agaccaaata catgcaaaca	240
gttccaaaata ttttcatcac cagcctggct ttgggagatc ttttacttct gctaacttgt	300
gtgccagtgg atgcaactca ctaccttgca gaaggatggc tgttcggaag aattggttgt	360
aaggigtctct ctttcatccg gctcacttct gtgggtgtgt cagtgttcac attaacaaatt	420
ctcagcgctg acagatacaa ggcagttgtg aagccacttg agcgacagcc ctccaatgcc	480
atcctgaaga ctgtgtgtaa agctggctgc gctcggatcg tgtctatgat atttgctcta	540
ccgaggctia tattttcaaa tgtatacact ttccgagatc ccaataaaaa tatgacattt	600
gaatcatgia cctcttattc tgtctciaag aagctcttgc aagaaataca ttctctgctg	660
tgttctttag tgttctacat tatccactc tctattatct ctgtctacta ttccttgatt	720
gctaggaccc tttaaaaaag caccctgaac atacctactg aggaacaaag ccatgcccgt	780
aagcagattg aatcccgaaa gagaattgcc agaacggat tgggtgttgg ggctctgttt	840
gcccctctgt gggtgccaaa tcacctctg tacctctacc attcattcac ttctcaaacc	900
tatgtagacc cctctgccat gcatttcatt ttaccattt tctctcgggt ttggcttctc	960
agcaattctt gcgtaaaccc ctttgctctc tactggctga gcaaaagctt ccagaagcat	1020
tttaaagctc agttgttctg ttgcaaggcg gagcggcctg agcctcctgt tgcctgacacc	1080
tctcttacca ccctggctgt gatgggaacg gtcccgggca ctgggagcat acagatgtct	1140
gaaattagtg tgacctcgtt cactgggtgt agtgtgaagc aggcagagga cagattcgt	1200
agcaaaggag aagaactctt cactggagt gtcccaattc ttgttgaatt agatggtgat	1260
gttaacggcc acaagtctc tgtcagtga gaggggtgaag gtgatgcaac atacggaaaa	1320
cttaccctga agttcatctg cactactggc aaactgcctg ttccatggcc aacactagtc	1380
actactctgt gctatggtgt tcaatgcctt tcaagatacc cggatcataat gaaacggcat	1440
gactttttca agagtgccat gccgaaggt tatgtacagg aaaggacct cttcttcaaa	1500
gatgacggca actacaagac acgtgctgaa gtcaagtttg aaggtagtac cttgttaaat	1560
agaatcgagt taaaaggat tgaattcaag gaagatggca acattctggg acacaaattg	1620

502/518

gaatacaact ataactcaca caatgtatac atcatggcag acaaacaaaa gaatggaatc 1680
 aaagtgaact tcaagacccg ccacaacatt gaagatggaa gcgttcaact agcagacat 1740
 tatcaacaaa atactccaat tggcgaatggc cctgtccitt taccagacaa ccattacctg 1800
 tccacacaat ctgccctttc gaaagatccc aacgaaaaga gagaccacat ggtcctttctt 1860
 gagtttgtaa cagctgctgg gattacacat ggcatggatg aactgtacaa ctga 1914

<210> 224

<211> 2076

<212> DNA

<213> Human

<400> 224

atggcttcac ccagcctccc gggcagtgac tgctcccaaa tcattgatca cagtcatgtc 60
 cccgagtttg aggtggccac ctggatcaaa atcaccctta ttctgggtga cctgatcatc 120
 ttctgatgg gccctctggg gaacagcgcc accattcggg tcaccaggt gctgcagaag 180
 aaaggatact tgcagaagga ggtgacagac cacatggtga gtttggcttg ctcgacatc 240
 ttgggtgtcc tcatcggcat gcccatggag ttctacagca tcatctggaa tccccgacc 300
 acgtccagct acaccctgtc ctgcaagctg cacactttcc tcttcgaggc ctgcagctac 360
 gctacgctgc tgcacgtgct gacactcagc tttagcgct acatcgccat ctgtaccccc 420
 ttcaggtaca aggtgtgtc gggaccttgc caggtgaagc tgctgattgg cttcgtctgg 480
 gtcacctccg ccttgggtgg acctgccctg ctgtttgcca tgggtactga gtacccccctg 540
 gtgaacgtgc ccagccaccg gggctcact tgcaaccgct ccagcaccg ccaccacgag 600
 cagcccgaga cctccaatat gtccatctgt accaacctct ccagccgctg gaccgtgtc 660
 cagtccagca tcttcggcgc ctctgtgtc tacctcgtgg tctgtctctc cgtagccttc 720
 atgtgctgga acatgatgca ggtgctcatg aaaagccaga agggctcgtt ggccgggggc 780
 acgcggcctc cgcagctgag gaagtcagag agcgaagaga gcaggaccgc caggaggcag 840
 accatcatct tctgaggct gattgttgtg acattggccg tatgtcggat gcccaaccag 900
 attcggagga tcatggctgc ggccaaacct aagcacgact ggacgaggtc ctacttccgg 960
 gcgtacatga tctcctccc ctctcggag acgtttttct acctcagctc ggtcatcaac 1020

503/518

ccgctccgtg acacgggtgc ctgcagcag ttccggcggg tgttcgtgca ggtgctgtgc 1080
 tgccgcctgt cgctgcagca cgccaaccac gagaagcgcc tgcgcgtaca tgcgcactcc 1140
 accaccgaca gcgcccgtt tgtgcagcgc ccgttgctct tcgcgtcccg gcgccagtc 1200
 tctgcaagga gaactigaga gattttctta agcacttttc agagcgaggc cgagccccag 1260
 tctaagtccc agtcattgag tctcgagtca ctgagccca actcaggcgc gaaaccagcc 1320
 aattctgtgt cagagaatgg ttttcaggag catgaagtgt ctgcaaagg agaagaactc 1380
 ttacttgtag ttgtcccaat tcttggtgaa ttagatgggt atgttaacgg ccacaagttc 1440
 tctgtcagtg gagagggtga aggtgatgca acatacggaa aacttaccct gaagttcatc 1500
 tgcactactg gcaaactgcc tgttccatgg ccaacactag tcactactct gtgctatggt 1560
 gttcaatgct tttcaagata cccgatcat atgaaacggc atgacttttt caagagtgcc 1620
 atgcccgaag gttatgtaca ggaaaggacc atcttcttca aagatgacgg caactacaag 1680
 acacgtgctg aagtcagtt tgaagggtat acccttggtt atagaatcga gttaaaaggt 1740
 attgacttca aggaagatgg caacattctg ggacacaaat tggaatacaa ctataactca 1800
 cacaatgtat acatcatggc agacaaacaa aagaatggaa tcaaagtga cttcaagacc 1860
 cgccacaaca ttgaagatgg aagcgttcaa ctgacagacc attatcaaca aaatactcca 1920
 attggcgatg gccctgtcct tttaccagac aaccattacc tgtccacaca atctgccctt 1980
 tcgaaagatc ccaacgaaaa gagagaccac atggtccttc ttgagttgt aacagctgct 2040
 gggattacac atggcatgga tgaactgtac aactga 2076

<210> 225

<211> 1986

<212> DNA

<213> Human.

<400> 225

atggtcctc acctcttctg gctctgtctc ctccccttgg tgcgagccac cgagccccac 60
 gagggccggg ccgacgagca gagcgcggag gggcccttgg ccgtgcccac tgcctcgcac 120
 ttcttctctt ggaacaacta cactttctcc gactggcaga actttgtggg caggaggcgc 180
 tacggcgctg agtcccagaa cccacgggtg aaagccctgc tcattgtggc ttactccttc 240

504/518

atcattgtct tctcactctt tggcaacgtc ctggctctgt atgtcatctt caagaaccag 300
 cgaatgcact cggccaccag cctcttcac gtcaacctgg cagttgccga cataatgatc 360
 acgtctctca acacccccct cactttgggt cgctttgtga acagcacatg gatatttggg 420
 aagggcatgt gccatgtcag ccgctttgcc cagtactgtt cactgcacgt ctacagcactg 480
 acactgacag ccattgcggt ggatcgccac caggtcacat tgcacccccct gaaacccccg 540
 atctcaatca caaaggggt catctacac gtgtcatctt ggaccatggc tacgttcttt 600
 tcactccac atgtatctg ccagaaatta ttacattca aatacagta ggacattgtg 660
 cgctccctct gcctgccaga ctccctgag ccagctgacc tcttctggaa gtacctggac 720
 ttggccacct tcatctgt ctacatctg cccctctca tcatctctgt ggcctacgt 780
 cgtgtggcca agaaactgt gtgtgtaat atgattggcg atgtgaccac agagcagtac 840
 ttggccctgc ggcgcaaaaa gaagaagacc atcaagatgt tgaatgtgtt gtagtcctc 900
 ttggccctct gtgtgttccc cctcaactgc tacgtctccc tctgtccag caaggtcatc 960
 cgcaccaaca atgccctcta ctttgccctc cactggtttg ccatgagcag caccigtat 1020
 aacccccctc tatactgtgt gtgaacgag aacttcagga ttgagctaaa ggcattactg 1080
 agcatgtgtc aaagacctcc caagcctcag gaggacaggc caccctcccc agttccttcc 1140
 ttcaggtgtg cctggacaga gaagaatgat ggccagaggg ctccccctgc caataacctc 1200
 ctgcccacct cccaactcca gtctgggaag acagacctgt catctgtgga acccattgtg 1260
 acgatgagt ctagcaaagg agaagaactc ttcactggag ttgtcccaat tcttgttga 1320
 ttagatgtgt atgttaacgg ccacaagttc tctgtcagt gagagggtga aggtgatgca 1380
 acatacgga aacttacct gaagttcatc tgcactactg gcaaactgcc tgttccatgg 1440
 ccaacactag tcaactact gtgtatgtt gttaaatgt tttcaagata cccggatcat 1500
 atgaaacggc atgacttttt caagagtgc atgccgaag gttatgtaca ggaaaggacc 1560
 atcttcttca aagatgacgg caactacaag acacgtgtgt aagtcaagtt tgaaggatg 1620
 acccttgta atagaatcga gttaaaaggt attgacttca aggaagatgg caacattctg 1680
 ggacacaaat tgaatacaa ctataactca cacaatgtat acatcatggc agacaaacaa 1740
 aagaatggaa tcaaagtga cttcaagacc cgccacaaca ttgaagatgg aagcgttcaa 1800
 ctacgagacc attatcaaca aaatactcca attggcgatg gccctgtcct ttaccagac 1860
 aaccattacc tgtccacaca atctgccctt tcgaaagatc ccaacgaaa gagagaccac 1920
 atgtctctc ttgagttgt aacagctgtt gggattacac atggcatgga tgaactgtac 1980

505/518

aactga

1986

<210> 226

<211> 1905

<212> DNA

<213> Human

<400> 226

atgtggaaca gctctgacgc caactttctcc tgctaccatg agtctgtgct gggctatcgt	60
tatgtttgcag itagctgggg ggtgggtgtg gctgtgacag gcaccgtggg caatgtgctc	120
accctactgg ccttggccat ccagcccaag ctccgtaccc gattcaacct gctcatagcc	180
aacctcacac tggctgatct cctctactgc acgtctcttc agcccttctc tgtggacacc	240
tacctccacc tgcactggcg caccggtgcc acctcttgca gggatatttg gctcctcctt	300
tttgccctcca attctgtctc catctgacc ctctgcctca tcgcactggg acgtacctc	360
ctcatigccc accctaagct ttttcccaa gttttcagtg ccaaggggat agtgctggca	420
ctggtagaca cctgggttgt gggcgtggcc agctttgctc ccctctggcc tatttatatc	480
ctggtacctg tagtctgcac ctgcagcttt gaccgcatcc gaggccggcc ttacaccacc	540
atcctcatgg gcatctactt tgtgcttggg ctgagcagtg ttggcatctt ctattgcctc	600
atccaccgcc aggtcaaacg agcagcacag gcactggacc aatacaagtt gcgacaggca	660
agcatccact ccaacctgt ggccaggact gatgaggcca tgcctggctg tttccaggag	720
ctggacagca ggtagcatc aggaggaccc agtgaggga tttcatctga gccagtcagt	780
gctgccacca ccagaccct ggaaggggac tcatcagaag tgggagacca gatcaacagc	840
aagagagcta agcagatggc agagaaaagc cctccagaag catctgcaa agcccagcca	900
attaaaggag ccagaagagc tccgattct tcatcggaat ttgggaaggt gactcgaatg	960
tgttttgctg tgttctctg ctttgccctg agctacatcc cttcttgct gctcaacatt	1020
ctggatgcca gagtccaggc tccccgggtg gtccacatgc ttgctgcaa cctcacctgg	1080
ctcaatggtt gcatcaaccc tgtgctctat gcagccatga accgccaatt ccgccaagca	1140
tatggctcca ttttaaaaag agggccccgg agtttccata ggctccatgc tagcaaagga	1200
gaagaactct tcactggagt tgtcccaatt ctgttgaat tagatggtga tgttaacggc	1260

506/518

cacaagtict ctgtcagtgg agagggigaa ggtgatgcaa catacgaaa acttaccctg 1320
 aagttcatct gcactactgg caaactgcct gttccatggc caacactagt cactactctg 1380
 tgctatggig ttcaatgctt ttcaagatac ccggatcata tgaaacggca tgacttttct 1440
 aagagtcca tgcccgaagg ttatgtacag gaaaggacca tcttcttcaa agatgacggc 1500
 aactacaaga cactgctga agtcaagttt gaaggtgata ccttggtaa tagaatcgag 1560
 ttaaaaggta ttgacttcaa ggaagatggc aacattctgg gacacaaatt ggaatacaac 1620
 tataactcac acaatgtata catcatggca gacaaacaaa agaattggaat caaagtgaac 1680
 ttcaagaccc gccacaacat tgaagatgga agcgttcaac tagcagacca ttatcaacaa 1740
 aatactccaa ttggcgatgg cctgtcctt ttaccagaca accattacct gtccacacaa 1800
 tctgcccttt cgaaagatcc caacgaaaag agagaccaca tggctcttct tgagtttgta 1860
 acagctgctg ggattacaca tggcatggat gaactgtaca actga 1905

<210> 227

<211> 1764

<212> DNA

<213> Human

<400> 227

atgaactcca ccttggatgg taatcagagc agccaccctt ttgcctctt ggcatttggc 60
 tatttgaaa ctgtcaattt ttgccttttg gaagtattga ttattgtctt tctaactgta 120
 ttgattattt ctggcaacat cattgtgatt ttgtatttc actgtgcacc ttgttgaac 180
 catcacacta caagttattt tatccagact atggcataatg ctgacctttt tgttggggtg 240
 agctgcgtgg tcccttcttt atcactcctc catcaccccc ttccagtaga ggagtccttg 300
 acttgccaga tatttggttt tglagtatca gttctgaaga gcgtctccat ggcttctctg 360
 gcctgtatca gcattgatag atacattgcc attactaaac ctttaacctt taatactctg 420
 gttacacctt ggagactacg cctgtgtatt ttcctgattt ggctatactc gacctgggc 480
 ttcttgctt cctttttcca ctggggcaaa cctggatata atggagatgt gtttcagtgg 540
 tgtgcggagt cctggcacac cgactcctac ttcacctgt tcatcgtgat gatgttatat 600
 gccccagcag ccttatttgt ctgcttcacc tatttcaaca tcttccgat ctgccaacag 660

507/518

cacacaaagg atatcagcga aaggcaagcc cgcttcagca gccagagtgg ggagactggg 720
 gaagtgcagg cctgtcctga taagcgctat gccatgggcc tgtttcgaat cactagtgtgta 780
 ttttacatcc tctggttgcc atataatcct tacttcttgt tggaaagctc cactggccac 840
 agcaaccgct tcgcatcctt ctgaccacc tggcttgcta ttagtaacag tttctgcaac 900
 tgtgtaatat atagtctctc caacagtgtg ttccaaagag gactaaagcg cctctcaggg 960
 gctatgtgtg ctctctgtgc aagtcagact acagccaacg acccttacac agttagaagc 1020
 aaaggccctc ttaatggatg tcataatcgt agcaaaggag aagaactctt cactggagtt 1080
 gtcccaattc ttgttgaatt agatgggatg gttacggcc acaagtctc tgtcagtgtg 1140
 gaggggtgaag gtgatgcaac atacggaaaa cttaccctga agttcatctg cactactggc 1200
 aaactgcctg ttccatggcc aacactagtc actactctgt gctatgggtg tcaatgcttt 1260
 tcaagatacc cggatcataat gaaacggcat gactttttca agagtccat gccgaaggt 1320
 tatgtacagg aaaggacat ctctctcaaa gatgacggca actacaagac acgtgctgaa 1380
 gtcaagtttg aagggtgata ccttgttaat agaatcgagt taaaaggatg tgacttcaag 1440
 gaagatggca acattctggg acacaaattg gaatacaact ataactcaca caatgtatac 1500
 atcatggcag acaaacaaaa gaatggaatc aaagtgaact tcaagaccgg ccacaacatt 1560
 gaagatggaa gcgttcaact agcagacat tatcaacaaa atactccaat tggcgatggc 1620
 cctgtccttt taccagacaa ccattacctg tccacacaa ctgcccttc gaaagatccc 1680
 aacgaaaaga gagaccacat ggtccttctt gagtttgtta cagctgctgg gattacacat 1740
 ggcatggatg aactgtacaa ctga 1764

<210> 228

<211> 3570

<212> DNA

<213> Human

<400> 228

atgccggggc cgctagggct gctctgcttc ctgccctgg ggctgctcgg ctggccggg 60
 cccagcggcg cggcgccgcc tctctgcgcg gcgccctgca gctgcgacgg cgaccgtcgg 120
 gtggactgct ccgggaaggg gcigacggcc gtgcccgagg ggctcagcgc ctaccccaa 180

508/518

gcgctggata tcagtatgaa caacattact cagttgccag aagatgcatt taagaacttt 240
 ccttttctag aagagctaca attggcgggc aacgaccttt cttttatcca cccaaaggcc 300
 ttgtctgggt tgaagaact caaagttcta acgctccaga ataatcagtt gaaaacagta 360
 cccagigaag ccattcgagg gctgagtgtt ttgcagtcct tgcgtttaga tgccaacat 420
 attacctcag tccccgagga cagttttgaa ggacttggtc agttacggca tctgtggctg 480
 gatgacaaca gcttgacgga ggtgcctgtg caccctctca gcaatctgcc caccctacag 540
 gcgctgaccc tggctctcaa caagatctca agcatccctg actttgcatt taccaacctt 600
 tcaagcctgg tagttctgca tcttcataac aataaaatta gaagcctgag tcaacactgt 660
 tttgatggac tagataacct ggagacctta gacttgaatt ataataactt gggggaattt 720
 cctcaggcta ttaaagccct tcttagcctt aaagagctag gatttcatag taattctatt 780
 tctgttatcc ctgatggagc atttgatggt aatccactct taagaactat acatttgtat 840
 gataatcctc tgtcttttgt ggggaactca gcatttcaca atttatctga tcttcattcc 900
 ctagtcatte gtgggtgaag catgggtcag cagttcccca atcttacagg aactgtccac 960
 ctggaaagtc tgactttgac aggtacaaag ataagcagca tacctaataa ttgtgttcaa 1020
 gaacaaaaga tgcttaggac ttgggacttg tcttacaata atataagaga ccttccaagt 1080
 tttaatggtt gccatgctct ggaagaaatt tctttacagc gtaatcaaat ctaccaataa 1140
 aaggaaggca cctttcaagg cctgatatct ctaaggattc tagatctgag tagaaacctg 1200
 atacatgaaa ttcacagtag agcttttgcc acacttgggc caataactaa cctagatgta 1260
 agtttcaatg aattaacttc ctttctacg gaaggcctga atgggctaaa tcaactgaaa 1320
 cttgtgggca acttcaagct gaaagaagcc ttagcagcaa aagactttgt taacctcagg 1380
 tctttatcag taccataatg ttatcagtgc tgtgcatttt ggggttgtga ctcttatgca 1440
 aatttaaaca cagaagataa cagcctccag gaccacagtg tggcacagga gaaaggtact 1500
 gctgatgcag caaatgtcac aagcactctt gaaaatgaag aacatagtca aataattatc 1560
 cattgtacac cttaacagg tgcctttaag cccigtgaat atttactggg aagctggatg 1620
 attcgtctta ctgtgtggtt cattttcttg gtigcattat ttttcaacct gcttgttatt 1680
 ttaacaacat ttgcacttg tacatcactg ccttcgtcca aattgtttat aggcttgatt 1740
 tctgtgtcta acttattcat gggaatctat actggcatcc taacttttct tgatgctgtg 1800
 tcttggggca gattcgctga atttggcatt tgggtggcaa ctggcagttg ctgcaaagta 1860
 gctgggtttc ttgcagtttt ctctcagaa agtgccatat ttttattaat gctagcaact 1920

509/518

gtcgaaagaa gcttatctgc aaaagatata atgaaaaatg ggaagagcaa tcatctcaaa 1980
 cagttccggg ttgctgccct tttggcttcc ctaggigcta cagtagcagg ctgttttccc 2040
 cttttccata gaggggaata ttctgcatca cccctttgtt tgccatttcc tacaggigaa 2100
 acgccatcat taggattcac tgtaacgtta gtgctattaa actcactagc atttttatta 2160
 atggccgtta tctacactaa gctatactgc aacttggaaa aagaggacct ctgagaaaac 2220
 tcacaatcta gcatgattaa gcatgtcgct tggctaactc tcaccaattg catcttttcc 2280
 tgccctgtgg cgtttttttc atttgcacca ttgatcactg caatctctat cagccccgaa 2340
 ataatgaagt ctgttactct gatatttttt ccattgccctg ctigccctgaa tccagtccctg 2400
 tatgttttct tcaacccaaa gtttaaagaa gacttgaagt tactgaagcg acgtgttacc 2460
 aagaaaagt gatcagtttc agtttccatc agtagccaag gtggttgtct ggaacaggat 2520
 ttctactacg actgtggcat gtactacatc ttgcagggca acctgactgt ttgcgactgc 2580
 tgcgaatcgt ttcttttaac aaagccagta tcatgcaaac acttgataaa atcacacagc 2640
 tgccttgcct tggcagtggc ctcttgccaa agacctgagg gctacttggtc cgactgtggc 2700
 acacagtcgg cccactctga ttatgcagat gaagaagatt cctttgtctc agacagttct 2760
 gaccaggctg aggcctgtgg acgagcctgc ttctaccaga gtagaggatt ccccttggtg 2820
 cgctatgcct acaatctacc aagagttaaa gacactagca aaggagaaga actcttactc 2880
 ggagtgttcc caattcttgt tgaattagat ggigatgtta acggccacaa gttctctgtc 2940
 agtggagagg gtgaaggiga tgcaacatac ggaaaactta ccttgaagtt catctgcact 3000
 actggcaaac tgcctgttcc atggccaaca ctagtacta ctctgtgcta tgggtttcaa 3060
 tgcttttcaa gatacccgga tcatatgaaa cggcatgact ttttcaagag tgccatgccc 3120
 gaaggttatg tacaggaaag gaccatcttc ttcaaagatg acggcaacta caagacacgt 3180
 gctgaagtca agtttgaagg tgataccctt gttaatagaa tcgagttaaa aggtattgac 3240
 ttcaaggaag atggcaacat tctgggacac aaattggaat acaactataa ctacacaaat 3300
 gtatacatca tggcagacaa acaaaagaat ggaatcaaag tgaacttcaa gaccgcccac 3360
 aacattgaag atggaagcgt tcaactagca gaccattatc aacaaaatac tccaattggc 3420
 gatggccctg tctttttacc agacaacctt tactgttcca cacaatctgc cttttcgaaa 3480
 gatcccaacg aaaagagaga ccacatggtc cttcttgagt ttgtaacagc tgcgtggatt 3540
 acacatggca tggatgaact gtacaactga 3570

510/518

<210> 229

<211> 1761

<212> DNA

<213> Human

<400> 229

```

atggigaata atttctccca agctgaggct gaggagctgt gttacaagaa cgtgaacgaa   60
tcttgatta aaactcctta ctgccaggt cctcgatcta tctctacgc cgtccttggt   120
tttggggctg tgctggcagc gtttggaac ttactggta tgattgctat ccttcacttc   180
aaacaactgc acacacctac aaactttctg attgcgtgc tggcctgtgc tgacttcttg   240
gtgggagtc cgtgatgcc cttcagcaca gtgaggtctg tggagagctg ttggtacttt   300
ggggacagtt actgtaaatt ccatacatgt tttagacacat ccttctgttt tgcttcttta   360
tttcatttat gctgtatctc tttgataga tacattgctg ttactgatcc tctgacctat   420
ccaaccaagt ttactgtgtc agtttcaggg atatgcattg ttctttcctg gttcttttct   480
gtcacataca gcttttcgat cttttacacg ggagccaacg aagaaggaat tgaggaatta   540
gtagttgctc taacctgtgt aggaggctgc caggctccac tgaatcaaaa ctgggtccta   600
ctttgttttc ttctattctt tatacccaat gtgcctatgg tgtttatata cagtaagata   660
tttttggtgg ccaagcatca ggctaggaag atagaaagta cagccagcca agctcagtc   720
tctcagaga gttacaagga aagagtagca aaaagagaga gaaaggctgc caaaccttg   780
ggaattgcta tggcagcatt tcttgtctct tggctacat acctcgtga tgcagtgatt   840
gatgcttata tgaattttat aactcctcct tatgtttatg agattttagt ttggttgttt   900
tattataatt cagctatgaa ccccttgatt tatgctttct ttaccaatg gtttgggaag   960
gcaataaaac ttattgtaag cggcaaggtc ttaaggactg attcgtcaac aactaattta  1020
ttttctgaag aagtagagac agatgctagc aaaggagaag aactcttcac tggagttgtc  1080
ccaattcttg ttgaattaga tgggatgtt aacggccaca agttctctgt cagtggagag  1140
ggtgaagggt atgcaacata cggaaaactt acctgaagt tcatctgcac tactggcaaa  1200
ctgctgttc catggccaac actagtcact actctgtgct atggtgttca atgcttttca  1260
agatacccg atcatatgaa acggcatgac ttttcaaga gtgcatgcc cgaaggttat  1320
gtacaggaaa ggaccatctt cttcaaagat gacggcaact acaagacacg tgctgaagtc  1380

```

511/518

aagtttgaag gigataccct tgtaataga atcgagttaa aaggtattga cttcaaggaa 1440
gatggcaaca ttctgggaca caaatggaa tacaactata actcacaaa tgtatacatc 1500
atggcagaca aacaaaagaa tggaatcaaa gtgaacttca agacccgcca caacattgaa 1560
gatggaagcg ttcaactagc agaccattat caacaaaata ctccaattgg cgaiggccct 1620
gtccttttac cagacaacca ttacctgtcc acacaatctg ccctttcgaa agatcccaac 1680
gaaaagagag accacatggt ccttcttgag ttgttaacag ctgctgggat tacacatggc 1740
atggatgaac tgtacaactg a 1761

<210> 230

<211> 5433

<212> DNA

<213> Human

<400> 230

atgaccccag ccgtgccct cttactgtct gtgattctgt ccctgcgcct ggccaccgcc 60
ttcgaccccg cccccagtgc ctgctctgcc ctggcctcgg gtgtgctcta cggggccttc 120
tcgcigcagg acctctttcc taccatcgcc tcgggctgct cctggacctt ggagaacctt 180
gacccacca agtactccct ctacctgccc ttcaaccgcc aggagcaggt gtgcgcacac 240
tttgccccc gcctgtgcc cctggaccac taccigtgca actttacctg cctgcgcctt 300
agccccgagg aggcggtggc ccaggcggag tcagaggtgg ggccggcaga agaggaggag 360
gcagaggcgg cagcggggtt ggagctgtgc agcggctcag gcccctttac cttcctgcac 420
ttcgacaaga acttcgtgca gctgtgccig tggctgagc cctccgaggc cccgcgcctg 480
ctggcgcccg ctgccctagc cticcgttt gtcgaggtct tgctcatcaa caacaacaac 540
tctagccaat tcacctgtgg tgtgctctgc cgctggagtg aggagtgtgg ccgcgtgcc 600
ggcagggcct gcggctttgc tcagccaggc tgcagctgcc ctggagaggc gggggccggc 660
tccaccacca ccacatctcc aggcctcct gctgcccaca cctgttcaa tgccttggtg 720
cccgggggcc cagccccacc tgcctaggcc gatttgcact cggggagcag caatgatctg 780
ttcacaaccg agatgagata tggtagggag ccggaagagg aaccgaaagt gaaaaccag 840
tgcccgaggt ctgcagatga gcctgggcta tacatggcgc agacaggcga cccggcggt 900

512/518

gaggagtggc ccccgctggag cgtgtgttcc ctgacgtgtg ggcagggctc gcaggcgcgg 960
 acccgctcct gtgtgtcctc cccctatggg accctgtgca gcggggccct gcgggagacc 1020
 aggccttgca acaattcagc cacctgcccc gtgcacggcg tgtgggagga gtgggggtcc 1080
 tggagcctgt gctcccgag ctgcgggcgg ggtccccga gccgatgag gacctgcgtg 1140
 cccccccagc acggcggcaa ggcttgcgag ggtcctgagc tgcagactaa gctctgcagt 1200
 atggctgcct gcccggtgga aggcacgtgg ttagaatggg gtccctgggg cccatgctcc 1260
 acgtcctgtg ccaatgggac ccaacagcgc agccggaagt gcagcgtggc gggcccagcc 1320
 tgggccacat gcacgggtgc cctcactgac acccgggagt gcagcaacct cgagtccccg 1380
 gccactgata gcaagtgggg gccatggaat gcgtggagcc tgtgtcttaa gacgtgtgac 1440
 acaggctggc agcgccgctt ccgcatgtgc caggccacgg gcacgcaggg ctacccctgc 1500
 gagggcacgg gagaggaggt gaagccttgt agtgaaga ggtgtccagc cttccatgag 1560
 atgtgcaggg atgagtacgt gatgtgatg acgtggaaga aggcagctgc tggcgagatc 1620
 atctacaaca agtcccccc gaatgcctca ggtcttgcca gccgccgtg cctcctcagt 1680
 gcccaaggcg tggcgtactg ggggctgccc agctttgctc gctgcatctc ccatgagtac 1740
 cgctacctgt atctgtcact tagggagcac ctggccaagg ggcagcgcat gctggcaggc 1800
 gagggcatgt cgcaggiggt gcgcagcctg caggagctac tggcccggcg cacctactat 1860
 agtggggacc tgccttctc tgtggacatt ctgaggaatg tcatgacac ctttaagagg 1920
 gccacctagc tgcctcggc tcatgatgtg cagcgcttct tccaggctgt gagcttcagt 1980
 gtggatgcgg aaaacaagga gaagtgggac gatgtcagc aggtgtcccc tggctctgtg 2040
 cacctgctcc gtgtcgtgga ggacttcatt cacctgggtg gcgatgtct caaggccttc 2100
 cagagctctc tgattgtcac agataatcta gtatcagca ttcagcgaga gccgtctca 2160
 gctgtgtcca gtgacatcac gttccccatg cggggccgcc ggggcatgaa ggactgggtg 2220
 cggcactcag aggaccgctt ctctctgccc aaggaggctg tcagcctctc ctcccaggg 2280
 aagccagcca catctggggc agcaggcagc cctggcaggg ggagggggcc aggaacggtg 2340
 cctcctggcc caggccactc ccaccagcgc ctctcccag cagacctga tgagtctcc 2400
 tactttgtga tcgggtgtgt actctaccgc accctggcc tcatcctgcc gcctcccagg 2460
 cccccgtgg ccgtcacatc ccgggtgatg acagtactg tgcgcccccc taccagcct 2520
 ccagctgagc cctcatcac tgtggagctc tcctacatca tcaatgggac cacgatccc 2580
 catgtcgcca gctgggacta ctccagagca gatgccagct caggagactg ggacactgaa 2640

513/518

aattgccaga ccctggagac ccaggcagct cacacccgct gccagtgcc a gcacctgtcc 2700
acctttgtct tactagccca gccgcccaag gacctgacct tggagctggc aggtcccccc 2760
tcggtcccc tggatcggt ctgtgcagtg tcgtgcatgg cgctgcttac cctgctcgcc 2820
atctatgccg ccttttggag gtccataaaa tctgaacgct ccatcatctt gctgaacttc 2880
tgccgtgcc tcttggcatc caacatcctg atcctcgtgg gccagtcgcc ggtgctgagc 2940
aagggcggtg gcacatgac ggctgccttc ctgcacttct tctttctctc ctcccttttg 3000
tgggtgctta ccgaggcctg gcagtcctac ctggctgtca ttgggcggat gcgcacccgc 3060
ctcgctcgca agcgcttctt ctgcctgggc tggggtctgc ctgccctggg ggtggccgtg 3120
tctgttggct ttaccggaac gaaaggatac ggtacatcca gctactgtg gctctccctg 3180
gagggcggtc tgcctacgc ctttgtgggc cctgcagccg tcatgtctt ggtgaacatg 3240
ctcatcgga tcatgtctt caacaagctc atggcacgtg atggcatctc cgacaaatcc 3300
aagaagcaga gggccgggtc ggagcggtgc ccttgggcca gctgctctt cccctgtca 3360
gcgtgtggag cggtcgccag cccctgtctc agctcagctt cggccaggaa cgcatggcc 3420
tcactctgga gctcctgcgt ggtgctgccc ctgctggcgc tcacctggat gctgcccgtc 3480
ctggctatga cagaccgccg ttccgtctc ttccaggccc tctttgtgt cttcaactcc 3540
gcgcagggct ttgtcatcac tgcgtgcac tgcctcctgc gccgagaggt ccagatgtg 3600
gtgaagtgcc agatgggggt gtgccgggt gatgagagcg aagactcccc tgactcgtgt 3660
aagaacgggc agctgcagat cctgtcagac ttgtaaaagg atgtggatct ggcttgtcaa 3720
acagtgtgt tcaaggaggt caacacttg aaccgtcca ccatcacggg cacactatcc 3780
cgctgtccc tggatgagga tggagagccc aagtcctgcc tcgtgggccc tgagggcagc 3840
ctcagcttct caccactgcc tgggaatac ctggtgccc tggcagctc accagggtg 3900
ggggagcctc cgccccaca ggaggccaac cctgtttaca tgtgtgggga ggggtggcctg 3960
cggcagctgg acctacatg gctgcggccc actgagccag gctctgagg agactacatg 4020
gtgctgcccc ggccgacttt gagcctgcag cctggcggtg ggggtggagg tggtaggat 4080
gccccaggg cccggccgga ggggaccccc cggcgagctg ccaagacagt ggcccacact 4140
gaaggctacc ccagcttct gtccgtggac cactcgggcc tggggctggg ccttgcctat 4200
ggatctctcc agaattcccta tggatgacc ttccaaccgc caccgccgac acccagcgcc 4260
cgccaagtgc ccgagccagg ggagcgagc cggaccaatg ctgcaccgt gcccggtct 4320
accatgaaga tgggtctcct ggagcgaag aaattacggt attcagacct ggactttgag 4380

514/518

gtgatgcaca cccggaaacg gcattcagaa ctctaccacg agctcaacca gaagtccac 4440
 actttcgacc gctaccgcag ccagtcacag gccaaagagg agaagcggtg gagtggtcc 4500
 tcgggtgggg cggccgagcg gagcgtgtgc accgataagc ccagccctgg ggagcgcccc 4560
 agcttgctcc aacatcggcg ccatcagagc tggagcacct tcaaattctat gacacigggc 4620
 tcgctgcccc ccaagccccg agaacggctg actctgcacc gggcagcagc ctgggagccc 4680
 acagaaccac cggatgggta ctccagaca gaggtggcta gcaaaggaga agaactcttc 4740
 actggagttg tccaattct tgttgaatta gatggtgatg ttaacggcca caagtctct 4800
 gtcagtggag aggggtgaagg tgatgcaaca tacggaaaac ttacctgaa gttcatctgc 4860
 actactggca aactgcctgt tccatggcca acactagta ctactctgtg ctatggtgtt 4920
 caatgctttt caagataccc ggatcataatg aaacggcatg acttttcaa gaggccatg 4980
 cccgaaggtt atgtacagga aaggaccatc ttcttcaaag atgacggcaa ctacaagaca 5040
 cgtgctgaag tcaagtttga aggtgatacc ctgtttaata gaatcgagtt aaaaggtatt 5100
 gacttcaagg aagatggcaa cattctggga cacaatttg aatacaacta taactcacac 5160
 aatgtatata tcatggcaga caaacaaaag aatggaatca aagtgaactt caagaccgc 5220
 cacaacattg aagatggaag cgttcaacta gcagaccatt atcaacaaaa tactccaatt 5280
 ggcatggcc ctgtcctttt accagacaac cattacctgt ccacacaatc tgccctttcg 5340
 aaagatccca acgaaaagag agaccacatg gtccttcttg agtttgaac agctgctggg 5400
 attacacatg gcatggatga actgtacaac tga 5433

<210> 231

<211> 1692

<212> DNA

<213> Human

<400> 231

atggatgggt caaacgtgac atcatttggt gttgaggaac ccacgaacat ctcaactggc 60
 aggaacgcct cagtcgggaa tgcacatcgg caaatcccca tcgtgcactg ggtcattatg 120
 agcatctccc cagtggggtt tgttgagaat gggattctcc tctggttcct gtgcttccgg 180
 atgagaagaa atcccttcac tgtctacatc acccactgt ctatcgaga catctcactg 240

515/518

```

ctctctgta tttcatctt gtctatcgac tatgctttag attatgagct ttcttciggc 300
cattactaca caattgtcac attatcagtg acitttctgt ttggctacaa cacgggcctc 360
tatctgctga cggccattag tgtggagagg tgccgtgcag tccittaccc catctggtag 420
cgatgccatc gcccgaagta ccagtcggca ttggctctgt cccttctgtg ggctctttct 480
tgcttggtag ccacatgga gtatgtcatg tgcacgcaca gagaagaaga gagtcactct 540
cggaatgact gccgagcagt catcatcttt atagccatcc tgagcttccct ggtcttcacg 600
ccccatgac tgggtgccag caccatcttg gtcgtgaaga tccggaagaa cacgtgggct 660
tccattccct ccaagcttta catagtcac atggcacca tcattatatt cctcatcttc 720
gctatgcccc tgagactcct ttacctgctg tactatgagt attggctgcac ctttgggaac 780
ctacaccaca ttccctgct cttctccaca atcaacagta gcgccaaccc tticatttac 840
ttctttgtgg gaagcagtaa gaagaagaga ttcaaggagt ccttaaaagt tgttctgacc 900
agggctttca aagatgaaat gcaacctcgg cgccagaaag acaattgtaa tacggtcaca 960
gttgagactg tcgtcgctag caaaggagaa gaactcttca ctggagtgt cccaattctt 1020
gttgaattag atggtagtgt taacggccac aagtctctg tcagtggaaga gggatgaagg 1080
gatgcaacat acggaaaact taccctgaag ttcatctgca ctactggcaa actgcctgtt 1140
ccatggccaa cactagtcac tactctgtgc tatgggtgtc aatgcctttc aagatacccg 1200
gatcatatga aacggcatga ctttttcaag agtgccatgc ccgaaggta tgtacaggaa 1260
aggaccatct tcttcaaaga tgacggcaac tacaagacac gtgctgaagt caagtttgaa 1320
ggatgataccc ttgttaatag aatcgagta aaaggtattg acttcaagga agatggcaac 1380
attctgggac acaaattgga atacaactat aactcacaca atgtatacat catggcagac 1440
aaacaaaaga atggaatcaa agtgaacttc aagaccgcc acaacattga agatggaagc 1500
gttcaactag cagaccatta tcaacaaaat actccaattg gcgatggccc tgcctttta 1560
ccagacaacc attacctgtc cacacaatct gccctttcga aagatcccaa cgaaaagaga 1620
gaccacatgg tccttcttga gtttgtaaca gctgctggga ttacacatgg catggatgaa 1680
ctgtacaact ga 1692

```

<210> 232

<211> 2124

<212> DNA

516/518

<213> Human

<400> 232

```

atgcagatgg ccgatgcagc cacgatagcc accatgaata aggcagcagg cggggacaag   60
ctagcagaac tcttcagtct ggtcccgac cttctggagg cggccaacac gagtggtaac  120
gcgtcgctgc agcttccgga ctgtggtgagg gagctggggc tggagtggcc ggacggcgcg  180
ccgccaggac atccccggg cagcggcggg gcagagagcg cggacacaga ggcccggtg  240
cggattctca tcagcgtggt gtactgggtg gtgtgcgcc tggggttggc gggcaacctg  300
ctggttctct acctgatgaa gagcatgcag ggctggcgca agtcctctat caacctcttc  360
gtaccaacc tggcgctgac ggactttcag ttgtgtctca cctgccctt ctggcggtg  420
gagaacgctc ttgacttcaa atggcccttc ggcaaggcca tgtgtaagat cgtgtccatg  480
gtgacgtcca tgaacatgta cgccagcgtg ttcttctca ctgccatgag tgtgacgcgc  540
taccattcgg tggcctcggc tctgaagagc caccggacc gaggacacgg ccggggcgac  600
tgctcgggcc ggagcctggg ggacagctgc tgcctctcgg ccaaggcgct gtgtgtgtg  660
atctgggctt tggccgcgt ggctcgtg cccagtcca tttctccac cacggtcaag  720
gtgatggcg aggagctgtg cctggtgctg ttcccgaca agttgctgg cgcgcacagg  780
cagttctggc tgggcctcta ccactcgcag aaggtgctgc tgggcttcgt gctgccgctg  840
ggcatcatta tcttgtgcta cctgtgtgtg gtgcgttca tcgccgaccg ccgcgcggcg  900
gggaccaaag gaggggccc ggtagccgga ggacggcca ccggagccag cggccggaga  960
ctgtcgaagg tcacaaatc agtgaccatc gttgtcctgt ccttcttct gtgttggctg 1020
cccaaccagg cgtcaccac ctggagcatc ctcatcaagt tcaacgggt gcccttcagc 1080
caggagtatt tcctgtgcca ggtatacgcg ttccctgtga gcgtgtgct agcgactcc 1140
aacagctgcc tcaacccgt cctctactgc ctgtgcgcc gcgagttccg caaggcgctc 1200
aagagcctgc tgtggcgcat cgcgtctct tcgatcaca gcatgcgcc cttaccgcc 1260
actaccaagc cggagcacga ggatcagggg ctgcaggccc cggcgccgcc ccacgggcc 1320
gcggagccgg acctgtctta ctaccacct ggctcgtg tctacagcg gggcgctac 1380
gacctgtgc ccagcagctc tgcctacact agcaaaggag aagaactct cactggagt 1440
gtcccaattc ttgtgaatt agatggtgat gttacggcc acaagttct tgtcagtga 1500
gagggtgaag gtgatgaac atacggaaa cttacctga agttcatct cactactggc 1560

```

517/518

```

aaactgcctg ttccatggcc aacactagtc actactctgt gctatgggtg tcaatgcctt 1620
tcaagatacc cggatcatat gaaacggcat gactttttca agagtgccat gcccgaaggt 1680
tatgtacagg aaaggacat cttcttcaaa gatgacggca actacaagac acgtgcigaa 1740
gtcaagttag aaggtagtac ccttgtaa ataatcgagt taaaaggtag tgacttcaag 1800
gaagatggca acattctggg acacaaattg gaatacaact ataactcaca caatgtatag 1860
atcatggcag acaaacaaaa gaatggaatc aaagtgaact tcaagaccgc ccacaacatt 1920
gaagatggaa gcgttcaact agcagacat tatcaacaaa atactccaat tggcgtatgg 1980
cctgtccttt taccagacaa ccattacctg tccacacaat ctgccctttc gaaagatccc 2040
aacgaaaaga gagaccacat ggtccttctt gagtttgtaa cagctgctgg gattacacat 2100
ggcatggatg aactgtacaa ctga 2124

```

<210> 233

<211> 2241

<212> DNA

<213> Human

<400> 233

```

atgacgtcca cctgcaccaa cagcacgcgc gagagtaaca gcagccacac gtgcatgccc 60
ctctccaaaa tggccatcag cctggcccac ggcatcatcc gctcaaccgt gctggttatc 120
ttctcgcgcg cctctttcgt cggcaacata gtcttgccgc tagtgttgca gcgcaagccg 180
cagctgctgc aggtgaccaa ccgttttacc tttaacctcc tcgtcaccga cctgctgcag 240
atttcgctcg tggccccctg ggtgggtggc acctcigtgc ctctcttcctg gcccctcaac 300
agccacttct gcacggccct ggttagcctc accacctgt tcgccttcgc cagcgtcaac 360
accattgtct tgggtgcagt ggtatgctac ttgtccatca tccacctct ctctaccgc 420
tccaagatga cccagcgccg cggttacctg ctctctatg gcacctggat tggggccatc 480
ctgcagagca ctctccact ctacggctgg ggccaggctg cctttgatga gcgcaatgct 540
ctctgctcca tgatctgggg ggccagcccc agctacacta ttctcagcgt ggtgtccttc 600
atcgtcattc cactgattgt catgattgcc tgctactccg tgggtgtctg tgcagcccgg 660
aggcagcatg ctctgctgta caatgtcaag agacacagct tggaaagtgc agtcaaggac 720

```

518/518

tggtgtggaga atgaggatga agagggagca gagaagaagg aggagttcca ggatgagagt	780
gagtttcgcc gccagcatga aggtgaggtc aaggccaagg agggcagaat ggaagccaag	840
gacggcagcc tgaaggccaa ggaaggaagc acggggacca gtgagagtag ttagaggcc	900
aggggcagcg aggaggtcag agagagcagc acggtggcca gcgacggcag catggagggt	960
aaggaaggca gcaccaaagt tgaggagaac agcatgaagg cagacaaggg tcgcacagag	1020
gtcaaccagt gcagcatga ctgggtgaa gatgacatgg agtttggtga agacgacatc	1080
aatttcagtg aggatgacgt cgaggcagtg aacatcccgg agagcctccc acccagtcgt	1140
cgtaacagca acagcaaccc tcctctgccc aggtgctacc agtgcaaagc tgctaaagtg	1200
atcttcatca tcattttctc ctatgtgcta tccctggggc cctactgctt ttagcagtc	1260
ctggccgtgt ggggtgatgt cgaaaccag gtacccagtg gggtgatcac cataatcatc	1320
tggtttttct tcctgcagtg ctgcatccac ccctatgtct atggctacat gcacaagacc	1380
attaagaagg aaatccagga catgctgaag aagtcttct gcaaggaaaa gccccgaaa	1440
gaagatagcc acccagacct gcccggaaca gagggtagga ctgaaggcaa gattgtccct	1500
tcctacgatt ctgctacitt tcctgctagc aaaggagaag aactcttcac tggagttgtc	1560
ccaattcttg ttgaattaga tggatgatgt aacggccaca agttctctgt cagtgagag	1620
ggtgaaggtg atgcaacata cggaaaactt accctgaagt tcctctgcac tactggcaaa	1680
ctgccgtgtc catggccaac actagtcact actctgtgct atgggtgttca atgcttttca	1740
agataccggg atcatatgaa acggcatgac tttttcaaga gtgcatgcc cgaaggttat	1800
gtacaggaaa ggaccatctt cttcaaagat gacggcaact acaagacacg tgctgaagtc	1860
aagtttgaag gtgataccct tgttaataga atcgagttaa aaggtattga cttcaaggaa	1920
gatggcaaca ttctgggaca caaattggaa tacaactata actcacacaa tgtatacatc	1980
atggcagaca aacaaaagaa tggaatcaaa gtgaacttca agaccgcca caqattgaa	2040
gatggaagcg ttcaactagc agaccattat caacaaaata ctccaattgg cgatggccct	2100
gtcctttttac cagacaacca ttacctgtcc acacaatctg ccttttcgaa agatcccaac	2160
gaaaagagag accacatggg cttctttgag ttgttaacag ctgctgggat tacacatggc	2220
atggatgaac tgtacaactg a	2241

INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP03/01901

A. CLASSIFICATION OF SUBJECT MATTER
Int.Cl⁷ G01N33/50, G01N33/15, C12N15/09

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
Int.Cl⁷ G01N33/50, G01N33/15, C12N15/09

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched
Jitsuyo Shinan Koho 1922-1996 Toroku Jitsuyo Shinan Koho 1994-2003
Kokai Jitsuyo Shinan Koho 1971-2003 Jitsuyo Shinan Toroku Koho 1996-2003

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 00/49416 A (UNIVERSITY COURT OF THE UNIVERSITY OF GLASGOW),	1-6, 11, 12, 22-28
Y	24 August, 2000 (24.08.00), & AU 200026797 A & NO 200103997 A & CN 1372642 A & JP 2002-541439 A	7-10, 13-21
Y	Mercuty™ Pathway Profiling System User Manual, CLONTECH, 02 March, 2001 (02.03.01), pages 1 to 27	7-10, 13-21
Y	Bo-yeon KIM, Involvement of SH2-SH2-SH3 domain of phospholipase Cyl in NF-κB signaling, FEBS Letters, vol.472, pages 45 to 49, 2000	7-10, 13-21

☐ Further documents are listed in the continuation of Box C.

☐ See patent family annex.

* Special categories of cited documents: "A" document defining the general state of the art which is not considered to be of particular relevance "E" earlier document but published on or after the international filing date "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) "O" document referring to an oral disclosure, use, exhibition or other means "P" document published prior to the international filing date but later than the priority date claimed	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art "&" document member of the same patent family
---	--

Date of the actual completion of the international search
23 April, 2003 (23.04.03)

Date of mailing of the international search report
13 May, 2003 (13.05.03)

Name and mailing address of the ISA/
Japanese Patent Office

Authorized officer

Facsimile No.

Telephone No.

A. 発明の属する分野の分類 (国際特許分類 (IPC))

Int. Cl.⁷ G01N 33/50 G01N 33/15 C12N 15/09

B. 調査を行った分野

調査を行った最小限資料 (国際特許分類 (IPC))

Int. Cl.⁷ G01N 33/50 G01N 33/15 C12N 15/09

最小限資料以外の資料で調査を行った分野に含まれるもの

日本国実用新案公報 1922-1996年
 日本国公開実用新案公報 1971-2003年
 日本国登録実用新案公報 1994-2003年
 日本国実用新案登録公報 1996-2003年

国際調査で使用した電子データベース (データベースの名称、調査に使用した用語)

C. 関連すると認められる文献

引用文献の カテゴリー*	引用文献名 及び一部の箇所が関連するときは、その関連する箇所の表示	関連する 請求の範囲の番号
X	WO 00/49416 A (UNIVERSITY COURT OF THE UNIVERSITY OF GLASGOW) 2000.08.24	1-6, 11, 12, 22-28
Y	& AU 200026797 A & NO 200103997 A & CN 1372642 A & JP 2002-541439 A	7-10, 13-21
Y	Mercuty™ Pathway Profiling System User Manual, CLONTECH, 2001.03.02, p.1-27	7-10, 13-21

☒ C欄の続きにも文献が列挙されている。☐ パテントファミリーに関する別紙を参照。

* 引用文献のカテゴリー

「A」 特に関連のある文献ではなく、一般的技術水準を示すもの
 「E」 国際出願日前の出願または特許であるが、国際出願日以後に公表されたもの
 「L」 優先権主張に疑義を提起する文献又は他の文献の発行日若しくは他の特別な理由を確立するために引用する文献 (理由を付す)
 「O」 口頭による開示、使用、展示等に言及する文献
 「P」 国際出願日前で、かつ優先権の主張の基礎となる出願

の日の後に公表された文献

「T」 国際出願日又は優先日後に公表された文献であって出願と矛盾するものではなく、発明の原理又は理論の理解のために引用するもの
 「X」 特に関連のある文献であって、当該文献のみで発明の新規性又は進歩性がないと考えられるもの
 「Y」 特に関連のある文献であって、当該文献と他の1以上の文献との、当業者にとって自明である組合せによって進歩性がないと考えられるもの
 「&」 同一パテントファミリー文献

国際調査を完了した日

23.04.03

国際調査報告の発送日

13.05.03

国際調査機関の名称及びあて先

日本国特許庁 (ISA/JP)
 郵便番号100-8915
 東京都千代田区霞が関三丁目4番3号

特許庁審査官 (権限のある職員)

宮澤 浩



2J 9407

電話番号 03-3581-1101 内線 3251

C (続き) . 関連すると認められる文献		
引用文献の カテゴリー*	引用文献名 及び一部の箇所が関連するときは、その関連する箇所の表示	関連する 請求の範囲の番号
Y	Bo-yeon KIM, Involvement of SH2-SH2-SH3 domain of phospholipase C γ 1 in NF- κ B signaling, FEBS Letters, vol. 472, p. 45-49, 2000	7-10, 13-21

**This Page is Inserted by IFW Indexing and Scanning
Operations and is not part of the Official Record**

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

- ☐ BLACK BORDERS
- ☐ IMAGE CUT OFF AT TOP, BOTTOM OR SIDES
- ☐ FADED TEXT OR DRAWING
- ☐ BLURRED OR ILLEGIBLE TEXT OR DRAWING
- ☐ SKEWED/SLANTED IMAGES
- ☒ COLOR OR BLACK AND WHITE PHOTOGRAPHS
- ☐ GRAY SCALE DOCUMENTS
- ☒ LINES OR MARKS ON ORIGINAL DOCUMENT
- ☐ REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY
- ☐ OTHER: _____

IMAGES ARE BEST AVAILABLE COPY.

As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.

THIS PAGE BLANK (USPTO)